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(21) International Application Number: PCT/IB98/02122 (22) International Filing Date: 17 December 1998 (17.12.98) (30) Priority Data: <table border="0"><tr><td>60/069,957</td><td>17 December 1997 (17.12.97)</td><td>US</td></tr><tr><td>60/074,121</td><td>9 February 1998 (09.02.98)</td><td>US</td></tr><tr><td>60/081,563</td><td>13 April 1998 (13.04.98)</td><td>US</td></tr><tr><td>60/096,116</td><td>10 August 1998 (10.08.98)</td><td>US</td></tr></table> (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): BOUGUELERET, Lydie [FR/FR]; 108, avenue Victor Hugo, F-92170 Vanves (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire de Tours, F-75006 Paris (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		60/069,957	17 December 1997 (17.12.97)	US	60/074,121	9 February 1998 (09.02.98)	US	60/081,563	13 April 1998 (13.04.98)	US	60/096,116	10 August 1998 (10.08.98)	US	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
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(54) Title: EXTENDED cDNAs FOR SECRETED PROTEINS (57) Abstract <p>The sequences of extended cDNAs encoding secreted proteins are disclosed. The extended cDNAs can be used to express secreted proteins or portions thereof or to obtain antibodies capable of specifically binding to the secreted proteins. The extended cDNAs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. The extended cDNAs may also be used to design expression vectors and secretion vectors.</p>														

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EXTENDED cDNAs for secreted proteins

The present application relates to extended cDNAs which were disclosed in several United States Provisional Patent Applications. Table I lists the SEQ ID Nos. of the extended cDNAs in the present application, the SEQ ID Nos. of the identical or nearly identical extended cDNAs in the provisional applications, and the identities of the provisional applications in which the extended cDNAs were disclosed.

Background of the Invention

The estimated 50,000-100,000 genes scattered along the human chromosomes offer tremendous promise for the understanding, diagnosis, and treatment of human diseases. In addition, probes capable of specifically hybridizing to loci distributed throughout the human genome find applications in the construction of high resolution chromosome maps and in the identification of individuals.

In the past, the characterization of even a single human gene was a painstaking process, requiring years of effort. Recent developments in the areas of cloning vectors, DNA sequencing, and computer technology have merged to greatly accelerate the rate at which human genes can be isolated, sequenced, mapped, and characterized. Cloning vectors such as yeast artificial chromosomes (YACs) and bacterial artificial chromosomes (BACs) are able to accept DNA inserts ranging from 300 to 1000 kilobases (kb) or 100-400 kb in length respectively, thereby facilitating the manipulation and ordering of DNA sequences distributed over great distances on the human chromosomes. Automated DNA sequencing machines permit the rapid sequencing of human genes. Bioinformatics software enables the comparison of nucleic acid and protein sequences, thereby assisting in the characterization of human gene products.

Currently, two different approaches are being pursued for identifying and characterizing the genes distributed along the human genome. In one approach, large fragments of genomic DNA are isolated, cloned, and sequenced. Potential open reading frames in these genomic sequences are identified using bio-informatics software. However, this approach entails sequencing large stretches of human DNA which do not encode proteins in order to find the protein encoding sequences scattered throughout the genome. In addition to requiring extensive sequencing, the bio-informatics software may mischaracterize the genomic sequences obtained. Thus, the software may produce false positives in which non-coding DNA is mischaracterized as coding DNA or false negatives in which coding DNA is mislabeled as non-coding DNA.

An alternative approach takes a more direct route to identifying and characterizing human genes. In this approach, complementary DNAs (cDNAs) are synthesized from isolated messenger RNAs (mRNAs) which encode human proteins. Using this approach, sequencing is only performed on DNA which is derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to isolate or purify extended cDNAs which include sequences adjacent to the EST sequences. The extended cDNAs may contain all of the sequence of the EST which was used to obtain them or only a portion of the sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include

portions of the coding sequence of the gene from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters.

In the past, the short EST sequences which could be used to isolate or purify extended cDNAs were often
5 obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3' untranslated region of the mRNA. In part, the prevalence of EST sequences derived from the 3' end of the mRNA is a result of the fact that typical techniques for obtaining cDNAs, are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs. (Adams et al., *Nature* 377:174, 1996, Hillier et al., *Genome Res.* 6:807-828, 1996).

In addition, in those reported instances where longer cDNA sequences have been obtained, the reported
10 sequences typically correspond to coding sequences and do not include the full 5' untranslated region of the mRNA from which the cDNA is derived. Such incomplete sequences may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences derived from the 5' ends of mRNAs which can be used to obtain extended cDNAs which may include the 5' sequences contained in the 5' ESTs.

15 While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. Of the 50,000-100,000 protein coding genes, those genes encoding proteins which are secreted from the cell in which they are synthesized, as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often involved in cell to cell communication and
20 may be responsible for producing a clinically relevant response in their target cells.

In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon- α , interferon- β , interferon- γ , and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy induced neutropenia and
25 multiple sclerosis. For these reasons, extended cDNAs encoding secreted proteins or portions thereof represent a particularly valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are encoded by the signal sequences
30 located at the 5' ends of the coding sequences of genes encoding secreted proteins. Because these signal peptides will direct the extracellular secretion of any protein to which they are operably linked, the signal sequences may be exploited to direct the efficient secretion of any protein by operably linking the signal sequences to a gene encoding the protein for which secretion is desired. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cell in which it is produced. Signal sequences encoding signal peptides

also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5' portions of the genes for secretory proteins which encode signal peptides.

- 5 Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross, S.H. et al.,
10 Purification of CpG Islands using a Methylated DNA Binding Column, *Nature Genetics* 6: 236-244 (1994)). The second consists of isolating human genomic DNA sequences containing *SpeI* binding sites by the use of *SpeI* binding protein. (Mortlock et al., *Genome Res.* 6:327-335, 1996). Both of these approaches have their limits due to a lack of specificity or of comprehensiveness.

- 5' ESTs and extended cDNAs obtainable therefrom may be used to efficiently identify and isolate upstream
15 regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. (Theil et al., *BioFactors* 4:87-93, (1993). Once identified and characterized, these regulatory regions may be utilized in gene therapy or protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

- In addition, ESTs containing the 5' ends of secretory protein genes or extended cDNAs which include
20 sequences adjacent to the sequences of the ESTs may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5' coding sequences of genes encoding secretory proteins.

Summary of the Invention

- The present invention relates to purified, isolated, or recombinant extended cDNAs which encode secreted
25 proteins or fragments thereof. Preferably, the purified, isolated or recombinant cDNAs contain the entire open reading frame of their corresponding mRNAs, including a start codon and a stop codon. For example, the extended cDNAs may include nucleic acids encoding the signal peptide as well as the mature protein. Alternatively, the extended cDNAs may contain a fragment of the open reading frame. In some embodiments, the fragment may encode only the sequence of the mature protein. Alternatively, the fragment may encode only a portion of the mature protein. A further aspect of the
30 present invention is a nucleic acid which encodes the signal peptide of a secreted protein.

The present extended cDNAs were obtained using ESTs which include sequences derived from the authentic 5' ends of their corresponding mRNAs. As used herein the terms "EST" or "5' EST" refer to the short cDNAs which were used to obtain the extended cDNAs of the present invention. As used herein, the term "extended cDNA" refers to the cDNAs which include sequences adjacent to the 5' EST used to obtain them. The extended cDNAs may contain all or a

portion of the sequence of the EST which was used to obtain them. The term "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5' EST. As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual extended cDNA clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The extended cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus, creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately 10^4 - 10^6 fold purification of the native message. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the extended cDNA is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the extended cDNAs will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched extended cDNAs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More preferably, the enriched extended cDNAs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched extended cDNAs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. "Stringent", "moderate," and "low" hybridization conditions are as defined in Example 29.

Unless otherwise indicated, a "complementary" sequence is fully complementary. Thus, extended cDNAs encoding secreted polypeptides or fragments thereof which are present in cDNA libraries in which one or more extended cDNAs encoding secreted polypeptides or fragments thereof make up 5% or more of the number of nucleic acid inserts in the backbone molecules are "enriched recombinant extended cDNAs" as defined herein. Likewise, extended cDNAs encoding secreted polypeptides or fragments thereof which are in a population of plasmids in which one or more extended cDNAs of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are "enriched recombinant extended cDNAs" as defined herein. However, extended

cDNAs encoding secreted polypeptides or fragments thereof which are in cDNA libraries in which the extended cDNAs encoding secreted polypeptides or fragments thereof constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in which backbone molecules having a cDNA insert encoding a secreted polypeptide are extremely rare, are not "enriched recombinant extended cDNAs."

5 In particular, the present invention relates to extended cDNAs which were derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are
10 transported across the membrane of the endoplasmic reticulum.

Extended cDNAs encoding secreted proteins may include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the extended cDNAs. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough" endoplasmic reticulum. Generally,
15 secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the
20 cell membrane.

The extended cDNAs of the present invention have several important applications. For example, they may be used to express the entire secreted protein which they encode. Alternatively, they may be used to express portions of the secreted protein. The portions may comprise the signal peptides encoded by the extended cDNAs or the mature proteins encoded by the extended cDNAs (i.e. the proteins generated when the signal peptide is cleaved off). The
25 portions may also comprise polypeptides having at least 10 consecutive amino acids encoded by the extended cDNAs. Alternatively, the portions may comprise at least 15 consecutive amino acids encoded by the extended cDNAs. In some embodiments, the portions may comprise at least 25 consecutive amino acids encoded by the extended cDNAs. In other embodiments, the portions may comprise at least 40 amino acids encoded by the extended cDNAs.

Antibodies which specifically recognize the entire secreted proteins encoded by the extended cDNAs or
30 fragments thereof having at least 10 consecutive amino acids, at least 15 consecutive amino acids, at least 25 consecutive amino acids, or at least 40 consecutive amino acids may also be obtained as described below. Antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the signal peptides encoded by the extended cDNAs may also be obtained.

In some embodiments, the extended cDNAs include the signal sequence. In other embodiments, the extended cDNAs may include the full coding sequence for the mature protein (i.e. the protein generated when the signal polypeptide is cleaved off). In addition, the extended cDNAs may include regulatory regions upstream of the translation start site or downstream of the stop codon which control the amount, location, or developmental stage of gene expression. As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating or controlling a variety of human conditions. The extended cDNAs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes mRNA which includes the sequence of one of the strands of the extended cDNA in which thymidine residues in the sequence of the extended cDNA are replaced by uracil residues in the mRNA.

The extended cDNAs or genomic DNAs obtained therefrom may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. In addition, the present invention is useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body. Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the extended cDNAs such as promoters or upstream regulatory sequences.

In addition, the present invention may also be used for gene therapy to control or treat genetic diseases. Signal peptides may also be fused to heterologous proteins to direct their extracellular secretion.

One embodiment of the present invention is a purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 40-140 and 242-377 or a sequence complementary thereto. In one aspect of this embodiment, the nucleic acid is recombinant.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 40-140 and 242-377 or one of the sequences complementary thereto. In one aspect of this embodiment, the nucleic acid comprises at least 15, 25, 30, 40, 50, 75, or 100 consecutive bases of one of the sequences of SEQ ID NOs: 40-140 and 242-377 or one of the sequences complementary thereto. The nucleic acid may be a recombinant nucleic acid.

Another embodiment of the present invention is a purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 40-140 and 242-377 or a sequence complementary to one of the sequences of SEQ ID NOs: 40-140 and 242-377. In one aspect of this embodiment, the nucleic acid is recombinant.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising the full coding sequences of one of SEQ ID NOs: 40-140 and 242-377, wherein the full coding sequence optionally comprises the sequence encoding signal peptide as well as the sequence encoding mature protein. In a preferred embodiment, the isolated or purified nucleic acid comprises the full coding sequence of one of SEQ ID Nos. 40, 42-44, 46, 48, 49, 51, 53, 5 60, 62-72, 76-78, 80-83, 85-88, 90, 93, 94, 97, 99-102, 104, 107-125, 127, 132, 135-138, 140 and 242-377 wherein the full coding sequence comprises the sequence encoding signal peptide and the sequence encoding mature protein. In one aspect of this embodiment, the nucleic acid is recombinant.

A further embodiment of the present invention is a purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 40-140 and 242-377 which encode a mature protein. In a preferred embodiment, the purified or 10 isolated nucleic acid comprises the nucleotides of one of SEQ ID NOs: 40-44, 46, 48, 49, 51-53, 55, 56, 58-72, 75-78, 80-88, 90, 93, 94, 97, 99-125, 127, 132, 133, 135-138, 140, and 242-377 which encode a mature protein. In one aspect of this embodiment, the nucleic acid is recombinant.

Yet another embodiment of the present invention is a purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 40-140 and 242-377 which encode the signal peptide. In a preferred embodiment, 15 the purified or isolated nucleic acid comprises the nucleotides of SEQ ID NOs: 40, 42-46, 48, 49, 51, 53, 57, 60, 62-73, 76-78, 80-83, 85-88, 90, 93-95, 97, 99-102, 104, 107-125, 127, 128, 130, 132, 134-140 and 242-377 which encode the signal peptide. In one aspect of this embodiment, the nucleic acid is recombinant.

Another embodiment of the present invention is a purified or isolated nucleic acid encoding a polypeptide having the sequence of one of the sequences of SEQ ID NOs: 141-241 and 378-513.

20 Another embodiment of the present invention is a purified or isolated nucleic acid encoding a polypeptide having the sequence of a mature protein included in one of the sequences of SEQ ID NOs: 141-241 and 378-513. In a preferred embodiment, the purified or isolated nucleic acid encodes a polypeptide having the sequence of a mature protein included in one of the sequences of SEQ ID NOs: 141-145, 147, 149, 150, 152-154, 156, 157, 159-172, 176-179, 181-189, 191, 194, 195, 198, 200-226, 228, 233, 234, 236-239, 241 and 378-513.

25 Another embodiment of the present invention is a purified or isolated nucleic acid encoding a polypeptide having the sequence of a signal peptide included in one of the sequences of SEQ ID NOs: 141-241 and 378-513. In a preferred embodiment, the purified or isolated nucleic acid encodes a polypeptide having the sequence of a signal peptide included in one of the sequences of SEQ ID NOs: 141, 143-147, 149, 150, 152, 154, 158, 161, 163-174, 177-179, 181-184, 186-189, 191, 194-196, 198, 200-203, 205, 208-226, 228, 229, 231, 233, 235-241, and 378-513.

30 Yet another embodiment of the present invention is a purified or isolated protein comprising the sequence of one of SEQ ID NOs: 141-241 and 378-513.

Another embodiment of the present invention is a purified or isolated polypeptide comprising at least 10 consecutive amino acids of one of the sequences of SEQ ID NOs: 141-241 and 378-513. In one aspect of this embodiment, the purified or isolated polypeptide comprises at least 15, 20, 25, 35, 50, 75, 100, 150 or 200 consecutive

amino acids of one of the sequences of SEQ ID NOs: 141-241 and 378-513. In still another aspect, the purified or isolated polypeptide comprises at least 25 consecutive amino acids of one of the sequences of SEQ ID NOs: 141-241 and 378-513.

Another embodiment of the present invention is an isolated or purified polypeptide comprising a signal peptide
5 of one of the polypeptides of SEQ ID NOs: 141-241 and 378-513. In a preferred embodiment, the isolated or purified polypeptide comprises a signal peptide of one of the polypeptides of SEQ ID NOs: 141, 143-147, 149, 150, 152, 154, 158, 161, 163-174, 177-179, 181-184, 186-189, 191, 194-196, 198, 200-203, 205, 208-226, 228, 229, 231, 233, 235-241, and 378-513.

Yet another embodiment of the present invention is an isolated or purified polypeptide comprising a mature
10 protein of one of the polypeptides of SEQ ID NOs: 141-241 and 378-513. In a preferred embodiment, the isolated or purified polypeptide comprises a mature protein of one of the polypeptides of SEQ ID NOs: 141-145, 147, 149, 150, 152-154, 156, 157, 159-172, 176-179, 181-189, 191, 194, 195, 198, 200-226, 228, 233, 234, 236-239, 241 and 378-513.

A further embodiment of the present invention is a method of making a protein comprising one of the
15 sequences of SEQ ID NO: 141-241 and 378-513, comprising the steps of obtaining a cDNA comprising one of the sequences of sequence of SEQ ID NO: 40-140 and 242-377, inserting the cDNA in an expression vector such that the cDNA is operably linked to a promoter, and introducing the expression vector into a host cell whereby the host cell produces the protein encoded by said cDNA. In one aspect of this embodiment, the method further comprises the step of isolating the protein.

20 Another embodiment of the present invention is a protein obtainable by the method described in the preceding paragraph.

Another embodiment of the present invention is a method of making a protein comprising the amino acid sequence of the mature protein contained in one of the sequences of SEQ ID NO: 141-241 and 378-513, comprising the steps of obtaining a cDNA comprising one of the nucleotides sequence of sequence of SEQ ID NO: 40-140 and 242-377
25 which encode for the mature protein, inserting the cDNA in an expression vector such that the cDNA is operably linked to a promoter, and introducing the expression vector into a host cell whereby the host cell produces the mature protein encoded by the cDNA. In one aspect of this embodiment, the method further comprises the step of isolating the protein.

Another embodiment of the present invention is a mature protein obtainable by the method described in the
30 preceding paragraph.

In a preferred embodiment, the above method comprises a method of making a protein comprising the amino acid sequence of the mature protein contained in one of the sequences of SEQ ID NO: 141-145, 147, 149, 150, 152-154, 156, 157, 159-172, 176-179, 181-189, 191, 194, 195, 198, 200-226, 228, 233, 234, 236-239, 241 and 378-513, comprising the steps of obtaining a cDNA comprising one of the nucleotides sequence of sequence of SEQ ID NO:

40-44, 46, 48, 49, 51-53, 55, 56, 58-72, 75-78, 80-88, 90, 93, 94, 97, 99-125, 127, 132, 133, 135-138, 140, and 242-377 which encode for the mature protein, inserting the cDNA in an expression vector such that the cDNA is operably linked to a promoter, and introducing the expression vector into a host cell whereby the host cell produces the mature protein encoded by the cDNA. In one aspect of this embodiment, the method further comprises the step of
5 isolating the protein.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids comprising the sequence of one of SEQ ID NOs: 40-140 and 242-377 or a sequence complementary thereto described herein.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids
10 comprising the full coding sequences of one of SEQ ID NOs: 40-140 and 242-377, wherein the full coding sequence comprises the sequence encoding signal peptide and the sequence encoding mature protein described herein.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids comprising the nucleotides of one of SEQ ID NOs: 40-140 and 242-377 which encode a mature protein which are described herein. Preferably, the host cell contains the purified or isolated nucleic acids comprising the nucleotides of
15 one of SEQ ID NOs: 40-44, 46, 48, 49, 51-53, 55, 56, 58-72, 75-78, 80-88, 90, 93, 94, 97, 99-125, 127, 132, 133, 135-138, 140, and 242-377 which encode a mature protein.

Another embodiment of the present invention is a host cell containing the purified or isolated nucleic acids comprising the nucleotides of one of SEQ ID NOs: 40-140 and 242-377 which encode the signal peptide which are described herein. Preferably, the host cell contains the purified or isolated nucleic acids comprising the nucleotides of
20 one of SEQ ID Nos.: 40, 42-46, 48, 49, 51, 53, 57, 60, 62-73, 76-78, 80-83, 85-88, 90, 93-95, 97, 99-102, 104, 107-125, 127, 128, 130, 132, 134-140 and 242-377 which encode the signal peptide.

Another embodiment of the present invention is a purified or isolated antibody capable of specifically binding to a protein having the sequence of one of SEQ ID NOs: 141-241 and 378-513. In one aspect of this embodiment, the antibody is capable of binding to a polypeptide comprising at least 10 consecutive amino acids of the sequence of one of
25 SEQ ID NOs: 141-241 and 378-513.

Another embodiment of the present invention is an array of cDNAs or fragments thereof of at least 15 nucleotides in length which includes at least one of the sequences of SEQ ID NOs: 40-140 and 242-377, or one of the sequences complementary to the sequences of SEQ ID NOs: 40-140 and 242-377, or a fragment thereof of at least 15 consecutive nucleotides. In one aspect of this embodiment, the array includes at least two of the sequences of SEQ ID
30 NOs: 40-140 and 242-377, the sequences complementary to the sequences of SEQ ID NOs: 40-140 and 242-377, or fragments thereof of at least 15 consecutive nucleotides. In another aspect of this embodiment, the array includes at least five of the sequences of SEQ ID NOs: 40-140 and 242-377, the sequences complementary to the sequences of SEQ ID NOs: 40-140 and 242-377, or fragments thereof of at least 15 consecutive nucleotides.

A further embodiment of the invention encompasses purified polynucleotides comprising an insert from a clone deposited in a deposit having an accession number selected from the group consisting of the accession numbers listed in Table VI or a fragment thereof comprising a contiguous span of at least 8, 10, 12, 15, 20, 25, 40, 60, 100, or 200 nucleotides of said insert. An additional embodiment of the invention encompasses purified polypeptides which

5 comprise, consist of, or consist essentially of an amino acid sequence encoded by the insert from a clone deposited in a deposit having an accession number selected from the group consisting of the accession numbers listed in Table VI, as well as polypeptides which comprise a fragment of said amino acid sequence consisting of a signal peptide, a mature protein, or a contiguous span of at least 5, 8, 10, 12, 15, 20, 25, 40, 60, 100, or 200 amino acids encoded by said insert.

10 An additional embodiment of the invention encompasses purified polypeptides which comprise a contiguous span of at least 5, 8, 10, 12, 15, 20, 25, 40, 60, 100, or 200 amino acids of SEQ ID NOs: 158, 174, 175, 196, 226, 231, 232, wherein said contiguous span comprises at least one of the amino acid positions which was not shown to be identical to a public sequence in any of Figures 11 to 15. Also encompassed by the invention are purified polynucleotides encoding said polypeptides.

Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they are derived.

Figure 2 is an analysis of the 43 amino terminal amino acids of all human SwissProt proteins to determine the

20 frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Figure 3 shows the distribution of von Heijne scores for 5' ESTs in each of the categories described herein and the probability that these 5' ESTs encode a signal peptide.

Figure 4 shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

25 Figure 5 shows the tissues from which the mRNAs corresponding to the 5' ESTs in each of the categories described herein were obtained.

Figure 6 illustrates a method for obtaining extended cDNAs.

Figure 7 is a map of pED6dpc2. pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SSt cDNAs are cloned between EcoRI and NotI. PED vectors are described in Kaufman et al.

30 (1991), NAR 19: 4485-4490.

Figure 8 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags.

Figure 9 describes the transcription factor binding sites present in each of these promoters.

Figure 10 is an alignment of the protein of SEQ ID NO: 217 with the human protein TFAR19 that may play a role in apoptosis (Genbank accession number AF014955, SEQ ID NO: 516).

Figure 11 is an alignment of the proteins of SEQ ID NOs: 174, 175 and 232 with a human secreted protein (Genseq accession number W36955, SEQ ID NO: 517).

5 Figure 12 is an alignment of the protein of SEQ ID NO: 231 with the human E25 protein (Genbank accession number AF038953, SEQ ID NO: 515).

Figure 13 is an alignment of the protein of SEQ ID NO: 196 with the human seventransmembrane protein (Genbank accession number Y11395, SEQ ID NO: 518).

10 Figure 14 is an alignment of the protein of SEQ ID NOs: 158 with the murine subunit 7a of the COP9 complex (Genbank accession number AF071316, SEQ ID NO: 519).

Figure 15 is an alignment of the protein of SEQ ID NO: 226 with the bovine subunit B14.5B of the NADH-ubiquinone oxidoreductase complex (Arizmendi *et al*, *FEBS Lett.*, 313 : 80-84 (1992) and Swissprot accession number Q02827, SEQ ID NO: 514).

Detailed Description of the Preferred Embodiment

15 I. Obtaining 5' ESTs

The present extended cDNAs were obtained using 5' ESTs which were isolated as described below.

A. Chemical Methods for Obtaining mRNAs having Intact 5' Ends

In order to obtain the 5' ESTs used to obtain the extended cDNAs of the present invention, mRNAs having intact 5' ends must be obtained. Currently, there are two approaches for obtaining such mRNAs. One of these
20 approaches is a chemical modification method involving derivatization of the 5' ends of the mRNAs and selection of the derivatized mRNAs. The 5' ends of eucaryotic mRNAs possess a structure referred to as a "cap" which comprises a guanosine methylated at the 7 position. The cap is joined to the first transcribed base of the mRNA by a 5', 5'-triphosphate bond. In some instances, the 5' guanosine is methylated in both the 2 and 7 positions. Rarely, the 5' guanosine is trimethylated at the 2, 7 and 7 positions. In the chemical method for obtaining mRNAs having intact 5'
25 ends, the 5' cap is specifically derivatized and coupled to a reactive group on an immobilizing substrate. This specific derivatization is based on the fact that only the ribose linked to the methylated guanosine at the 5' end of the mRNA and the ribose linked to the base at the 3' terminus of the mRNA, possess 2', 3'-cis diols. Optionally, where the 3' terminal ribose has a 2', 3'-cis diol, the 2', 3'-cis diol at the 3' end may be chemically modified, substituted, converted, or eliminated, leaving only the ribose linked to the methylated guanosine at the 5' end of the mRNA with a 2', 3'-cis diol. A
30 variety of techniques are available for eliminating the 2', 3'-cis diol on the 3' terminal ribose. For example, controlled alkaline hydrolysis may be used to generate mRNA fragments in which the 3' terminal ribose is a 3'-phosphate, 2'-phosphate or (2', 3')-cyclophosphate. Thereafter, the fragment which includes the original 3' ribose may be eliminated from the mixture through chromatography on an oligo-dT column. Alternatively, a base which lacks the 2', 3'-cis diol

may be added to the 3' end of the mRNA using an RNA ligase such as T4 RNA ligase. Example 1 below describes a method for ligation of pCp to the 3' end of messenger RNA.

EXAMPLE 1

Ligation of the Nucleoside Diphosphate pCp to the 3' End of Messenger RNA

5 1 µg of RNA was incubated in a final reaction medium of 10 µl in the presence of 5 U of T₄ phage RNA ligase in the buffer provided by the manufacturer (Gibco - BRL), 40 U of the RNase inhibitor RNasin (Promega) and, 2 µl of ³²pCp (Amersham #PB 10208).

The incubation was performed at 37°C for 2 hours or overnight at 7-8°C.

Following modification or elimination of the 2', 3'-cis diol at the 3' ribose, the 2', 3'-cis diol present at the 5' end of the mRNA may be oxidized using reagents such as NaBH₄, NaBH₃CN, or sodium periodate, thereby converting the 2', 3'-cis diol to a dialdehyde. Example 2 describes the oxidation of the 2', 3'-cis diol at the 5' end of the mRNA with sodium periodate.

EXAMPLE 2

Oxidation of 2', 3'-cis diol at the 5' End of the mRNA

15 0.1 OD unit of either a capped oligoribonucleotide of 47 nucleotides (including the cap) or an uncapped oligoribonucleotide of 46 nucleotides were treated as follows. The oligoribonucleotides were produced by in vitro transcription using the transcription kit "AmpliScribe T7" (Epicentre Technologies). As indicated below, the DNA template for the RNA transcript contained a single cytosine. To synthesize the uncapped RNA, all four NTPs were included in the in vitro transcription reaction. To obtain the capped RNA, GTP was replaced by an analogue of the cap, 20 m7G(5')ppp(5')G. This compound, recognized by polymerase, was incorporated into the 5' end of the nascent transcript during the step of initiation of transcription but was not capable of incorporation during the extension step. Consequently, the resulting RNA contained a cap at its 5' end. The sequences of the oligoribonucleotides produced by the in vitro transcription reaction were:

+ Cap:

25 5'm7GpppGCAUCCUACUCCCAUCCAAUCCACCCUAACUCCUCCCAUCUCCAC-3' (SEQ ID NO:1)

-Cap:

5'-pppGCAUCCUACUCCCAUCCAAUCCACCCUAACUCCUCCCAUCUCCAC-3' (SEQ ID NO:2)

The oligoribonucleotides were dissolved in 9 µl of acetate buffer (0.1 M sodium acetate, pH 5.2) and 3 µl of freshly prepared 0.1 M sodium periodate solution. The mixture was incubated for 1 hour in the dark at 4°C or room 30 temperature. Thereafter, the reaction was stopped by adding 4 µl of 10% ethylene glycol. The product was ethanol precipitated, resuspended in 10 µl or more of water or appropriate buffer and dialyzed against water.

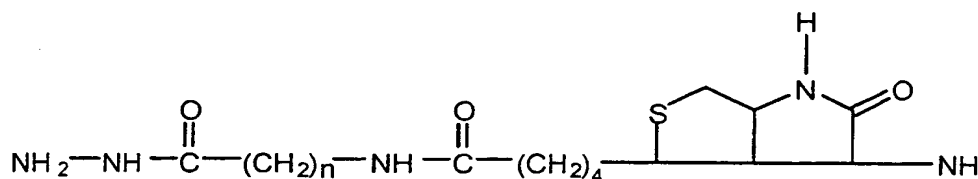
The resulting aldehyde groups may then be coupled to molecules having a reactive amine group, such as hydrazine, carbazide, thiocarbazide or semicarbazide groups, in order to facilitate enrichment of the 5' ends of the mRNAs. Molecules having reactive amine groups which are suitable for use in selecting mRNAs having intact 5' ends

include avidin, proteins, antibodies, vitamins, ligands capable of specifically binding to receptor molecules, or oligonucleotides. Example 3 below describes the coupling of the resulting dialdehyde to biotin.

EXAMPLE 3

Coupling of the Dialdehyde with Biotin

- 5 The oxidation product obtained in Example 2 was dissolved in 50 μ l of sodium acetate at a pH of between 5 and 5.2 and 50 μ l of freshly prepared 0.02 M solution of biotin hydrazide in a methoxyethanol/water mixture (1:1) of formula:



- 10 In the compound used in these experiments, $n=5$. However, it will be appreciated that other commercially available hydrazides may also be used, such as molecules of the formula above in which n varies from 0 to 5.

The mixture was then incubated for 2 hours at 37°C. Following the incubation, the mixture was precipitated with ethanol and dialyzed against distilled water.

Example 4 demonstrates the specificity of the biotinylation reaction.

15

EXAMPLE 4

Specificity of Biotinylation

The specificity of the biotinylation for capped mRNAs was evaluated by gel electrophoresis of the following samples:

- 20 Sample 1. The 46 nucleotide uncapped in vitro transcript prepared as in Example 2 and labeled with ^{32}pCp as described in Example 1.

Sample 2. The 46 nucleotide uncapped in vitro transcript prepared as in Example 2, labeled with ^{32}pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

- 25 Sample 3. The 47 nucleotide capped in vitro transcript prepared as in Example 2 and labeled with ^{32}pCp as described in Example 1.

Sample 4. The 47 nucleotide capped in vitro transcript prepared as in Example 2, labeled with ^{32}pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

- 30 Samples 1 and 2 had identical migration rates, demonstrating that the uncapped RNAs were not oxidized and biotinylated. Sample 3 migrated more slowly than Samples 1 and 2, while Sample 4 exhibited the slowest migration.

The difference in migration of the RNAs in Samples 3 and 4 demonstrates that the capped RNAs were specifically biotinylated.

In some cases, mRNAs having intact 5' ends may be enriched by binding the molecule containing a reactive amine group to a suitable solid phase substrate such as the inside of the vessel containing the mRNAs, magnetic beads, chromatography matrices, or nylon or nitrocellulose membranes. For example, where the molecule having a reactive amine group is biotin, the solid phase substrate may be coupled to avidin or streptavidin. Alternatively, where the molecule having the reactive amine group is an antibody or receptor ligand, the solid phase substrate may be coupled to the cognate antigen or receptor. Finally, where the molecule having a reactive amine group comprises an oligonucleotide, the solid phase substrate may comprise a complementary oligonucleotide.

10 The mRNAs having intact 5' ends may be released from the solid phase following the enrichment procedure. For example, where the dialdehyde is coupled to biotin hydrazide and the solid phase comprises streptavidin, the mRNAs may be released from the solid phase by simply heating to 95 degrees Celsius in 2% SDS. In some methods, the molecule having a reactive amine group may also be cleaved from the mRNAs having intact 5' ends following enrichment. Example 5 describes the capture of biotinylated mRNAs with streptavidin coated beads and the release of the
15 biotinylated mRNAs from the beads following enrichment.

EXAMPLE 5

Capture and Release of Biotinylated mRNAs Using Streptavidin Coated Beads

The streptavidin-coated magnetic beads were prepared according to the manufacturer's instructions (CPG Inc., USA). The biotinylated mRNAs were added to a hybridization buffer (1.5 M NaCl, pH 5 - 6). After incubating for 30
20 minutes, the unbound and nonbiotinylated material was removed. The beads were washed several times in water with 1% SDS. The beads obtained were incubated for 15 minutes at 95°C in water containing 2% SDS.

Example 6 demonstrates the efficiency with which biotinylated mRNAs were recovered from the streptavidin coated beads.

EXAMPLE 6

Efficiency of Recovery of Biotinylated mRNAs

25 The efficiency of the recovery procedure was evaluated as follows. RNAs were labeled with ³²pCp, oxidized, biotinylated and bound to streptavidin coated beads as described above. Subsequently, the bound RNAs were incubated for 5, 15 or 30 minutes at 95°C in the presence of 2% SDS.

The products of the reaction were analyzed by electrophoresis on 12% polyacrylamide gels under denaturing
30 conditions (7 M urea). The gels were subjected to autoradiography. During this manipulation, the hydrazone bonds were not reduced.

Increasing amounts of nucleic acids were recovered as incubation times in 2% SDS increased, demonstrating that biotinylated mRNAs were efficiently recovered.

In an alternative method for obtaining mRNAs having intact 5' ends, an oligonucleotide which has been derivatized to contain a reactive amine group is specifically coupled to mRNAs having an intact cap. Preferably, the 3' end of the mRNA is blocked prior to the step in which the aldehyde groups are joined to the derivatized oligonucleotide, as described above, so as to prevent the derivatized oligonucleotide from being joined to the 3' end of the mRNA. For example, pCp may be attached to the 3' end of the mRNA using T4 RNA ligase. However, as discussed above, blocking the 3' end of the mRNA is an optional step. Derivatized oligonucleotides may be prepared as described below in Example 7.

EXAMPLE 7

Derivatization of the Oligonucleotide

10 An oligonucleotide phosphorylated at its 3' end was converted to a 3' hydrazide in 3' by treatment with an aqueous solution of hydrazine or of dihydrazide of the formula $H_2N(R1)NH_2$ at about 1 to 3 M, and at pH 4.5, in the presence of a carbodiimide type agent soluble in water such as 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide at a final concentration of 0.3 M at a temperature of 8°C overnight.

The derivatized oligonucleotide was then separated from the other agents and products using a standard
15 technique for isolating oligonucleotides.

As discussed above, the mRNAs to be enriched may be treated to eliminate the 3' OH groups which may be present thereon. This may be accomplished by enzymatic ligation of sequences lacking a 3' OH, such as pCp, as described above in Example 1. Alternatively, the 3' OH groups may be eliminated by alkaline hydrolysis as described in Example 8 below.

20

EXAMPLE 8

Alkaline Hydrolysis of mRNA

The mRNAs may be treated with alkaline hydrolysis as follows. In a total volume of 100µl of 0.1N sodium hydroxide, 1.5µg mRNA is incubated for 40 to 60 minutes at 4°C. The solution is neutralized with acetic acid and precipitated with ethanol.

25

Following the optional elimination of the 3' OH groups, the diol groups at the 5' ends of the mRNAs are oxidized as described below in Example 9.

EXAMPLE 9

Oxidation of Diols

Up to 1 OD unit of RNA was dissolved in 9 µl of buffer (0.1 M sodium acetate, pH 6-7 or water) and 3 µl of
30 freshly prepared 0.1 M sodium periodate solution. The reaction was incubated for 1 h in the dark at 4°C or room temperature. Following the incubation, the reaction was stopped by adding 4 µl of 10% ethylene glycol. Thereafter the mixture was incubated at room temperature for 15 minutes. After ethanol precipitation, the product was resuspended in 10µl or more of water or appropriate buffer and dialyzed against water.

Following oxidation of the diol groups at the 5' ends of the mRNAs, the derivatized oligonucleotide was joined to the resulting aldehydes as described in Example 10.

EXAMPLE 10

Reaction of Aldehydes with Derivatized Oligonucleotides

5 The oxidized mRNA was dissolved in an acidic medium such as 50 μ l of sodium acetate pH 4-6. 50 μ l of a solution of the derivatized oligonucleotide was added such that an mRNA:derivatized oligonucleotide ratio of 1:20 was obtained and mixture was reduced with a borohydride. The mixture was allowed to incubate for 2 h at 37°C or overnight (14 h) at 10°C. The mixture was ethanol precipitated, resuspended in 10 μ l or more of water or appropriate buffer and dialyzed against distilled water. If desired, the resulting product may be analyzed using acrylamide gel
10 electrophoresis, HPLC analysis, or other conventional techniques.

Following the attachment of the derivatized oligonucleotide to the mRNAs, a reverse transcription reaction may be performed as described in Example 11 below.

EXAMPLE 11

Reverse Transcription of mRNAs

15 An oligodeoxyribonucleotide was derivatized as follows. 3 OD units of an oligodeoxyribonucleotide of sequence ATCAAGAATTCGCACGAGACCATTA (SEQ ID NO:3) having 5'-OH and 3'-P ends were dissolved in 70 μ l of a 1.5 M hydroxybenzotriazole solution, pH 5.3, prepared in dimethylformamide/water (75:25) containing 2 μ g of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide. The mixture was incubated for 2 h 30 min at 22°C. The mixture was then precipitated twice in LiClO₄/acetone. The pellet was resuspended in 200 μ l of 0.25 M hydrazine and incubated at 8°C
20 from 3 to 14 h. Following the hydrazine reaction, the mixture was precipitated twice in LiClO₄/acetone.

The messenger RNAs to be reverse transcribed were extracted from blocks of placenta having sides of 2 cm which had been stored at -80°C. The mRNA was extracted using conventional acidic phenol techniques. Oligo-dT chromatography was used to purify the mRNAs. The integrity of the mRNAs was checked by Northern-blotting.

The diol groups on 7 μ g of the placental mRNAs were oxidized as described above in Example 9. The
25 derivatized oligonucleotide was joined to the mRNAs as described in Example 10 above except that the precipitation step was replaced by an exclusion chromatography step to remove derivatized oligodeoxyribonucleotides which were not joined to mRNAs. Exclusion chromatography was performed as follows:

10 ml of AcA34 (BioSeptra#230151) gel were equilibrated in 50 ml of a solution of 10 mM Tris pH 8.0, 300 mM NaCl, 1 mM EDTA, and 0.05% SDS. The mixture was allowed to sediment. The supernatant was eliminated and
30 the gel was resuspended in 50 ml of buffer. This procedure was repeated 2 or 3 times.

A glass bead (diameter 3 mm) was introduced into a 2 ml disposable pipette (length 25 cm). The pipette was filled with the gel suspension until the height of the gel stabilized at 1 cm from the top of the pipette. The column was then equilibrated with 20 ml of equilibration buffer (10 mM Tris HCl pH 7.4, 20 mM NaCl).

10 μ l of the mRNA which had been reacted with the derivatized oligonucleotide were mixed in 39 μ l of 10 mM urea and 2 μ l of blue-glycerol buffer, which had been prepared by dissolving 5 mg of bromophenol blue in 60% glycerol (v/v), and passing the mixture through a filter with a filter of diameter 0.45 μ m.

The column was loaded. As soon as the sample had penetrated, equilibration buffer was added. 100 μ l
5 fractions were collected. Derivatized oligonucleotide which had not been attached to mRNA appeared in fraction 16 and later fractions. Fractions 3 to 15 were combined and precipitated with ethanol.

The mRNAs which had been reacted with the derivatized oligonucleotide were spotted on a nylon membrane and hybridized to a radioactive probe using conventional techniques. The radioactive probe used in these hybridizations was an oligodeoxyribonucleotide of sequence TAATGGTCTCGTGCGAATTCTTGAT (SEQ ID NO:4) which was
10 anticomplementary to the derivatized oligonucleotide and was labeled at its 5' end with 32 P. 1/10th of the mRNAs which had been reacted with the derivatized oligonucleotide was spotted in two spots on the membrane and the membrane was visualized by autoradiography after hybridization of the probe. A signal was observed, indicating that the derivatized oligonucleotide had been joined to the mRNA.

The remaining 9/10 of the mRNAs which had been reacted with the derivatized oligonucleotide was reverse
15 transcribed as follows. A reverse transcription reaction was carried out with reverse transcriptase following the manufacturer's instructions. To prime the reaction, 50 pmol of nonamers with random sequence were used.

A portion of the resulting cDNA was spotted on a positively charged nylon membrane using conventional methods. The cDNAs were spotted on the membrane after the cDNA:RNA heteroduplexes had been subjected to an alkaline hydrolysis in order to eliminate the RNAs. An oligonucleotide having a sequence identical to that of the derivatized
20 oligonucleotide was labeled at its 5' end with 32 P and hybridized to the cDNA blots using conventional techniques. Single-stranded cDNAs resulting from the reverse transcription reaction were spotted on the membrane. As controls, the blot contained 1 pmol, 100 fmol, 50 fmol, 10 fmol and 1 fmol respectively of a control oligodeoxyribonucleotide of sequence identical to that of the derivatized oligonucleotide. The signal observed in the spots containing the cDNA indicated that approximately 15 fmol of the derivatized oligonucleotide had been reverse transcribed.

25 These results demonstrate that the reverse transcription can be performed through the cap and, in particular, that reverse transcriptase crosses the 5'-P-P-P-5' bond of the cap of eukaryotic messenger RNAs.

The single stranded cDNAs obtained after the above first strand synthesis were used as template for PCR reactions. Two types of reactions were carried out. First, specific amplification of the mRNAs for the alpha globin, dehydrogenase, pp15 and elongation factor E4 were carried out using the following pairs of oligodeoxyribonucleotide
30 primers.

alpha-globin

GLO-S: CCG ACA AGA CCA ACG TCA AGG CCG C (SEQ ID NO:5)

GLO-As: TCA CCA GCA GGC AGT GGC TTA GGA G 3' (SEQ ID NO:6)

dehydrogenase

-18-

3 DH-S: AGT GAT TCC TGC TAC TTT GGA TGG C (SEQ ID NO:7)

3 DH-As: GCT TGG TCT TGT TCT GGA GTT TAG A (SEQ ID NO:8)

pp15

PP15-S: TCC AGA ATG GGA GAC AAG CCA ATT T (SEQ ID NO:9)

5 PP15-As: AGG GAG GAG GAA ACA GCG TGA GTC C (SEQ ID NO:10)

Elongation factor E4

EFA1-S: ATG GGA AAG GAA AAG ACT CAT ATC A (SEQ ID NO:11)

EF1A-As: AGC AGC AAC AAT CAG GAC AGC ACA G (SEQ ID NO:12)

10 Non specific amplifications were also carried out with the antisense (_As) oligodeoxyribonucleotides of the pairs described above and a primer chosen from the sequence of the derivatized oligodeoxyribonucleotide (ATCAAGAATTCGCACGAGACCATTA) (SEQ ID NO:13).

A 1.5% agarose gel containing the following samples corresponding to the PCR products of reverse transcription was stained with ethidium bromide. (1/20th of the products of reverse transcription were used for each PCR reaction).

15 Sample 1: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the presence of cDNA.

Sample 2: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the absence of added cDNA.

20 Sample 3: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the presence of cDNA.

Sample 4: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the absence of added cDNA.

Sample 5: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the presence of cDNA.

25 Sample 6: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the absence of added cDNA.

Sample 7: The products of a PCR reaction using the EIE4 primers of SEQ ID NOs 11 and 12 in the presence of added cDNA.

30 Sample 8: The products of a PCR reaction using the EIE4 primers of SEQ ID NOs 11 and 12 in the absence of added cDNA.

In Samples 1, 3, 5 and 7, a band of the size expected for the PCR product was observed, indicating the presence of the corresponding sequence in the cDNA population.

PCR reactions were also carried out with the antisense oligonucleotides of the globin and dehydrogenase primers (SEQ ID NOs 6 and 8) and an oligonucleotide whose sequence corresponds to that of the derivatized

oligonucleotide. The presence of PCR products of the expected size in the samples corresponding to samples 1 and 3 above indicated that the derivatized oligonucleotide had been incorporated.

The above examples summarize the chemical procedure for enriching mRNAs for those having intact 5' ends. Further detail regarding the chemical approaches for obtaining mRNAs having intact 5' ends are disclosed in

5 International Application No. WO96/34981, published November 7, 1996.

Strategies based on the above chemical modifications to the 5' cap structure may be utilized to generate cDNAs which have been selected to include the 5' ends of the mRNAs from which they are derived. In one version of such procedures, the 5' ends of the mRNAs are modified as described above. Thereafter, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5' end of the mRNA. Single stranded RNAs
10 are eliminated to obtain a population of cDNA/mRNA heteroduplexes in which the mRNA includes an intact 5' end. The resulting heteroduplexes may be captured on a solid phase coated with a molecule capable of interacting with the molecule used to derivatize the 5' end of the mRNA. Thereafter, the strands of the heteroduplexes are separated to recover single stranded first cDNA strands which include the 5' end of the mRNA. Second strand cDNA synthesis may then proceed using conventional techniques. For example, the procedures disclosed in WO 96/34981 or in Carninci, P. et
15 al. High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. *Genomics* 37:327-336 (1996) may be employed to select cDNAs which include the sequence derived from the 5' end of the coding sequence of the mRNA.

Following ligation of the oligonucleotide tag to the 5' cap of the mRNA, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5' end of the mRNA. Following elimination of the RNA component of the resulting heteroduplex using standard techniques, second strand cDNA synthesis is conducted with a
20 primer complementary to the oligonucleotide tag.

Figure 1 summarizes the above procedures for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they are derived.

B. Enzymatic Methods for Obtaining mRNAs having Intact 5' Ends

Other techniques for selecting cDNAs extending to the 5' end of the mRNA from which they are derived are
25 fully enzymatic. Some versions of these techniques are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EPO 625572 and Kato et al. Construction of a Human Full-Length cDNA Bank. *Gene* 150:243-250 (1994).

Briefly, in such approaches, isolated mRNA is treated with alkaline phosphatase to remove the phosphate
30 groups present on the 5' ends of uncapped incomplete mRNAs. Following this procedure, the cap present on full length mRNAs is enzymatically removed with a decapping enzyme such as T4 polynucleotide kinase or tobacco acid pyrophosphatase. An oligonucleotide, which may be either a DNA oligonucleotide or a DNA-RNA hybrid oligonucleotide having RNA at its 3' end, is then ligated to the phosphate present at the 5' end of the decapped mRNA using T4 RNA

ligase. The oligonucleotide may include a restriction site to facilitate cloning of the cDNAs following their synthesis. Example 12 below describes one enzymatic method based on the doctoral thesis of Dumas.

EXAMPLE 12

Enzymatic Approach for Obtaining 5' ESTs

5 Twenty micrograms of PolyA⁺ RNA were dephosphorylated using Calf Intestinal Phosphatase (Biolabs). After a phenol chloroform extraction, the cap structure of mRNA was hydrolysed using the Tobacco Acid Pyrophosphatase (purified as described by Shinshi et al., *Biochemistry* 15: 2185-2190, 1976) and a hemi 5'DNA/RNA-3' oligonucleotide having an unphosphorylated 5' end, a stretch of adenosine ribophosphate at the 3' end, and an EcoRI site near the 5' end was ligated to the 5'P ends of mRNA using the T4 RNA ligase (Biolabs). Oligonucleotides suitable for use in this
10 procedure are preferably 30-50 bases in length. Oligonucleotides having an unphosphorylated 5' end may be synthesized by adding a fluorochrome at the 5' end. The inclusion of a stretch of adenosine ribophosphates at the 3' end of the oligonucleotide increases ligation efficiency. It will be appreciated that the oligonucleotide may contain cloning sites other than EcoRI.

Following ligation of the oligonucleotide to the phosphate present at the 5' end of the decapped mRNA, first
15 and second strand cDNA synthesis may be carried out using conventional methods or those specified in EP0 625,572 and Kato et al. Construction of a Human Full-Length cDNA Bank. *Gene* 150:243-250 (1994), and Dumas Milne Edwards, *supra*. The resulting cDNA may then be ligated into vectors such as those disclosed in Kato et al. Construction of a Human Full-Length cDNA Bank. *Gene* 150:243-250 (1994) or other nucleic acid vectors known to those skilled in the art using techniques such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 2d Ed., Cold
20 Spring Harbor Laboratory Press, 1989.

II. Characterization of 5' ESTs

The above chemical and enzymatic approaches for enriching mRNAs having intact 5' ends were employed to obtain 5' ESTs. First, mRNAs were prepared as described in Example 13 below.

EXAMPLE 13

Preparation of mRNA

25 Total human RNAs or PolyA⁺ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as described below. The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczynski, P and Sacchi, N., *Analytical Biochemistry* 162:156-159, 1987). PolyA⁺ RNA was isolated from total RNA (LABIMO) by
30 two passes of oligodT chromatography, as described by Aviv and Leder (Aviv, H. and Leder, P., *Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972) in order to eliminate ribosomal RNA.

The quality and the integrity of the poly A⁺ were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded. Contamination of the PolyA⁺ mRNAs by ribosomal sequences was checked using RNAs blots and a probe derived from the sequence of the 28S RNA. Preparations of mRNAs with less

than 5% of ribosomal RNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed mRNAs was examined using PCR.

Following preparation of the mRNAs, the above described chemical and/or the enzymatic procedures for
5 enriching mRNAs having intact 5' ends discussed above were employed to obtain 5' ESTs from various tissues. In both approaches an oligonucleotide tag was attached to the cap at the 5' ends of the mRNAs. The oligonucleotide tag had an EcoRI site therein to facilitate later cloning procedures.

Following attachment of the oligonucleotide tag to the mRNA by either the chemical or enzymatic methods, the integrity of the mRNA was examined by performing a Northern blot with 200-500ng of mRNA using a probe
10 complementary to the oligonucleotide tag.

EXAMPLE 14

cDNA Synthesis Using mRNA Templates Having Intact 5' Ends

For the mRNAs joined to oligonucleotide tags using both the chemical and enzymatic methods, first strand cDNA synthesis was performed using reverse transcriptase with random nonamers as primers. In order to protect
15 internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of RNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

For both the chemical and the enzymatic methods, the second strand of the cDNA was synthesized with a Klenow fragment using a primer corresponding to the 5' end of the ligated oligonucleotide described in Example 12.
20 Preferably, the primer is 20-25 bases in length. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

Following cDNA synthesis, the cDNAs were cloned into pBlueScript as described in Example 15 below.

EXAMPLE 15

Insertion of cDNAs into BlueScript

25 Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was used during cDNA synthesis, the EcoRI site present in the tag was the only site which was hemi-methylated. Consequently, only the EcoRI site in the oligonucleotide tag was susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (AcA, Biosepra). Fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was
30 directionally cloned into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

Clones containing the oligonucleotide tag attached were selected as described in Example 16 below.

EXAMPLE 16

Selection of Clones Having the Oligonucleotide Tag Attached Thereto

The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows. Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang et al., *Gene* 127:95-8, 1993) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry et al., *Biotechniques*, 13: 124-131, 1992. In this procedure, the single stranded DNA was hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide described in Example 13. Preferably, the primer has a length of 20-25 bases. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as the ThermoSequenase obtained from Amersham Pharmacia Biotech. Alternatively, protocols such as the Gene Trapper kit (Gibco BRL) may be used. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5' tag oligonucleotide was estimated to typically rank between 90 and 98% using dot blot analysis.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP). A copy of the MTP was stored for future needs. Then the libraries were transferred into 96 MTP and sequenced as described below.

EXAMPLE 17

Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE 9600 thermocyclers (Perkin-Elmer), using standard SETA-A and SETA-B primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers (Perkin Elmer, Applied Biosystems Division, Foster City, CA). Sequencing reactions were performed using PE 9600 thermocyclers (Perkin Elmer) with standard dye-primer chemistry and ThermoSequenase (Amersham Life Science). The primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs used in the sequencing reactions were purchased from Boehringer. Sequencing buffer, reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with EtOH, resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel. Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and the sequence data were collected and analyzed using the ABI Prism DNA Sequencing Analysis Software, version 2.1.2.

The sequence data from the 44 cDNA libraries made as described above were transferred to a proprietary database, where quality control and validation steps were performed. A proprietary base-caller ("Trace"), working using a Unix system automatically flagged suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the noise level. The proprietary base-caller also performed an automatic trimming. Any stretch of 25 or

fewer bases having more than 4 suspect peaks was considered unreliable and was discarded. Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may contain 1 to 5 bases belonging to the above mentioned sequences at their 5' end. If needed, these can easily be removed on a case by case basis.

5 Thereafter, the sequences were transferred to the proprietary NETGENE™ Database for further analysis as described below.

Following sequencing as described above, the sequences of the 5' ESTs were entered in a proprietary database called NETGENE™ for storage and manipulation. It will be appreciated by those skilled in the art that the data could be stored and manipulated on any medium which can be read and accessed by a computer. Computer readable media
10 include magnetically readable media, optically readable media, or electronically readable media. For example, the computer readable media may be a hard disc, a floppy disc, a magnetic tape, CD-ROM, RAM, or ROM as well as other types of other media known to those skilled in the art.

In addition, the sequence data may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, the sequence data may be stored as text in a word processing file, such as
15 MicrosoftWORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE.

The computer readable media on which the sequence information is stored may be in a personal computer, a network, a server or other computer systems known to those skilled in the art. The computer or other system preferably includes the storage media described above, and a processor for accessing and manipulating the sequence data.

20 Once the sequence data has been stored it may be manipulated and searched to locate those stored sequences which contain a desired nucleic acid sequence or which encode a protein having a particular functional domain. For example, the stored sequence information may be compared to other known sequences to identify homologies, motifs implicated in biological function, or structural motifs.

Programs which may be used to search or compare the stored sequences include the MacPattern (EMBL),
25 BLAST, and BLAST2 program series (NCBI), basic local alignment search tool programs for nucleotide (BLASTN) and peptide (BLASTX) comparisons (Altschul et al, *J. Mol. Biol.* 215: 403 (1990)) and FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, 85: 2444 (1988)). The BLAST programs then extend the alignments on the basis of defined match and mismatch criteria.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-
30 helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

Before searching the cDNAs in the NETGENE™ database for sequence motifs of interest, cDNAs derived from mRNAs which were not of interest were identified and eliminated from further consideration as described in Example 18 below.

EXAMPLE 18

5

Elimination of Undesired Sequences from Further Consideration

5' ESTs in the NETGENE™ database which were derived from undesired sequences such as transfer RNAs, ribosomal RNAs, mitochondrial RNAs, procaryotic RNAs, fungal RNAs, Alu sequences, L1 sequences, or repeat sequences were identified using the FASTA and BLASTN programs with the parameters listed in Table II.

To eliminate 5' ESTs encoding tRNAs from further consideration, the 5' EST sequences were compared to the
10 sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human. The comparison was performed using FASTA on both strands of the 5' ESTs. Sequences having more than 80% homology over more than 60 nucleotides were identified as tRNA. Of the 144,341 sequences screened, 26 were identified as tRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding rRNAs from further consideration, the 5' EST sequences were compared to the
15 sequences of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S = 108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as rRNAs. Of the 144,341 sequences screened, 3,312 were identified as rRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding mtRNAs from further consideration, the 5' EST sequences were compared to
20 the sequences of the two known mitochondrial genomes for which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38 sequences. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S = 108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as mtRNAs. Of the 144,341 sequences screened, 6,110 were identified as mtRNAs and eliminated from further consideration.

25 Sequences which might have resulted from exogenous contaminants were eliminated from further consideration by comparing the 5' EST sequences to release 46 of the EMBL bacterial and fungal divisions using BLASTN with the parameter S = 144. All sequences having more than 90% homology over at least 40 nucleotides were identified as exogenous contaminants. Of the 42 cDNA libraries examined, the average percentages of procaryotic and fungal sequences contained therein were 0.2% and 0.5% respectively. Among these sequences, only one could be
30 identified as a sequence specific to fungi. The others were either fungal or procaryotic sequences having homologies with vertebrate sequences or including repeat sequences which had not been masked during the electronic comparison.

In addition, the 5' ESTs were compared to 6093 Alu sequences and 1115 L1 sequences to mask 5' ESTs containing such repeat sequences from further consideration. 5' ESTs including THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats were also eliminated from further consideration. On average, 11.5% of

the sequences in the libraries contained repeat sequences. Of this 11.5%, 7% contained Alu repeats, 3.3% contained L1 repeats and the remaining 1.2% were derived from the other types of repetitive sequences which were screened. These percentages are consistent with those found in cDNA libraries prepared by other groups. For example, the cDNA libraries of Adams et al. contained between 0% and 7.4% Alu repeats depending on the source of the RNA which was used to prepare the cDNA library (Adams et al., *Nature* 377:174, 1996).

The sequences of those 5' ESTs remaining after the elimination of undesirable sequences were compared with the sequences of known human mRNAs to determine the accuracy of the sequencing procedures described above.

EXAMPLE 19

Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described above, the sequences of 5' ESTs derived from known sequences were identified and compared to the known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5' ESTs to identify those matching an entry in the public human mRNA database. The 6655 5' ESTs which matched a known human mRNA were then realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5' EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy.

This analysis revealed that the sequences incorporated in the NETGENE™ database had an accuracy of more than 99.5%.

To determine the efficiency with which the above selection procedures select cDNAs which include the 5' ends of their corresponding mRNAs, the following analysis was performed.

EXAMPLE 20

Determination of Efficiency of 5' EST Selection

To determine the efficiency at which the above selection procedures isolated 5' ESTs which included sequences close to the 5' end of the mRNAs from which they were derived, the sequences of the ends of the 5' ESTs which were derived from the elongation factor 1 subunit α and ferritin heavy chain genes were compared to the known cDNA sequences for these genes. Since the transcription start sites for the elongation factor 1 subunit α and ferritin heavy chain are well characterized, they may be used to determine the percentage of 5' ESTs derived from these genes which included the authentic transcription start sites.

For both genes, more than 95% of the cDNAs included sequences close to or upstream of the 5' end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5' ESTs from ESTs in the NETGENE™ database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for comparison. For those 5' ESTs derived from mRNAs included in the GeneBank database, more than 85% had their 5' ends close to the 5' ends of the known sequence. As some of the mRNA

sequences available in the GenBank database are deduced from genomic sequences, a 5' end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5' ends of their corresponding mRNAs.

The EST libraries made above included multiple 5' ESTs derived from the same mRNA. The sequences of such 5' ESTs were compared to one another and the longest 5' ESTs for each mRNA were identified. Overlapping cDNAs were assembled into continuous sequences (contigs). The resulting continuous sequences were then compared to public databases to gauge their similarity to known sequences, as described in Example 21 below.

EXAMPLE 21

Clustering of the 5' ESTs and Calculation of Novelty Indices for cDNA Libraries

10 For each sequenced EST library, the sequences were clustered by the 5' end. Each sequence in the library was compared to the others with BLASTN2 (direct strand, parameters S = 107). ESTs with High Scoring Segment Pairs (HSPs) at least 25 bp long, having 95% identical bases and beginning closer than 10 bp from each EST 5' end were grouped. The longest sequence found in the cluster was used as representative of the cluster. A global clustering between libraries was then performed leading to the definition of super-contigs.

15 To assess the yield of new sequences within the EST libraries, a novelty rate (NR) was defined as: $NR = 100 \times (\text{Number of new unique sequences found in the library} / \text{Total number of sequences from the library})$. Typically, novelty rating range between 10% and 41% depending on the tissue from which the EST library was obtained. For most of the libraries, the random sequencing of 5' EST libraries was pursued until the novelty rate reached 20%.

Following characterization as described above, the collection of 5' ESTs in NETGENE™ was screened to 20 identify those 5' ESTs bearing potential signal sequences as described in Example 22 below.

EXAMPLE 22

Identification of Potential Signal Sequences in 5' ESTs

The 5' ESTs in the NETGENE™ database were screened to identify those having an uninterrupted open reading frame (ORF) longer than 45 nucleotides beginning with an ATG codon and extending to the end of the EST.

25 Approximately half of the cDNA sequences in NETGENE™ contained such an ORF. The ORFs of these 5' ESTs were searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, G. A New Method for Predicting Signal Sequence Cleavage Sites. *Nucleic Acids Res.* 14:4683-4690 (1986). Those 5' EST sequences encoding a 15 amino acid long stretch with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those 5' ESTs which matched a known human 30 mRNA or EST sequence and had a 5' end more than 20 nucleotides downstream of the known 5' end were excluded from further analysis. The remaining cDNAs having signal sequences therein were included in a database called SIGNALTAG™.

To confirm the accuracy of the above method for identifying signal sequences, the analysis of Example 23 was performed.

EXAMPLE 23**Confirmation of Accuracy of Identification of Potential Signal Sequences in 5' ESTs**

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino terminal amino acids of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5' region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was calculated based on either the assumption that 10% of human proteins are secreted or the assumption that 20% of human proteins are secreted. The results of this analysis are shown in Figures 2 and 3.

Using the above method of identifying secretory proteins, 5' ESTs for human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor all of which are polypeptides which are known to be secreted, were obtained. Thus, the above method successfully identified those 5' ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5' ESTs actually functions as a signal peptide, the signal sequences from the 5' ESTs may be cloned into a vector designed for the identification of signal peptides. Some signal peptide identification vectors are designed to confer the ability to grow in selective medium on host cells which have a signal sequence operably inserted into the vector. For example, to confirm that a 5' EST encodes a genuine signal peptide, the signal sequence of the 5' EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637. Growth of host cells containing signal sequence selection vectors having the signal sequence from the 5' EST inserted therein confirms that the 5' EST encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs into expression vectors such as pXT1 (as described below), or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

Those 5' ESTs which encoded a signal peptide, as determined by the method of Example 22 above, were further grouped into four categories based on their homology to known sequences. The categorization of the 5' ESTs is described in Example 24 below.

EXAMPLE 24

Categorization of 5' ESTs Encoding a Signal Peptide

Those 5' ESTs having a sequence not matching any known vertebrate sequence nor any publicly available EST sequence were designated "new." Of the sequences in the SIGNALTAG™ database, 947 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

5 Those 5' ESTs having a sequence not matching any vertebrate sequence but matching a publicly known EST were designated "EST-ext", provided that the known EST sequence was extended by at least 40 nucleotides in the 5' direction. Of the sequences in the SIGNALTAG™ database, 150 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

10 Those ESTs not matching any vertebrate sequence but matching a publicly known EST without extending the known EST by at least 40 nucleotides in the 5' direction were designated "EST." Of the sequences in the SIGNALTAG™ database, 599 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs matching a human mRNA sequence but extending the known sequence by at least 40 nucleotides in the 5' direction were designated "VERT-ext." Of the sequences in the SIGNALTAG™ database, 23 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category. Included in this category was a 5' EST which
15 extended the known sequence of the human translocase mRNA by more than 200 bases in the 5' direction. A 5' EST which extended the sequence of a human tumor suppressor gene in the 5' direction was also identified.

Figure 4 shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

Each of the 5' ESTs was categorized based on the tissue from which its corresponding mRNA was obtained,
20 as described below in Example 25.

EXAMPLE 25

Categorization of Expression Patterns

Figure 5 shows the tissues from which the mRNAs corresponding to the 5' ESTs in each of the above described categories were obtained.

25 In addition to categorizing the 5' ESTs by the tissue from which the cDNA library in which they were first identified was obtained, the spatial and temporal expression patterns of the mRNAs corresponding to the 5' ESTs, as well as their expression levels, may be determined as described in Example 26 below. Characterization of the spatial and temporal expression patterns and expression levels of these mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail
30 below.

In addition, 5' ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from lack of expression, over expression, or under expression of an mRNA corresponding to a 5' EST. By comparing mRNA expression patterns and quantities in samples taken from healthy

individuals with those from individuals suffering from a particular disease, 5' ESTs responsible for the disease may be identified.

It will be appreciated that the results of the above characterization procedures for 5' ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5' ESTs. It will also be appreciated that if it is desired to defer characterization until extended cDNAs have been obtained rather than characterizing the ESTs themselves, the above characterization procedures can be applied to characterize the extended cDNAs after their isolation.

EXAMPLE 26

Evaluation of Expression Levels and Patterns of mRNAs

Corresponding to 5' ESTs or Extended cDNAs

Expression levels and patterns of mRNAs corresponding to 5' ESTs or extended cDNAs (obtainable as described below) may be analyzed by solution hybridization with long probes as described in International Patent Application No. WO 97/05277. Briefly, a 5' EST, extended cDNA, or fragment thereof corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3, T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the 5' EST or extended cDNA has 100 or more nucleotides. The plasmid is linearized and transcribed in the presence of ribonucleotides comprising modified ribonucleotides (i.e. biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (i.e. RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

The 5' ESTs, extended cDNAs, or fragments thereof may also be tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK Patent Application No. 2 305 241 A. In this method, cDNAs are prepared from a cell, tissue, organism or other source of nucleic acid for which it is desired to determine gene expression patterns. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction endonuclease, called an "anchoring enzyme," having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5' or 3' most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a "tagging endonuclease" is ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short "tag" fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the "tagging endonuclease" to generate short "tag" fragments derived from the cDNAs in the second pool. The "tags" resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce "ditags." In some embodiments, the ditags are concatamerized to produce ligation products containing from 2 to 200 ditags. The tag sequences are then determined and compared to the sequences of the 5' ESTs or extended cDNAs to determine which 5' ESTs or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5' ESTs or extended cDNAs in the cell, tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of full length cDNAs (i.e. extended cDNAs which include the coding sequence for the signal peptide, the coding sequence for the mature protein, and a stop codon), extended cDNAs, 5' ESTs or fragments of the full length cDNAs, extended cDNAs, or 5' ESTs of sufficient length to permit specific detection of gene expression. Preferably, the fragments are at least 15 nucleotides in length. More preferably, the fragments are at least 100 nucleotides in length. More preferably, the fragments are more than 100 nucleotides in length. In some embodiments the fragments may be more than 500 nucleotides in length.

For example, quantitative analysis of gene expression may be performed with full length cDNAs, extended cDNAs, 5' ESTs, or fragments thereof in a complementary DNA microarray as described by Schena et al. (*Science* 270:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* 93:10614-10619, 1996). Full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are amplified by PCR and arrayed from 96-well microtiter plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 cm² microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a fluorescence laser scanning device fitted with a custom filter set. Accurate differential expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with full length cDNAs, extended cDNAs, 5' ESTs, or fragments thereof in complementary DNA arrays as described by Pietu et al. (*Genome Research* 6:492-503, 1996). The full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides.

After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the 5' ESTs or extended cDNAs can be done through high density nucleotide arrays as described by Lockhart et al. (Nature Biotechnology 14: 1675-1680, 1996) and Sosnowsky et al. (Proc. Natl. Acad. Sci. 94:1119-1123, 1997). Oligonucleotides of 15-50 nucleotides corresponding to sequences of the 5' ESTs or extended cDNAs are synthesized directly on the chip (Lockhart et al., *supra*) or synthesized and then addressed to the chip (Sosnowski et al., *supra*). Preferably, the oligonucleotides are about 20 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart et al., *supra* and application of different electric fields (Sosnowsky et al., Proc. Natl. Acad. Sci. 94:1119-1123), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5' EST or extended cDNA from which the oligonucleotide sequence has been designed.

III. Use of 5' ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs

Once 5' ESTs which include the 5' end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended cDNAs which contain sequences adjacent to the 5' ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site, the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide. Such extended cDNAs are referred to herein as "full length cDNAs." Alternatively, the extended cDNAs may include only the sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Example 27 below describes a general method for obtaining extended cDNAs. Example 28 below describes the cloning and sequencing of several extended cDNAs, including extended cDNAs which include the entire coding sequence and authentic 5' end of the corresponding mRNA for several secreted proteins.

The methods of Examples 27, 28, and 29 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of the secreted proteins encoded by the genes corresponding to the 5' ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 10 amino acids of one of the proteins encoded by the sequences of SEQ ID NOs: 40-140 and 242-377. In further embodiments, the extended cDNAs encode at least 20 amino acids of the proteins encoded by the sequences of SEQ ID NOs: 40-140 and 242-377. In further embodiments, the extended cDNAs encode at least 30 amino acids of the sequences of SEQ ID NOs: 40-140 and

242-377. In a preferred embodiment, the extended cDNAs encode a full length protein sequence, which includes the protein coding sequences of SEQ ID NOs: 40-140 and 242-377.

EXAMPLE 27

General Method for Using 5' ESTs to Clone and Sequence Extended cDNAs

5 The following general method has been used to quickly and efficiently isolate extended cDNAs including sequence adjacent to the sequences of the 5' ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5' EST in the NETGENE™ database, including those 5' ESTs encoding secreted proteins. The method is summarized in Figure 6.

1. Obtaining Extended cDNAs

10 a) First strand synthesis

The method takes advantage of the known 5' sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly 14dT primer containing a 49 nucleotide sequence at its 5' end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3' end of the mRNA. For example, the primer may have the following sequence: 5'-ATC GTT GAG ACT CGT ACC AGC AGA GTC ACG AGA GAG ACT ACA CGG
15 TAC TGG TTT TTT TTT TTT TTVN -3' (SEQ ID NO:14). Those skilled in the art will appreciate that other sequences may also be added to the poly dT sequence and used to prime the first strand synthesis. Using this primer and a reverse transcriptase such as the Superscript II (Gibco BRL) or Rnase H Minus M-MLV (Promega) enzyme, a reverse transcript anchored at the 3' polyA site of the RNAs is generated.

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the
20 alkaline hydrolysis and the residual poly dT primer are eliminated with an exclusion column such as an AcA34 (Biosepra) matrix as explained in Example 11.

b) Second strand synthesis

A pair of nested primers on each end is designed based on the known 5' sequence from the 5' EST and the known 3' end added by the poly dT primer used in the first strand synthesis. Software used to design primers are either
25 based on GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), or based on the octamer frequency disparity method (Griffais et al., *Nucleic Acids Res.* 19: 3887-3891, 1991 such as PC-Rare (<http://bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html>)).

Preferably, the nested primers at the 5' end are separated from one another by four to nine bases. The 5' primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

30 Preferably, the nested primers at the 3' end are separated from one another by four to nine bases. For example, the nested 3' primers may have the following sequences: (5'- CCA GCA GAG TCA CGA GAG AGA CTA CAC GG -3'(SEQ ID NO:15), and 5'- CAC GAG AGA GAC TAC ACG GTA CTG G -3' (SEQ ID NO:16). These primers were selected because they have melting temperatures and specificities compatible with their use in PCR. However, those skilled in the art will appreciate that other sequences may also be used as primers.

The first PCR run of 25 cycles is performed using the Advantage Tth Polymerase Mix (Clontech) and the outer primer from each of the nested pairs. A second 20 cycle PCR using the same enzyme and the inner primer from each of the nested pairs is then performed on 1/2500 of the first PCR product. Thereafter, the primers and nucleotides are removed.

5 **2. Sequencing of Full Length Extended cDNAs or Fragments Thereof**

Due to the lack of position constraints on the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon thus yielding a nested PCR product containing the whole coding sequence. Such a full length extended cDNA undergoes a direct cloning procedure as described in section a below. However, in some cases, the
10 second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are submitted to a modified procedure described in section b below.

a) Nested PCR products containing complete ORFs

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST
15 sequence, it is cloned in an appropriate vector such as pED6dpc2, as described in section 3.

b) Nested PCR products containing incomplete ORFs

When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products as described
20 in the following section.

Once the full coding sequence has been completely determined, new primers compatible for PCR use are designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, i.e. the polyA tract and sometimes the polyadenylation signal, as illustrated in figure 6. Such full length extended cDNAs are
25 then cloned into an appropriate vector as described in section 3.

c) Sequencing extended cDNAs

Sequencing of extended cDNAs is performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

In order to sequence PCR fragments, primer walking is performed using software such as OSP to choose
30 primers and automated computer software such as ASMG (Sutton et al., *Genome Science Technol.* 1: 9-19, 1995) to construct contigs of walking sequences including the initial 5' tag using minimum overlaps of 32 nucleotides. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

Completion of the sequencing of a given extended cDNA fragment is assessed as follows. Since sequences located after a polyA tract are difficult to determine precisely in the case of uncloned products, sequencing and primer

walking processes for PCR products are interrupted when a polyA tract is identified in extended cDNAs obtained as described in case b. The sequence length is compared to the size of the nested PCR product obtained as described above. Due to the limited accuracy of the determination of the PCR product size by gel electrophoresis, a sequence is considered complete if the size of the obtained sequence is at least 70 % the size of the first nested PCR product. If the length of the sequence determined from the computer analysis is not at least 70% of the length of the nested PCR product, these PCR products are cloned and the sequence of the insertion is determined. When Northern blot data are available, the size of the mRNA detected for a given PCR product is used to finally assess that the sequence is complete. Sequences which do not fulfill the above criteria are discarded and will undergo a new isolation procedure.

Sequence data of all extended cDNAs are then transferred to a proprietary database, where quality controls and validation steps are carried out as described in example 15.

3. Cloning of Full Length Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into the expression vector pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA) as follows. The structure of pED6dpc2 is shown in Figure 7. pED6dpc2 vector DNA is prepared with blunt ends by performing an EcoRI digestion followed by a fill in reaction. The blunt ended vector is dephosphorylated. After removal of PCR primers and ethanol precipitation, the PCR product containing the full coding sequence or the extended cDNA obtained as described above is phosphorylated with a kinase subsequently removed by phenol-Sevag extraction and precipitation. The double stranded extended cDNA is then ligated to the vector and the resulting expression plasmid introduced into appropriate host cells.

Since the PCR products obtained as described above are blunt ended molecules that can be cloned in either direction, the orientation of several clones for each PCR product is determined. Then, 4 to 10 clones are ordered in microtiter plates and subjected to a PCR reaction using a first primer located in the vector close to the cloning site and a second primer located in the portion of the extended cDNA corresponding to the 3' end of the mRNA. This second primer may be the antisense primer used in anchored PCR in the case of direct cloning (case a) or the antisense primer located inside the 3'UTR in the case of indirect cloning (case b). Clones in which the start codon of the extended cDNA is operably linked to the promoter in the vector so as to permit expression of the protein encoded by the extended cDNA are conserved and sequenced. In addition to the ends of cDNA inserts, approximately 50 bp of vector DNA on each side of the cDNA insert are also sequenced.

The cloned PCR products are then entirely sequenced according to the aforementioned procedure. In this case, contig assembly of long fragments is then performed on walking sequences that have already contigated for uncloned PCR products during primer walking. Sequencing of cloned amplicons is complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends.

4. Computer Analysis of Full Length Extended cDNA

Sequences of all full length extended cDNAs are then submitted to further analysis as described below and using the parameters found in Table II with the following modifications. For screening of miscellaneous subdivisions of Genbank, FASTA was used instead of BLASTN and 15 nucleotide of homology was the limit instead of 17. For Alu detection, BLASTN was used with the following parameters: S = 72; identity = 70%; and length = 40 nucleotides.

- 5 Polyadenylation signal and polyA tail which were not search for the 5' ESTs were searched. For polyadenylation signal detection the signal (AATAAA) was searched with one permissible mismatch in the last ten nucleotides preceding the 5' end of the polyA. For the polyA, a stretch of 8 amino acids in the last 20 nucleotides of the sequence was searched with BLAST2N in the sense strand with the following parameters (W = 6, S = 10, E = 1000, and identity = 90%). Finally, patented sequences and ORF homologies were searched using, respectively, BLASTN and BLASTP on GenSEQ
- 10 (Derwent's database of patented nucleotide sequences) and SWISSPROT for ORFs with the following parameters (W = 8 and B = 10). Before examining the extended full length cDNAs for sequences of interest, extended cDNAs which are not of interest are searched as follows.

a) Elimination of undesired sequences

- Although 5'ESTs were checked to remove contaminant sequences as described in Example 18, a last verification was
- 15 carried out to identify extended cDNAs sequences derived from undesired sequences such as vector RNAs, transfer RNAs, ribosomal rRNAs, mitochondrial RNAs, prokaryotic RNAs and fungal RNAs using the FASTA and BLASTN programs on both strands of extended cDNAs as described below.

- To identify the extended cDNAs encoding vector RNAs, extended cDNAs are compared to the known sequences of vector RNA using the FASTA program. Sequences of extended cDNAs with more than 90% homology over
- 20 stretches of 15 nucleotides are identified as vector RNA.

To identify the extended cDNAs encoding tRNAs, extended cDNA sequences were compared to the sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human. Sequences of extended cDNAs having more than 80% homology over 60 nucleotides using FASTA were identified as tRNA.

- To identify the extended cDNAs encoding rRNAs, extended cDNA sequences were compared to the sequences
- 25 of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human. Sequences of extended cDNAs having more than 80% homology over stretches longer than 40 nucleotides using BLASTN were identified as rRNAs.

- To identify the extended cDNAs encoding mtRNAs, extended cDNA sequences were compared to the sequences of the two known mitochondrial genomes for which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38
- 30 sequences. Sequences of extended cDNAs having more than 80% homology over stretches longer than 40 nucleotides using BLASTN were identified as mtRNAs.

Sequences which might have resulted from other exogenous contaminants were identified by comparing extended cDNA sequences to release 105 of Genbank bacterial and fungal divisions. Sequences of extended cDNAs

having more than 90% homology over 40 nucleotides using BLASTN were identified as exogenous prokaryotic or fungal contaminants.

In addition, extended cDNAs were searched for different repeat sequences, including Alu sequences, L1 sequences, THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats. Sequences of extended cDNAs with more than 70% homology over 40 nucleotide stretches using BLASTN were identified as repeat sequences and masked in further identification procedures. In addition, clones showing extensive homology to repeats, i.e., matches of either more than 50 nucleotides if the homology was at least 75% or more than 40 nucleotides if the homology was at least 85% or more than 30 nucleotides if the homology was at least 90%, were flagged.

b) Identification of structural features

10 Structural features, e.g. polyA tail and polyadenylation signal, of the sequences of full length extended cDNAs are subsequently determined as follows.

A polyA tail is defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 20 nt of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not readable after such a polyA stretch. Stretches with 100% homology over 6 nucleotides are identified as polyA tails.

To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 bp preceding the polyA tail are searched for the canonic polyadenylation AAUAAA signal allowing one mismatch to account for possible sequencing errors and known variation in the canonical sequence of the polyadenylation signal.

c) Identification of functional features

20 Functional features, e.g. ORFs and signal sequences, of the sequences of full length extended cDNAs were subsequently determined as follows.

The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation initiation codon and ending with a stop codon. ORFs encoding at least 20 amino acids are preferred.

25 Each found ORF is then scanned for the presence of a signal peptide in the first 50 amino-acids or, where appropriate, within shorter regions down to 20 amino acids or less in the ORF, using the matrix method of von Heijne (Nuc. Acids Res. 14: 4683-4690 (1986)) and the modification described in Example 22.

d) Homology to either nucleotidic or proteic sequences

30 Sequences of full length extended cDNAs are then compared to known sequences on a nucleotidic or proteic basis.

Sequences of full length extended cDNAs are compared to the following known nucleic acid sequences: vertebrate sequences (Genbank), EST sequences (Genbank), patented sequences (Geneseqn) and recently identified sequences (Genbank daily releases) available at the time of filing for the priority documents. Full length cDNA sequences are also compared to the sequences of a private database (Genset internal sequences) in order to find sequences that

have already been identified by applicants. Sequences of full length extended cDNAs with more than 90% homology over 30 nucleotides using either BLASTN or BLAST2N as indicated in Table III are identified as sequences that have already been described. Matching vertebrate sequences are subsequently examined using FASTA; full length extended cDNAs with more than 70% homology over 30 nucleotides are identified as sequences that have already been described.

5 ORFs encoded by full length extended cDNAs as defined in section c) are subsequently compared to known amino acid sequences found in Swissprot release CHP, PIR release PIR# and Genpept release GPEPT public databases using BLASTP with the parameter $W=8$ and allowing a maximum of 10 matches. Sequences of full length extended cDNAs showing extensive homology to known protein sequences are recognized as already identified proteins.

In addition, the three-frame conceptual translation products of the top strand of full length extended cDNAs
10 are compared to publicly known amino acid sequences of Swissprot using BLASTX with the parameter $E=0.001$. Sequences of full length extended cDNAs with more than 70% homology over 30 amino acid stretches are detected as already identified proteins.

5. Selection of Cloned Full Length Sequences of the Present Invention

Cloned full length extended cDNA sequences that have already been characterized by the aforementioned
15 computer analysis are then submitted to an automatic procedure in order to preselect full length extended cDNAs containing sequences of interest.

a) Automatic sequence preselection

All complete cloned full length extended cDNAs clipped for vector on both ends are considered. First, a negative selection is operated in order to eliminate unwanted cloned sequences resulting from either contaminants or
20 PCR artifacts as follows. Sequences matching contaminant sequences such as vector RNA, tRNA, mtRNA, rRNA sequences are discarded as well as those encoding ORF sequences exhibiting extensive homology to repeats as defined in section 4 a). Sequences obtained by direct cloning using nested primers on 5' and 3' tags (section 1. case a) but lacking polyA tail are discarded. Only ORFs containing a signal peptide and ending either before the polyA tail (case a) or before the end of the cloned 3'UTR (case b) are kept. Then, ORFs containing unlikely mature proteins such as mature
25 proteins which size is less than 20 amino acids or less than 25% of the immature protein size are eliminated.

In the selection of the ORF, priority was given to the ORF and the frame corresponding to the polypeptides described in SignalTag Patents (United States Patent Application Serial Nos: 08/905,223; 08/905,135; 08/905,051; 08/905,144; 08/905,279; 08/904,468; 08/905,134; and 08/905,133). If the ORF was not found among the ORFs described in the SignalTag Patents, the ORF encoding the signal peptide with the highest score according to Von Heijne
30 method as defined in Example 22 was chosen. If the scores were identical, then the longest ORF was chosen.

Sequences of full length extended cDNA clones are then compared pairwise with BLAST after masking of the repeat sequences. Sequences containing at least 90% homology over 30 nucleotides are clustered in the same class. Each cluster is then subjected to a cluster analysis that detects sequences resulting from internal priming or from

alternative splicing, identical sequences or sequences with several frameshifts. This automatic analysis serves as a basis for manual selection of the sequences.

b) Manual sequence selection

Manual selection is carried out using automatically generated reports for each sequenced full length extended
5 cDNA clone. During this manual procedures, a selection is operated between clones belonging to the same class as follows. ORF sequences encoded by clones belonging to the same class are aligned and compared. If the homology between nucleotidic sequences of clones belonging to the same class is more than 90% over 30 nucleotide stretches or if the homology between amino acid sequences of clones belonging to the same class is more than 80% over 20 amino acid stretches, than the clones are considered as being identical. The chosen ORF is the best one according to the
10 criteria mentioned below. If the nucleotide and amino acid homologies are less than 90% and 80% respectively, the clones are said to encode distinct proteins which can be both selected if they contain sequences of interest.

Selection of full length extended cDNA clones encoding sequences of interest is performed using the following criteria. Structural parameters (initial tag, polyadenylation site and signal) are first checked. Then, homologies with known nucleic acids and proteins are examined in order to determine whether the clone sequence match a known
15 nucleic/proteic sequence and, in the latter case, its covering rate and the date at which the sequence became public. If there is no extensive match with sequences other than ESTs or genomic DNA, or if the clone sequence brings substantial new information, such as encoding a protein resulting from alternative slicing of an mRNA coding for an already known protein, the sequence is kept. Examples of such cloned full length extended cDNAs containing sequences of interest are described in Example 28. Sequences resulting from chimera or double inserts as assessed by homology to other
20 sequences are discarded during this procedure.

EXAMPLE 28

Cloning and Sequencing of Extended cDNAs

The procedure described in Example 27 above was used to obtain the extended cDNAs of the present invention. Using this approach, the full length cDNA of SEQ ID NO:17 was obtained. This cDNA falls into the "EST-
25 ext" category described above and encodes the signal peptide MKKVLLITAILAVAVG (SEQ ID NO: 18) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:19 was also obtained using this procedure. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MWWFQQGLSFLPSALVIWTS (SEQ ID NO:20) having a von Heijne score of 5.5.

30 Another full length cDNA obtained using the procedure described above has the sequence of SEQ ID NO:21. This cDNA, falls into the "EST-ext" category described above and encodes the signal peptide MVLTTLPANSANSPVNMPTTGPNLSYASSALSPCLT (SEQ ID NO:22) having a von Heijne score of 5.9.

The above procedure was also used to obtain a full length cDNA having the sequence of SEQ ID NO:23. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide ILSTVTALTFAXA (SEQ ID NO:24) having a von Heijne score of 5.5.

The full length cDNA of SEQ ID NO:25 was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LVLTLCTLPLAVA (SEQ ID NO:26) having a von Heijne score of 10.1.

The full length cDNA of SEQ ID NO:27 was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:28) having a von Heijne score of 10.7.

The above procedures were also used to obtain the extended cDNAs of the present invention. 5' ESTs expressed in a variety of tissues were obtained as described above. The appended sequence listing provides the tissues from which the extended cDNAs were obtained. It will be appreciated that the extended cDNAs may also be expressed in tissues other than the tissue listed in the sequence listing.

5' ESTs obtained as described above were used to obtain extended cDNAs having the sequences of SEQ ID NOs: 40-140 and 242-377. Table IV provides the sequence identification numbers of the extended cDNAs of the present invention, the locations of the full coding sequences in SEQ ID NOs: 40-140 and 242-377 (i.e. the nucleotides encoding both the signal peptide and the mature protein, listed under the heading FCS location in Table IV), the locations of the nucleotides in SEQ ID NOs: 40-140 and 242-377 which encode the signal peptides (listed under the heading SigPep Location in Table IV), the locations of the nucleotides in SEQ ID NOs: 40-140 and 242-377 which encode the mature proteins generated by cleavage of the signal peptides (listed under the heading Mature Polypeptide Location in Table IV), the locations in SEQ ID NOs: 40-140 and 242-377 of stop codons (listed under the heading Stop Codon Location in Table IV), the locations in SEQ ID NOs: 40-140 and 242-377 of polyA signals (listed under the heading Poly A Signal Location in Table IV) and the locations of polyA sites (listed under the heading Poly A Site Location in Table IV).

The polypeptides encoded by the extended cDNAs were screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid sequences which are well conserved amongst the members of a protein family. The conserved regions have been used to derive consensus patterns or matrices included in the PROSITE data bank, in particular in the file prosite.dat (Release 13.0 of November 1995, located at <http://expasy.hcuge.ch/sprot/prosite.html>. Prosite_convert and prosite_scan programs (http://ulrec3.unil.ch/ftpserveur/prosite_scan) were used to find signatures on the extended cDNAs.

For each pattern obtained with the prosite_convert program from the prosite.dat file, the accuracy of the detection on a new protein sequence has been tested by evaluating the frequency of irrelevant hits on the population of human secreted proteins included in the data bank SWISSPROT. The ratio between the number of hits on shuffled proteins (with a window size of 20 amino acids) and the number of hits on native (unshuffled) proteins was used as an index. Every pattern for which the ration was greater than 20% (one hit on shuffled proteins for 5 hits on native

-40-

proteins) was skipped during the search with prosite_scan. The program used to shuffle protein sequences (db_shuffled) and the program used to determine the statistics for each pattern in the protein data banks (prosite_statistics) are available on the ftp site http://ulrec3.unil.ch/ftpserveur/prosite_scan.

Table V lists the sequence identification numbers of the polypeptides of SEQ ID NOs: 141-241 and 378-513, the locations of the amino acid residues of SEQ ID NOs: 141-241 and 378-513 in the full length polypeptide (second column), the locations of the amino acid residues of SEQ ID NOs: 141-241 and 378-513 in the signal peptides (third column), and the locations of the amino acid residues of SEQ ID NOs: 141-241 and 378-513 in the mature polypeptide created by cleaving the signal peptide from the full length polypeptide (fourth column).

The nucleotide sequences of the sequences of SEQ ID NOs: 40-140 and 242-377 and the amino acid sequences encoded by SEQ ID NOs: 40-140 and 242-377 (i.e. amino acid sequences of SEQ ID NOs: 141-241 and 378-513) are provided in the appended sequence listing. In some instances, the sequences are preliminary and may include some incorrect or ambiguous sequences or amino acids. The sequences of SEQ ID NOs: 40-140 and 242-377 can readily be screened for any errors therein and any sequence ambiguities can be resolved by resequencing a fragment containing such errors or ambiguities on both strands. Nucleic acid fragments for resolving sequencing errors or ambiguities may be obtained from the deposited clones or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the ambiguity or error. Upon resolution of an error or ambiguity, the corresponding corrections can be made in the protein sequences encoded by the DNA containing the error or ambiguity. For example, in the sequences of the present invention, ambiguities in the sequence of SEQ ID NO: 131 were resolved. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein, and determining its sequence.

For each amino acid sequence, Applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing. Some of the amino acid sequences may contain "Xaa" designators. These "Xaa" designators indicate either (1) a residue which cannot be identified because of nucleotide sequence ambiguity or (2) a stop codon in the determined sequence where Applicants believe one should not exist (if the sequence were determined more accurately).

Cells containing the extended cDNAs (SEQ ID NOs: 40-140 and 242-377) of the present invention in the vector pED6dpc2, are maintained in permanent deposit by the inventors at Genset, S.A., 24 Rue Royale, 75008 Paris, France.

Pools of cells containing the extended cDNAs (SEQ ID NOs: 40-140 and 242-377), from which cells containing a particular polynucleotide are obtainable, were deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209 or the European Collection of Cell Cultures, Vaccine Research and Production Laboratory, Public Health Laboratory Service, Centre for Applied Microbiology and Research, Porton Down, Salisbury, Wiltshire SP4 0JG, United Kingdom. Each extended cDNA clone has been transfected into separate bacterial cells (E-

coli) for this composite deposit. Table VI lists the deposit numbers of the clones containing the extended cDNAs of the present invention. Table VII provides the internal designation number assigned to each SEQ ID NO and indicates whether the sequence is a nucleic acid sequence or a protein sequence.

Each extended cDNA can be removed from the pED6dpc2 vector in which it was deposited by performing a
5 NotI, PstI double digestion to produce the appropriate fragment for each clone. The proteins encoded by the extended cDNAs may also be expressed from the promoter in pED6dpc2.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone.

This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The design
10 of the oligonucleotide probe should preferably follow these parameters:

(a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

(b) Preferably, the probe is designed to have a T_m of approx. 80°C (assuming 2 degrees for each A or T and 4 degrees for each G or C). However, probes having melting temperatures between 40 °C and 80 °C may also be used provided that specificity is not lost.

15 The oligonucleotide should preferably be labeled with $(-^{32}\text{P})\text{ATP}$ (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantified by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4×10^6 dpm/pmol.

20 The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 $\mu\text{g/ml}$. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing
25 ampicillin at 100 $\mu\text{g/ml}$ and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is
30 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 $\mu\text{g/ml}$ of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1×10^6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to

1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

5 The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the extended cDNA insertion. For example, a PCR reaction may be conducted using a primer having the sequence
GGCCATACACTTGAGTGAC (SEQ ID NO:38) and a primer having the sequence ATATAGACAAACGCACACC (SEQ. ID.
NO:39). The PCR product which corresponds to the extended cDNA can then be manipulated using standard cloning
10 techniques familiar to those skilled in the art.

In addition to PCR based methods for obtaining extended cDNAs, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5' ESTs were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs or 5' ESTs. Example 29 below provides an example of such methods.

15

EXAMPLE 29

Methods for Obtaining Extended cDNAs or Nucleic Acids Homologous to Extended cDNAs or 5' ESTs

A full length cDNA library can be made using the strategies described in Examples 13, 14, 15, and 16 above by replacing the random nonamer used in Example 14 with an oligo-dT primer. For instance, the oligonucleotide of SEQ ID
20 NO:14 may be used.

Alternatively, a cDNA library or genomic DNA library may be obtained from a commercial source or made using techniques familiar to those skilled in the art. The library includes cDNAs which are derived from the mRNA corresponding to a 5' EST or which have homology to an extended cDNA or 5' EST. The cDNA library or genomic DNA library is hybridized to a detectable probe comprising at least 10 consecutive nucleotides from the 5' EST or extended
25 cDNA using conventional techniques. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises at least 20-30 consecutive nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises at least 30 nucleotides from the 5' EST or extended cDNA. In other embodiments, the probe comprises at least 40, at least 50, at least 75, at least 100, at least 150, or at least 200 consecutive nucleotides from the 5' EST or extended cDNA.

30 Techniques for identifying cDNA clones in a cDNA library which hybridize to a given probe sequence are disclosed in Sambrook et al., Molecular Cloning: A Laboratory Manual 2d Ed., Cold Spring Harbor Laboratory Press, 1989. The same techniques may be used to isolate genomic DNAs.

Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are identified and isolated for further manipulation as follows. A probe comprising at least 10 consecutive nucleotides from the 5' EST or extended

cDNA is labeled with a detectable label such as a radioisotope or a fluorescent molecule. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises 20-30 consecutive nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises at least 40, at least 50, at least 75, at least 100, at least 150, or at least 200 consecutive nucleotides from the 5' EST or extended cDNA.

Techniques for labeling the probe are well known and include phosphorylation with polynucleotide kinase, nick translation, in vitro transcription, and non-radioactive techniques. The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter and denatured. After incubation of the filter with a blocking solution, the filter is contacted with the labeled probe and incubated for a sufficient amount of time for the probe to hybridize to cDNAs or genomic DNAs containing a sequence capable of hybridizing to the probe.

By varying the stringency of the hybridization conditions used to identify extended cDNAs or genomic DNAs which hybridize to the detectable probe, extended cDNAs having different levels of homology to the probe can be identified and isolated. To identify extended cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction } G + C) \cdot (600/N)$ where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction } G + C) \cdot (0.63\% \text{ formamide}) \cdot (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook et al., supra.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the T_m . Preferably, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions. Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed

with 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

Extended cDNAs, nucleic acids homologous to extended cDNAs or 5' ESTs, or genomic DNAs which have hybridized to the probe are identified by autoradiography or other conventional techniques.

- 5 The above procedure may be modified to identify extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a Na⁺ concentration of approximately 1M. Following
- 10 hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C.

- Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following
- 15 hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide.

Extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs which have hybridized to the probe are identified by autoradiography.

- If it is desired to obtain nucleic acids homologous to extended cDNAs, such as allelic variants thereof or nucleic
- 20 acids encoding proteins related to the proteins encoded by the extended cDNAs, the level of homology between the hybridized nucleic acid and the extended cDNA or 5' EST used as the probe may readily be determined. To determine the level of homology between the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived are compared. For example, using the above methods, nucleic acids having at least 95% nucleic acid
- 25 homology to the extended cDNA or 5'EST from which the probe was derived may be obtained and identified. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA or 5'EST from which the probe was derived. The level of homology between the hybridized nucleic acid and the extended cDNA or 5' EST used as the probe may be further determined using BLAST2N; parameters may be adapted depending on the sequence length and degree of
- 30 homology studied. In such comparisons, the default parameters or the parameters listed in Tables II and III may be used.

To determine whether a clone encodes a protein having a given amount of homology to the protein encoded by the extended cDNA or 5' EST, the amino acid sequence encoded by the extended cDNA or 5' EST is compared to the amino acid sequence encoded by the hybridizing nucleic acid. Homology is determined to exist when an amino acid sequence in the extended cDNA or 5' EST is closely related to an amino acid sequence in the hybridizing nucleic acid. A

sequence is closely related when it is identical to that of the extended cDNA or 5' EST or when it contains one or more amino acid substitutions therein in which amino acids having similar characteristics have been substituted for one another. Using the above methods, one can obtain nucleic acids encoding proteins having at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the proteins encoded by the extended cDNA or 5' EST from which the probe was derived. Using the above methods and algorithms such as FASTA with parameters depending on the sequence length and degree of homology studied the level of homology may be determined. In determining the level of homology using FASTA, the default parameters or the parameters listed in Tables II or III may be used.

Alternatively, extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing poly A selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the poly A tail of the mRNA is hybridized to the mRNA and a reverse transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of the 5' EST for which an extended cDNA is desired. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the sequences of the 5' EST. More preferably, the primer comprises 20-30 consecutive nucleotides from the sequences of the 5' EST. In some embodiments, the primer comprises more than 30 nucleotides from the sequences of the 5' EST. If it is desired to obtain extended cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RTPCR may be performed as described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by contacting an mRNA comprising the sequence of the 5' EST for which an extended cDNA is desired with a primer comprising at least 10 consecutive nucleotides of the sequences complementary to the 5' EST, hybridizing the primer to the mRNAs, and reverse transcribing the hybridized primer to make a first cDNA strand from the mRNAs. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST. More preferably, the primer comprises 20-30 consecutive nucleotides from the 5' EST.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized. The second cDNA strand may be made by hybridizing a primer complementary to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or viral vectors capable of replicating in an appropriate host cell. For example, the host cell may be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double

stranded cDNA and cloning the double stranded cDNA are well known to those skilled in the art and are described in Current Protocols in Molecular Biology, John Wiley 503 Sons, Inc. 1997 and Sambrook et al. Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, 1989.

Alternatively, kits for obtaining full length cDNAs, such as the GeneTrapper (Cat. No. 10356-020, Gibco, BRL), may be used for obtaining full length cDNAs or extended cDNAs. In this approach, full length or extended cDNAs are prepared from mRNA and cloned into double stranded phagemids. The cDNA library in the double stranded phagemids is then rendered single stranded by treatment with an endonuclease, such as the Gene II product of the phage F1, and Exonuclease III as described in the manual accompanying the GeneTrapper kit. A biotinylated oligonucleotide comprising the sequence of a 5' EST, or a fragment containing at least 10 nucleotides thereof, is hybridized to the single stranded phagemids. Preferably, the fragment comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST. More preferably, the fragment comprises 20-30 consecutive nucleotides from the 5' EST. In some procedures, the fragment may comprise more than 30 consecutive nucleotides from the 5' EST. For example, the fragment may comprises at least 40, at least 50, at least 75, at least 100, at least 150, or at least 200 consecutive nucleotides from the 5' EST.

Hybrids between the biotinylated oligonucleotide and phagemids having inserts containing the 5' EST sequence are isolated by incubating the hybrids with streptavidin coated paramagnetic beads and retrieving the beads with a magnet. Thereafter, the resulting phagemids containing the 5' EST sequence are released from the beads and converted into double stranded DNA using a primer specific for the 5' EST sequence. The resulting double stranded DNA is transformed into bacteria. Extended cDNAs containing the 5' EST sequence are identified by colony PCR or colony hybridization.

A plurality of extended cDNAs containing full length protein coding sequences or sequences encoding only the mature protein remaining after the signal peptide is cleaved may be provided as cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

IV. Expression of Proteins Encoded by Extended cDNAs Isolated Using 5' ESTs

Extended cDNAs containing the full protein coding sequences of their corresponding mRNAs or portions thereof, such as cDNAs encoding the mature protein, may be used to express the secreted proteins or portions thereof which they encode as described in Example 30 below. If desired, the extended cDNAs may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. It will be appreciated that a plurality of extended cDNAs containing the full protein coding sequences or portions thereof may be simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

EXAMPLE 30

Expression of the Proteins Encoded by Extended cDNAs or Portions Thereof

To express the proteins encoded by the extended cDNAs or portions thereof, nucleic acids containing the coding sequence for the proteins or portions thereof to be expressed are obtained as described in Examples 27-29 and cloned into a suitable expression vector. If desired, the nucleic acids may contain the sequences encoding the signal

peptide to facilitate secretion of the expressed protein. For example, the nucleic acid may comprise the sequence of one of SEQ ID NOs: 40-140 and 242-377 listed in Table IV and in the accompanying sequence listing. Alternatively, the nucleic acid may comprise those nucleotides which make up the full coding sequence of one of the sequences of SEQ ID NOs: 40-140 and 242-377 as defined in Table IV above.

5 It will be appreciated that should the extent of the full coding sequence (i.e. the sequence encoding the signal peptide and the mature protein resulting from cleavage of the signal peptide) differ from that listed in Table IV as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the extent of the full coding sequences in the sequences of SEQ ID NOs. 40-140 and 242-377.

10 For example, the sequence of SEQ ID NO: 115 represents an alternatively spliced transcript of a previously identified mRNA. Accordingly, the scope of any claims herein relating to nucleic acids containing the full coding sequence of one of SEQ ID NOs. 40-140 and 242-377 is not to be construed as excluding any readily identifiable variations from or equivalents to the full coding sequences listed in Table IV. Similarly, should the extent of the full length polypeptides differ from those indicated in Table V as a result of any of the preceding factors, the scope of claims relating to polypeptides
15 comprising the amino acid sequence of the full length polypeptides is not to be construed as excluding any readily identifiable variations from or equivalents to the sequences listed in Table V.

Alternatively, the nucleic acid used to express the protein or portion thereof may comprise those nucleotides which encode the mature protein (i.e. the protein created by cleaving the signal peptide off) encoded by one of the sequences of SEQ ID NOs: 40-140 and 242-377 as defined in Table IV above.

20 It will be appreciated that should the extent of the sequence encoding the mature protein differ from that listed in Table IV as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the extent of the sequence encoding the mature protein in the sequences of SEQ ID NOs. 40-140 and 242-377. Accordingly, the scope of any claims herein relating to nucleic acids
25 containing the sequence encoding the mature protein encoded by one of SEQ ID Nos. 40-140 and 242-377 is not to be construed as excluding any readily identifiable variations from or equivalents to the sequences listed in Table IV. Thus, claims relating to nucleic acids containing the sequence encoding the mature protein encompass equivalents to the sequences listed in Table IV, such as sequences encoding biologically active proteins resulting from post-translational modification, enzymatic cleavage, or other readily identifiable variations from or equivalents to the secreted proteins in
30 addition to cleavage of the signal peptide. Similarly, should the extent of the mature polypeptides differ from those indicated in Table V as a result of any of the preceding factors, the scope of claims relating to polypeptides comprising the sequence of a mature protein included in the sequence of one of SEQ ID NOs. 141-241 and 378-513 is not to be construed as excluding any readily identifiable variations from or equivalents to the sequences listed in Table V. Thus, claims relating to polypeptides comprising the sequence of the mature protein encompass equivalents to the sequences

listed in Table IV, such as biologically active proteins resulting from post-translational modification, enzymatic cleavage, or other readily identifiable variations from or equivalents to the secreted proteins in addition to cleavage of the signal peptide. It will also be appreciated that should the biologically active form of the polypeptides included in the sequence of one of SEQ ID NOs. 141-241 and 378-513 or the nucleic acids encoding the biologically active form of the

5 polypeptides differ from those identified as the mature polypeptide in Table V or the nucleotides encoding the mature polypeptide in Table IV as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the amino acids in the biologically active form of the polypeptides and the nucleic acids encoding the biologically active form of the polypeptides. In such instances, the
10 claims relating to polypeptides comprising the mature protein included in one of SEQ ID NOs. 141-241 and 378-513 or nucleic acids comprising the nucleotides of one of SEQ ID NOs. 40-140 and 242-377 encoding the mature protein shall not be construed to exclude any readily identifiable variations from the sequences listed in Table IV and Table V.

In some embodiments, the nucleic acid used to express the protein or portion thereof may comprise those nucleotides which encode the signal peptide encoded by one of the sequences of SEQ ID NOs: 40-140 and 242-377 as
15 defined in Table IV above.

It will be appreciated that should the extent of the sequence encoding the signal peptide differ from that listed in Table IV as a result of a sequencing error, reverse transcription or amplification error, mRNA splicing, post-translational modification of the encoded protein, enzymatic cleavage of the encoded protein, or other biological factors, one skilled in the art would be readily able to identify the extent of the sequence encoding the signal peptide in the
20 sequences of SEQ ID NOs. 40-140 and 242-377. Accordingly, the scope of any claims herein relating to nucleic acids containing the sequence encoding the signal peptide encoded by one of SEQ ID Nos. 40-140 and 242-377 is not to be construed as excluding any readily identifiable variations from the sequences listed in Table IV. Similarly, should the extent of the signal peptides differ from those indicated in Table V as a result of any of the preceding factors, the scope of claims relating to polypeptides comprising the sequence of a signal peptide included in the sequence of one of SEQ ID
25 NOs. 141-241 and 378-513 is not to be construed as excluding any readily identifiable variations from the sequences listed in Table V.

Alternatively, the nucleic acid may encode a polypeptide comprising at least 10 consecutive amino acids of one of the sequences of SEQ ID NOs: 141-241 and 378-513. In some embodiments, the nucleic acid may encode a polypeptide comprising at least 15 consecutive amino acids of one of the sequences of SEQ ID NOs: 141-241 and 378-
30 513. In other embodiments, the nucleic acid may encode a polypeptide comprising at least 25 consecutive amino acids of one of the sequences of SEQ ID NOs: 141-241 and 378-513. In other embodiments, the nucleic acid may encode a polypeptide comprising at least 60, at least 75, at least 100 or more than 100 consecutive amino acids of one of the sequences of SEQ ID Nos: 141-241 and 378-513.

The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767.

The following is provided as one exemplary method to express the proteins encoded by the extended cDNAs corresponding to the 5' ESTs or the nucleic acids described above. First, the methionine initiation codon for the gene and the poly A signal of the gene are identified. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the extended cDNA lacks a poly A signal, this sequence can be added to the construct by, for example, splicing out the Poly A signal from pSG5 (Stratagene) using BglI and Sall restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex Thymidine Kinase promoter and the selectable neomycin gene. The extended cDNA or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the extended cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5' primer and BglII at the 5' end of the corresponding cDNA 3' primer, taking care to ensure that the extended cDNA is positioned in frame with the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1, now containing a poly A signal and digested with BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600ug/ml G418 (Sigma, St. Louis, Missouri). Preferably the expressed protein is released into the culture medium, thereby facilitating purification.

Alternatively, the extended cDNAs may be cloned into pED6dpc2 as described above. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. Preferably, the protein expressed from the extended cDNA is released into the culture medium thereby facilitating purification.

Proteins in the culture medium are separated by gel electrophoresis. If desired, the proteins may be ammonium sulfate precipitated or separated based on size or charge prior to electrophoresis.

As a control, the expression vector lacking a cDNA insert is introduced into host cells or organisms and the proteins in the medium are harvested. The secreted proteins present in the medium are detected using techniques such as Coomassie or silver staining or using antibodies against the protein encoded by the extended cDNA. Coomassie and silver staining techniques are familiar to those skilled in the art.

Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate 5' EST, extended cDNA, or portion thereof. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the 5' EST, extended cDNA, or portion thereof.

Secreted proteins from the host cells or organisms containing an expression vector which contains the extended cDNA derived from a 5' EST or a portion thereof are compared to those from the control cells or organism. The presence of a band in the medium from the cells containing the expression vector which is absent in the medium from the control cells indicates that the extended cDNA encodes a secreted protein. Generally, the band corresponding to the protein encoded by the extended cDNA will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, if the protein expressed from the above expression vectors does not contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector containing an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

The protein encoded by the extended cDNA may be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques.

If antibody production is not possible, the extended cDNA sequence or portion thereof may be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the extended cDNA or portion thereof is inserted in frame with the gene encoding the other half of

the chimera. The other half of the chimera may be β -globin or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to β -globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β -globin gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by

5 protease digestion.

One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene), which encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis et al.,

10 **(Basic Methods in Molecular Biology, L.G. Davis, M.D. Digner, and J.F. Battey, ed., Elsevier Press, NY, 1986)** and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using in vitro translation systems such as the In vitro Express™ Translation Kit (Stratagene).

Following expression and purification of the secreted proteins encoded by the 5' ESTs, extended cDNAs, or

15 fragments thereof, the purified proteins may be tested for the ability to bind to the surface of various cell types as described in Example 31 below. It will be appreciated that a plurality of proteins expressed from these cDNAs may be included in a panel of proteins to be simultaneously evaluated for the activities specifically described below, as well as other biological roles for which assays for determining activity are available.

EXAMPLE 31

20 Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

The proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof are cloned into expression vectors such as those described in Example 30. The proteins are purified by size, charge, immunochromatography or other techniques familiar to those skilled in the art. Following purification, the proteins are labeled using techniques known to those skilled in the art. The labeled proteins are incubated with cells or cell lines derived from a variety of organs or

25 tissues to allow the proteins to bind to any receptor present on the cell surface. Following the incubation, the cells are washed to remove non-specifically bound protein. The labeled proteins are detected by autoradiography. Alternatively, unlabeled proteins may be incubated with the cells and detected with antibodies having a detectable label, such as a fluorescent molecule, attached thereto.

Specificity of cell surface binding may be analyzed by conducting a competition analysis in which various

30 amounts of unlabeled protein are incubated along with the labeled protein. The amount of labeled protein bound to the cell surface decreases as the amount of competitive unlabeled protein increases. As a control, various amounts of an unlabeled protein unrelated to the labeled protein is included in some binding reactions. The amount of labeled protein bound to the cell surface does not decrease in binding reactions containing increasing amounts of unrelated unlabeled protein, indicating that the protein encoded by the cDNA binds specifically to the cell surface.

As discussed above, secreted proteins have been shown to have a number of important physiological effects and, consequently, represent a valuable therapeutic resource. The secreted proteins encoded by the extended cDNAs or portions thereof made according to Examples 27-29 may be evaluated to determine their physiological activities as described below.

5 EXAMPLE 32

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Cytokine, Cell Proliferation or Cell Differentiation Activity

As discussed above, secreted proteins may act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B5, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins encoded by the above extended cDNAs or portions thereof may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references: **Current Protocols in Immunology**, Ed. by J.E. Coligan et al., Greene Publishing Associates and Wiley-Interscience; Takai et al. *J. Immunol.* 137:3494-3500, 1986. Bertagnolli et al. *J. Immunol.* 145:1706-1712, 1990. Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991. Bertagnolli, et al. *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152:1756-1761, 1994.

In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in **Current Protocols in Immunology**. J.E. Coligan et al. Eds., Vol 1 pp. 3.12.1-3.12.14 John Wiley and Sons, Toronto. 1994; and Schreiber, R.D. **Current Protocols in Immunology**, *supra* Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

The proteins encoded by the cDNAs may also be assayed for the ability to regulate the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references: Bottomly, K., Davis, L.S. and Lipsky, P.E., Measurement of Human and Murine Interleukin 2 and Interleukin 4, **Current Protocols in Immunology**, J.E. Coligan et al. Eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 36:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Nordan, R., Measurement of Mouse and Human Interleukin 6 **Current Protocols in Immunology**. J.E. Coligan et al. Eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Bennett, F., Giannotti, J., Clark, S.C. and Turner, K.J., Measurement of Human Interleukin 11 **Current Protocols in Immunology**. J.E. Coligan et al. Eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J., Measurement of Mouse and Human Interleukin 9 **Current Protocols in Immunology**. J.E. Coligan et al., Eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

The proteins encoded by the cDNAs may also be assayed for their ability to regulate T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references: Chapter 3 (In Vitro Assays for Mouse Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans) in **Current Protocols in Immunology**, J.E. Coligan et al. Eds. Greene Publishing Associates and Wiley-Interscience; Weinberger et al., **Proc. Natl. Acad. Sci. USA** 77:6091-6095, 1980; Weinberger et al., **Eur. J. Immunol.** 11:405-411, 1981; Takai et al., **J. Immunol.** 137:3494-3500, 1986; Takai et al., **J. Immunol.** 140:508-512, 1988.

Those proteins which exhibit cytokine, cell proliferation, or cell differentiation activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 33

Assaying the Proteins Expressed from Extended cDNAs or Portions

Thereof for Activity as Immune System Regulators

The proteins encoded by the cDNAs may also be evaluated for their effects as immune regulators. For example, the proteins may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references: Chapter 3 (In Vitro Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) in **Current Protocols in Immunology**, J.E. Coligan et al. Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann et al., **Proc. Natl. Acad. Sci. USA** 78:2488-2492, 1981; Herrmann et al., **J. Immunol.** 128:1968-1974, 1982; Handa et al., **J. Immunol.** 135:1564-1572, 1985; Takai et al., **J. Immunol.** 137:3494-3500, 1986; Takai et al., **J. Immunol.** 140:508-512, 1988; Herrmann et al., **Proc. Natl. Acad. Sci. USA** 78:2488-2492, 1981; Herrmann et al., **J. Immunol.** 128:1968-1974, 1982; Handa et al., **J. Immunol.** 135:1564-1572, 1985; Takai et al., **J. Immunol.** 137:3494-3500, 1986; Bowman et al., **J. Virology** 61:1992-1998; Takai et al., **J. Immunol.** 140:508-512, 1988; Bertagnolli et al., **Cellular Immunology** 133:327-341, 1991; Brown et al., **J. Immunol.** 153:3079-3092, 1994.

The proteins encoded by the cDNAs may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Maliszewski, **J. Immunol.** 144:3028-3033, 1990; Mond, J.J. and Brunswick, M Assays for B Cell Function: *In vitro* Antibody Production, Vol 1 pp. 3.8.1-3.8.16 in **Current Protocols in Immunology**, J.E. Coligan et al Eds., John Wiley and Sons, Toronto. 1994.

The proteins encoded by the cDNAs may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 3 (In Vitro Assays for Mouse Lymphocyte

Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) in **Current Protocols in Immunology**, J.E. Coligan et al. Eds., Greene Publishing Associates and Wiley-Interscience; Takai et al., **J. Immunol.** 137:3494-3500, 1986; Takai et al., **J. Immunol.** 140:508-512, 1988; Bertagnoli et al., **J. Immunol.** 149:3778-3783, 1992.

The proteins encoded by the cDNAs may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Guery et al., **J. Immunol.** 134:536-544, 1995; Inaba et al., **Journal of Experimental Medicine** 173:549-559, 1991; Macatonia et al., **Journal of Immunology** 154:5071-5079, 1995; Porgador et al., **Journal of Experimental Medicine** 182:255-260, 1995; Nair et al., **Journal of Virology** 67:4062-4069, 1993; Huang et al., **Science** 264:961-965, 1994; Macatonia et al., **Journal of Experimental Medicine** 169:1255-1264, 1989; Bhardwaj et al., **Journal of Clinical Investigation** 94:797-807, 1994; and Inaba et al., **Journal of Experimental Medicine** 172:631-640, 1990.

The proteins encoded by the cDNAs may also be evaluated for their influence on the lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Darzynkiewicz et al., **Cytometry** 13:795-808, 1992; Gorczyca et al., **Leukemia** 7:659-670, 1993; Gorczyca et al., **Cancer Research** 53:1945-1951, 1993; Itoh et al., **Cell** 66:233-243, 1991; Zacharchuk, **Journal of Immunology** 145:4037-4045, 1990; Zamai et al., **Cytometry** 14:891-897, 1993; Gorczyca et al., **International Journal of Oncology** 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., **Blood** 84:111-117, 1994; Fine et al., **Cellular immunology** 155:111-122, 1994; Galy et al., **Blood** 85:2770-2778, 1995; Toki et al., **Proc. Nat. Acad Sci. USA** 88:7548-7551, 1991.

Those proteins which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of immune activity is beneficial. For example, the protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus,

myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

5 Using the proteins of the invention it may also be possible to regulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T-cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

10 Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte
15 antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7
20 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an
25 immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed
30 using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models

of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/pr/pr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to T cells in vivo, thereby activating the T cells.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acids encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 macroglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 34

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Hematopoiesis Regulating Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Johansson et al. **Cellular Biology** 15:141-151, 1995; Keller et al., **Molecular and Cellular Biology** 13:473-486, 1993; McClanahan et al., **Blood** 81:2903-2915, 1993.

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Freshney, M.G. Methylcellulose Colony Forming Assays, in **Culture of Hematopoietic Cells**. R.I. Freshney, et al. Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., **Proc. Natl. Acad. Sci. USA** 89:5907-5911, 1992; McNiece, I.K. and Briddell, R.A. Primitive Hematopoietic Colony Forming Cells with High Proliferative Potential, in **Culture of Hematopoietic Cells**. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., **Experimental Hematology** 22:353-359, 1994; Ploemacher, R.E. Cobblestone Area Forming Cell Assay, In **Culture of Hematopoietic Cells**. R.I. Freshney, et al. Eds. pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Spooncer, E., Dexter, M. and Allen, T. Long Term Bone Marrow Cultures in the Presence of Stromal Cells, in **Culture of Hematopoietic Cells**. R.I. Freshney, et al. Eds.

pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; and Sutherland, H.J. Long Term Culture Initiating Cell Assay, in **Culture of Hematopoietic Cells**. R.I. Freshney, et al. Eds. pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Those proteins which exhibit hematopoiesis regulatory activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoiesis is beneficial. For example, a protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 35

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Tissue Growth

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in International Patent Publication No. WO95/16035, International Patent Publication No. WO95/05846 and International Patent Publication No. WO91/07491.

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H1 and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Those proteins which are involved in the regulation of tissue growth may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of tissue growth is beneficial. For example, a protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or

nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and
5 other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair
10 processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

15 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to
20 tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate
25 growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

30 The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e., for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as

Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle
10 (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

15 A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

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EXAMPLE 36

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Reproductive Hormones or Cell Movement

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their ability to regulate reproductive hormones, such as follicle stimulating hormone. Numerous assays for such activity are familiar to
25 those skilled in the art, including the assays disclosed in the following references: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986. Chapter 6.12 (Measurement of Alpha and Beta Chemokines) *Current Protocols in Immunology*, J.E. Coligan et al. Eds. Greene Publishing Associates and Wiley-Interscience; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al. *APMIS* 103:140-146, 1995; Muller
30 et al. *Eur. J. Immunol.* 25:1744-1748; Gruber et al. *J. of Immunol.* 152:5860-5867, 1994; Johnston et al. *J. of Immunol.* 153:1762-1768, 1994.

Those proteins which exhibit activity as reproductive hormones or regulators of cell movement may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of reproductive hormones or cell movement are beneficial. For example, a protein of the present invention may also exhibit activin- or inhibin-related

activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals.

- 5 Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-B group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive
- 10 performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 36A

15 Assaying the Proteins Expressed from Extended cDNAs or
Portions Thereof for Chemotactic/Chemokinetic Activity

- The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for chemotactic/chemokinetic activity. For example, a protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells,
- 20 eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

- 25 A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 30 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12,

Measurement of alpha and beta Chemokins 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Mueller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol, 153:1762-1768, 1994.

EXAMPLE 37

5

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Blood Clotting

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res.

10 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Those proteins which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to

15 enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke). Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the

20 expression of the proteins as desired.

EXAMPLE 38

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Involvement in Receptor/Ligand Interactions

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for their involvement

25 in receptor/ligand interactions. Numerous assays for such involvement are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 7.28 (Measurement of Cellular Adhesion under Static Conditions 7.28.1-7.28.22) in Current Protocols in Immunology, J.E. Coligan et al. Eds. Greene Publishing Associates and Wiley-Interscience; Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160, 1989; Stoltenborg et al., J. Immunol. Methods

30 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995; Gyuris et al., Cell 75:791-803, 1993.

For example, the proteins of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion

molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

EXAMPLE 38A

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Anti-Inflammatory Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

EXAMPLE 38B

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Tumor Inhibition Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for tumor inhibition activity. In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or

circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

EXAMPLE 39

Identification of Proteins which Interact with Polypeptides Encoded by Extended cDNAs

Proteins which interact with the polypeptides encoded by extended cDNAs or portions thereof, such as receptor proteins, may be identified using two hybrid systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech). As described in the manual accompanying the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech), the extended cDNAs or portions thereof, are inserted into an expression vector such that they are in frame with DNA encoding the DNA binding domain of the yeast transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins which might interact with the polypeptides encoded by the extended cDNAs or portions thereof are inserted into a second expression vector such that they are in frame with DNA encoding the activation domain of GAL4. The two expression plasmids are transformed into yeast and the yeast are plated on selection medium which selects for expression of selectable markers on each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene. Transformants capable of growing on medium lacking histidine are screened for GAL4 dependent lacZ expression. Those cells which are positive in both the histidine selection and the lacZ assay contain plasmids encoding proteins which interact with the polypeptide encoded by the extended cDNAs or portions thereof.

Alternatively, the system described in Lustig et al., Methods in Enzymology 283: 83-99 (1997) may be used for identifying molecules which interact with the polypeptides encoded by extended cDNAs. In such systems, *in vitro* transcription reactions are performed on a pool of vectors containing extended cDNA inserts cloned downstream of a promoter which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into *Xenopus laevis* oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a desired activity or for interaction with a known polypeptide.

Proteins or other molecules interacting with polypeptides encoded by extended cDNAs can be found by a variety of additional techniques. In one method, affinity columns containing the polypeptide encoded by the extended cDNA or a portion thereof can be constructed. In some versions, of this method the affinity column contains chimeric proteins in which the protein encoded by the extended cDNA or a portion thereof is fused to glutathione S-transferase.

5 A mixture of cellular proteins or pool of expressed proteins as described above and is applied to the affinity column. Proteins interacting with the polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen et al. Electrophoresis, 18, 588-598 (1997). Alternatively, the proteins retained on the affinity column can be purified by electrophoresis based methods and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

10 Proteins interacting with polypeptides encoded by extended cDNAs or portions thereof can also be screened by using an Optical Biosensor as described in Edwards & Leatherbarrow, Analytical Biochemistry, 246, 1-6 (1997). The main advantage of the method is that it allows the determination of the association rate between the protein and other interacting molecules. Thus, it is possible to specifically select interacting molecules with a high or low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethyl dextran matrix) and a sample of test
15 molecules is placed in contact with the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/ or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extend a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can be one of the polypeptides encoded by extended cDNAs or a portion thereof and the test sample can be a collection of proteins extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or
20 chemical libraries, or phage displayed peptides. The tissues or cells from which the test proteins are extracted can originate from any species.

In other methods, a target protein is immobilized and the test population is a collection of unique polypeptides encoded by the extended cDNAs or portions thereof.

To study the interaction of the proteins encoded by the extended cDNAs or portions thereof with drugs, the
25 microdialysis coupled to HPLC method described by Wang et al., Chromatographia, 44, 205-208(1997) or the affinity capillary electrophoresis method described by Busch et al., J. Chromatogr. 777:311-328 (1997), the disclosures of which are incorporated herein by reference can be used.

The system described in U.S. Patent No. 5,654,150 may also be used to identify molecules which interact with the polypeptides encoded by the extended cDNAs. In this system, pools of extended cDNAs are transcribed and
30 translated *in vitro* and the reaction products are assayed for interaction with a known polypeptide or antibody.

It will be appreciated by those skilled in the art that the proteins expressed from the extended cDNAs or portions may be assayed for numerous activities in addition to those specifically enumerated above. For example, the expressed proteins may be evaluated for applications involving control and regulation of inflammation, tumor

proliferation or metastasis, infection, or other clinical conditions. In addition, the proteins expressed from the extended cDNAs or portions thereof may be useful as nutritional agents or cosmetic agents.

The proteins expressed from the extended cDNAs or portions thereof may be used to generate antibodies capable of specifically binding to the expressed protein or fragments thereof as described in Example 40 below. The antibodies may be capable of binding a full length protein encoded by one of the sequences of SEQ ID NOs. 40-140 and 242-377, a mature protein encoded by one of the sequences of SEQ ID NOs. 40-140 and 242-377, or a signal peptide encoded by one of the sequences of SEQ ID Nos. 40-140 and 242-377. Alternatively, the antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 10 amino acids of the sequences of SEQ ID NOs: 141-241 and 378-513. In some embodiments, the antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 15 amino acids of the sequences of SEQ ID NOs: 141-241 and 378-513. In other embodiments, the antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 25 amino acids of the sequences of SEQ ID NOs: 141-241 and 378-513. In further embodiments, the antibodies may be capable of binding fragments of the proteins expressed from the extended cDNAs which comprise at least 40 amino acids of the sequences of SEQ ID NOs: 141-241 and 378-513.

EXAMPLE 40

Production of an Antibody to a Human Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells as described in Example 30. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

A. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as Elisa, as originally described by Engvall, E., *Meth. Enzymol.* 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2.

B. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

V. Use of Extended cDNAs or Portions Thereof as Reagents

The extended cDNAs of the present invention may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the extended cDNAs (or genomic DNAs obtainable therefrom) may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, sequences from the extended cDNAs (or genomic DNAs obtainable therefrom) may be used to design PCR primers to be used in isolation, diagnostic, or forensic procedures.

EXAMPLE 41

Preparation of PCR Primers and Amplification of DNA

The extended cDNAs (or genomic DNAs obtainable therefrom) may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. The PCR primers are at least 10 bases, and preferably at least 12, 15, or 17 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C

ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in Methods in Molecular Biology 67: Humana Press, Totowa 1997. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 42

Use of Extended cDNAs as Probes

Probes derived from extended cDNAs or portions thereof (or genomic DNAs obtainable therefrom) may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded and may be made using techniques known in the art, including in vitro transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or in vitro transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 30 above.

PCR primers made as described in Example 41 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 43-47 below. Such analyses may utilize detectable probes or primers based on the sequences of the extended cDNAs isolated using the 5' ESTs (or genomic DNAs obtainable therefrom).

EXAMPLE 43

Forensic Matching by DNA Sequencing

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the extended cDNAs (or

genomic DNAs obtainable therefrom), is then utilized in accordance with Example 41 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample. Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

EXAMPLE 44

10 Positive Identification by DNA Sequencing

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of sequences from Table IV and the appended sequence listing. Preferably, 20 to 50 different primers are used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 41. Each of these DNA segments is sequenced, using the methods set forth in Example 43. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

EXAMPLE 45

20 Southern Blot Forensic Identification

The procedure of Example 44 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis et al. (Basic Methods in Molecular Biology, 1986, Elsevier Press. pp 62-65).

A panel of probes based on the sequences of the extended cDNAs (or genomic DNAs obtainable therefrom), or fragments thereof of at least 10 bases, are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis et al., supra). Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30

nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). In other embodiments, the probe comprises at least 40, at least 50, at least 75, at least 100, at least 150, or at least 200 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom).

Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing from the hybridization of a large sample of extended cDNAs (or genomic DNAs obtainable therefrom) will be a unique identifier. Since the restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the number of extended cDNA probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

EXAMPLE 46

Dot Blot Identification Procedure

Another technique for identifying individuals using the extended cDNA sequences disclosed herein utilizes a dot blot hybridization technique.

Genomic DNA is isolated from nuclei of subject to be identified. Oligonucleotide probes of approximately 30 bp in length are synthesized that correspond to at least 10, preferably 50 sequences from the extended cDNAs or genomic DNAs obtainable therefrom. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with P^{32} using polynucleotide kinase (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose filter containing the genomic sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis et al. *supra*). The ^{32}P labeled DNA fragments are sequentially hybridized with successively stringent conditions to detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood et al., *Proc. Natl. Acad. Sci. USA* 82(6):1585-1588 (1985)). A unique pattern of dots distinguishes one individual from another individual.

Extended cDNAs or oligonucleotides containing at least 10 consecutive bases from these sequences can be used as probes in the following alternative fingerprinting technique. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom). In other embodiments, the probe comprises at least 40, at least 50, at least 75, at least 100, at least 150, or at least 200 consecutive nucleotides from the extended cDNA (or genomic DNAs obtainable therefrom).

Preferably, a plurality of probes having sequences from different genes are used in the alternative fingerprinting technique. Example 47 below provides a representative alternative fingerprinting procedure in which the probes are derived from extended cDNAs.

EXAMPLE 47

5 Alternative "Fingerprint" Identification Technique

20-mer oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, of extended cDNA sequences (or genomic DNAs obtainable therefrom) using commercially available oligonucleotide services such as Genset, Paris, France. Cell samples from the test subject are processed for DNA using techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are
10 applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into wells and separated on 0.8% agarose gels. The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with P³². The nitrocellulose is prehybridized
15 with blocking solution and hybridized with the labeled probes. Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

The antibodies generated in Examples 30 and 40 above may be used to identify the tissue type or cell species
20 from which a sample is derived as described above.

EXAMPLE 48

Identification of Tissue Types or Cell Species by Means of Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of
25 antibody preparations according to Examples 30 and 40 which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that
30 reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

A. Immunohistochemical Techniques

Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, H., Chap. 26 in: **Basic 503 Clinical Immunology**, 3rd Ed. Lange, Los Altos, California (1980) or Rose, N. et al., Chap. 12 in: **Methods in Immunodiagnosis**, 2d Ed. John Wiley 503 Sons, New York (1980).

A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below. Alternatively, the specific antitissue antibodies can be labeled with ferritin or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example ^{125}I , and detected by overlaying the antibody treated preparation with photographic emulsion.

Preparations to carry out the procedures can comprise monoclonal or polyclonal antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about 4 μm , unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that signal using appropriate standards.

B. Identification of Tissue Specific Soluble Proteins

The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice

in the art. Insoluble cell components such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis, L. et al., Section 19-2 in: **Basic Methods in Molecular Biology** (P. Leder, ed), Elsevier, New York (1986), using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient volume of from 5 to 55 μ l, and containing from about 1 to 100 μ g protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. et al., (above) Section 19-3. One set of nitrocellulose blots is stained with Coomassie Blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 30 and 40. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

In either procedure A or B, a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other approaches, either the primary or secondary antibody is conjugated to a biotin molecule, which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

The visualization of tissue specific antigen binding at levels above those seen in control tissues to one or more tissue specific antibodies, prepared from the gene sequences identified from extended cDNA sequences, can identify tissues of unknown origin, for example, forensic samples, or differentiated tumor tissue that has metastasized to foreign bodily sites.

In addition to their applications in forensics and identification, extended cDNAs (or genomic DNAs obtainable therefrom) may be mapped to their chromosomal locations. Example 49 below describes radiation hybrid (RH) mapping of human chromosomal regions using extended cDNAs. Example 50 below describes a representative procedure for mapping an extended cDNA (or a genomic DNA obtainable therefrom) to its location on a human chromosome. Example 51 below describes mapping of extended cDNAs (or genomic DNAs obtainable therefrom) on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH).

EXAMPLE 49

Radiation hybrid mapping of Extended cDNAs to the human genome

Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones containing different portions of the human genome. This technique is described by Benham et al. (*Genomics* 4:509-517, 1989) and Cox et al., (*Science* 250:245-250, 1990). The random and independent nature of the subclones permits efficient mapping of any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering extended cDNAs (or genomic DNAs obtainable therefrom). In this approach, the frequency of breakage between markers is used to measure distance, allowing construction of fine resolution maps as has been done using conventional ESTs (Schuler et al., *Science* 274:540-546, 1996).

RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH) and thymidine kinase (TK) (Foster et al., *Genomics* 33:185-192, 1996), the region surrounding the Gorlin syndrome gene (Obermayr et al., *Eur. J. Hum. Genet.* 4:242-245, 1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers et al., *Genomics* 29:170-178, 1995), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer et al., *Genomics* 14:574-584, 1992) and 13 loci on the long arm of chromosome 5 (Warrington et al., *Genomics* 11:701-708, 1991).

EXAMPLE 50

Mapping of Extended cDNAs to Human Chromosomes using PCR techniques

Extended cDNAs (or genomic DNAs obtainable therefrom) may be assigned to human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from the extended cDNA sequence (or the sequence of a genomic DNA obtainable therefrom) to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich, H.A., PCR Technology; Principles and Applications for DNA Amplification. 1992. W.H. Freeman and Co., New York.

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase, and 1 μ Cu of a 32 P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance between the ends of the primer sequences in the extended cDNA from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-rodent somatic cell hybrids, BIOS

PCRable DNA (BIOS Corporation) and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS, Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets of human chromosomes for the presence of a given extended cDNA (or genomic DNA obtainable therefrom). DNA is isolated from the somatic
5 hybrids and used as starting templates for PCR reactions using the primer pairs from the extended cDNAs (or genomic DNAs obtainable therefrom). Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the extended cDNA (or genomic DNA obtainable therefrom) will yield an amplified fragment. The extended cDNAs (or genomic DNAs obtainable therefrom) are assigned to a chromosome by analysis of the segregation pattern of PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell
10 hybrids that give rise to an amplified fragment is the chromosome containing that extended cDNA (or genomic DNA obtainable therefrom). For a review of techniques and analysis of results from somatic cell gene mapping experiments. (See Ledbetter et al., *Genomics* 6:475-481 (1990).)

Alternatively, the extended cDNAs (or genomic DNAs obtainable therefrom) may be mapped to individual chromosomes using FISH as described in Example 51 below.

15

EXAMPLE 51

Mapping of Extended 5' ESTs to Chromosomes

Using Fluorescence in situ Hybridization

Fluorescence in situ hybridization allows the extended cDNA (or genomic DNA obtainable therefrom) to be mapped to a particular location on a given chromosome. The chromosomes to be used for fluorescence in situ
20 hybridization techniques may be obtained from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of an extended cDNA (or genomic DNA obtainable therefrom) is obtained by FISH as described by Cherif et al. (*Proc. Natl. Acad. Sci. U.S.A.*, 87:6639-6643, 1990). Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-stimulated blood cell donors. PHA-stimulated lymphocytes from healthy males are cultured for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10
25 μ M) is added for 17 h, followed by addition of 5-bromodeoxyuridine (5-BudR, 0.1 mM) for 6 h. Colcemid (1 μ g/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide and air dried. The extended cDNA (or genomic DNA obtainable therefrom) is labeled with biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda Research
30 Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia, Upssala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 μ g/ml), rinsed three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are denatured in 70% formamide, 2 X SSC for 2 min at

70°C, then dehydrated at 4°C. The slides are treated with proteinase K (10 µg/100 ml in 20 mM Tris-HCl, 2 mM CaCl₂) at 37°C for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is detected by avidin-FITC and amplified with additional layers of
5 biotinylated goat anti-avidin and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif et al., *supra.*). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular extended cDNA (or genomic DNA obtainable therefrom) may be localized to a particular cytogenetic R-band on a given
10 chromosome.

Once the extended cDNAs (or genomic DNAs obtainable therefrom) have been assigned to particular chromosomes using the techniques described in Examples 49-51 above, they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

EXAMPLE 52

15 Use of Extended cDNAs to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes of the organism from which
20 the extended cDNAs (or genomic DNAs obtainable therefrom) are obtained. This approach is described in Ramaiah Nagaraja et al. **Genome Research** 7:210-222, March 1997. Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector. The YAC inserts are screened using PCR or other methods to determine whether they include the extended cDNA (or genomic DNA obtainable therefrom) whose position is to be determined. Once an insert has been found which includes the extended cDNA (or genomic DNA obtainable therefrom),
25 the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome or in the region from which the extended cDNA (or genomic DNA obtainable therefrom) was derived. This process can be repeated for each insert in the YAC library to determine the location of each of the extended cDNAs (or genomic DNAs obtainable therefrom) relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms
30 chromosomes may be obtained.

As described in Example 53 below extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

EXAMPLE 53

Identification of genes associated with hereditary diseases or drug response

This example illustrates an approach useful for the association of extended cDNAs (or genomic DNAs obtainable therefrom) with particular phenotypic characteristics. In this example, a particular extended cDNA (or genomic DNA obtainable therefrom) is used as a test probe to associate that extended cDNA (or genomic DNA obtainable therefrom) with a particular phenotypic characteristic.

5 Extended cDNAs (or genomic DNAs obtainable therefrom) are mapped to a particular location on a human chromosome using techniques such as those described in Examples 49 and 50 or other techniques known in the art. A search of Mendelian Inheritance in Man (V. McKusick, **Mendelian Inheritance in Man** (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which contains the extended cDNA (or genomic DNA obtainable therefrom) to be a very gene rich region containing several known genes and several
10 diseases or phenotypes for which genes have not been identified. The gene corresponding to this extended cDNA (or genomic DNA obtainable therefrom) thus becomes an immediate candidate for each of these genetic diseases.

Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the extended cDNA (or genomic DNA obtainable therefrom) are used to screen genomic DNA, mRNA or cDNA obtained from the patients. Extended cDNAs (or genomic DNAs obtainable therefrom) that are not amplified in the patients can
15 be positively associated with a particular disease by further analysis. Alternatively, the PCR analysis may yield fragments of different lengths when the samples are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the extended cDNA may be responsible for the genetic disease.

VI. Use of Extended cDNAs (or genomic DNAs obtainable therefrom) to Construct Vectors

20 The present extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to construct secretion vectors capable of directing the secretion of the proteins encoded by genes inserted in the vectors. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 54 below.

25 EXAMPLE 54

Construction of Secretion Vectors

The secretion vectors of the present invention include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

30 A signal sequence from an extended cDNA (or genomic DNA obtainable therefrom), such as one of the signal sequences in SEQ ID NOs: 40-140 and 242-377 as defined in Table IV above, is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide. The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the

extended cDNA (or genomic DNA obtainable therefrom). Suitable hosts include mammalian cells, tissues or organisms; avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Many nucleic acid backbones suitable for use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and hplc. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors, the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

The extended cDNAs or 5' ESTs may also be used to clone sequences located upstream of the extended cDNAs or 5' ESTs which are capable of regulating gene expression, including promoter sequences, enhancer sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 55 describes a method for cloning sequences upstream of the extended cDNAs or 5' ESTs.

EXAMPLE 55

Use of Extended cDNAs or 5' ESTs to Clone UpstreamSequences from Genomic DNA

Sequences derived from extended cDNAs or 5' ESTs may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the
5 GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions using an outer adaptor primer provided in the kit and an outer gene specific primer. The gene specific primer
10 should be selected to be specific for the extended cDNA or 5' EST of interest and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. Each first PCR reaction contains 5ng of genomic DNA, 5 µl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 µM each of outer adaptor primer and outer gene specific primer, 1.1 mM of Mg(OAc)₂, and 1 µl of the Tth polymerase 50X mix in a total volume of 50 µl. The reaction cycle for the first PCR reaction is as follows: 1 min @ 94°C / 2 sec @ 94°C, 3 min @
15 72°C (7 cycles) / 2 sec @ 94°C, 3 min @ 67°C (32 cycles) / 5 min @ 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR reaction. For example, 5 µl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 µl volume having a composition identical to that of the first PCR reaction except
20 the nested primers are used. The first nested primer is specific for the adaptor, and is provided with the GenomeWalker™ kit. The second nested primer is specific for the particular extended cDNA or 5' EST for which the promoter is to be cloned and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. The reaction parameters of the second PCR reaction are as follows: 1 min @ 94°C / 2 sec @ 94°C, 3 min @ 72°C (6 cycles) / 2 sec @ 94°C, 3 min @ 67°C (25 cycles) / 5 min @ 67°C

25 The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques. Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated oligonucleotide comprising at least 15 nucleotides from the extended cDNA or 5' EST sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing
30 the extended cDNA or EST sequence are isolated as described in Example 29 above. Thereafter, the single stranded DNA containing the extended cDNA or EST sequence is released from the beads and converted into double stranded DNA using a primer specific for the extended cDNA or 5' EST sequence or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. DNAs containing the 5' EST or extended cDNA sequences are identified by colony PCR or colony hybridization.

Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the extended cDNAs or 5' ESTs with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

- 5 In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example 56.

EXAMPLE 56

Identification of Promoters in Cloned Upstream Sequences

- The genomic sequences upstream of the extended cDNAs or 5' ESTs are cloned into a suitable promoter
10 reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, p β gal-Basic, p β gal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech. Briefly, each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, β galactosidase, or green fluorescent protein. The sequences upstream of the extended cDNAs or 5' ESTs are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The
15 level of reporter protein is assayed and compared to the level obtained from a vector which lacks an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert. If necessary, the upstream sequences can be cloned into vectors which contain an enhancer for augmenting transcription levels from weak promoter sequences. A significant level of expression above that observed with the vector lacking an insert indicates that a promoter sequence is present in the
20 inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the results of the above described determination of expression patterns of the extended cDNAs and ESTs. For example, if the expression pattern analysis indicates that the mRNA corresponding to a particular extended cDNA or 5' EST is expressed in fibroblasts, the promoter reporter vector may be introduced into a human fibroblast cell line.

- 25 Promoter sequences within the upstream genomic DNA may be further defined by constructing nested deletions in the upstream DNA using conventional techniques such as Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether the deletion has reduced or obliterated promoter activity. In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate
30 potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

EXAMPLE 57

Cloning and Identification of Promoters

Using the method described in Example 55 above with 5' ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA TTG CCT G (SEQ ID NO:29) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:30), the promoter having the internal designation P13H2 (SEQ ID NO:31) was obtained.

5 Using the primer pairs GTA CCA GGGG ACT GTG ACC ATT GC (SEQ ID NO:32) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:33), the promoter having the internal designation P15B4 (SEQ ID NO:34) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:35) and GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:36), the promoter having the internal designation P29B6 (SEQ ID NO:37) was obtained.

Figure 8 provides a schematic description of the promoters isolated and the way they are assembled with the
10 corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start sites using the computer program MatInspector release 2.0, August 1996.

Figure 9 describes the transcription factor binding sites present in each of these promoters. The columns
15 labeled matrix provides the name of the MatInspector matrix used. The column labeled position provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled "orientation" indicates the DNA strand on which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of
20 the site found.

The promoters and other regulatory sequences located upstream of the extended cDNAs or 5' ESTs may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described in Example 26 above. For
25 example, if a promoter which confers a high level of expression in muscle is desired, the promoter sequence upstream of an extended cDNA or 5' EST derived from an mRNA which is expressed at a high level in muscle, as determined by the method of Example 26, may be used in the expression vector.

Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able to drive expression of the inserted gene. The
30 promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences using the procedures of Examples 55-57, proteins which interact with the promoter may be identified as described in Example 58 below.

5

EXAMPLE 58**Identification of Proteins Which Interact with Promoter Sequences, Upstream****Regulatory Sequences, or mRNA**

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the art. Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1). Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem.

A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to select cells expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression vectors or in vitro transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNase protection analysis.

VII. Use of Extended cDNAs (or Genomic DNAs Obtainable Therefrom) in Gene Therapy

The present invention also comprises the use of extended cDNAs (or genomic DNAs obtainable therefrom) in gene therapy strategies, including antisense and triple helix strategies as described in Examples 57 and 58 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the expression of the protein encoded by the mRNA. The antisense sequences may prevent gene expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes

to translate the mRNA. Alternatively, the antisense sequences may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

5

EXAMPLE 59**Preparation and Use of Antisense Oligonucleotides**

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the extended cDNA (or genomic DNA obtainable therefrom).

The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an
10 intracellular duplex having sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green et al., *Ann. Rev. Biochem.* 55:569-597 (1986) and Izant and Weintraub, *Cell* 36:1007-1015 (1984).

In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from
15 that which is normally transcribed in the cell. The antisense molecules may be transcribed using in vitro transcription systems such as those which employ T7 or SP6 polymerase to generate the transcript. Another approach involves transcription of the antisense nucleic acids in vivo by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be
20 synthesized in vitro. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity. Examples of modifications suitable for use in antisense strategies are described by Rossi et al., *Pharmacol. Ther.* 50(2):245-254, (1991).

25 Various types of antisense oligonucleotides complementary to the sequence of the extended cDNA (or genomic DNA obtainable therefrom) may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International Application No. PCT WO94/23026 are used. In these molecules, the 3' end or both the 3' and 5' ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense
30 oligonucleotides.

In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141.

In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523 are used. These double- or single-stranded oligonucleotides comprise one or

more, respectively, inter- or intra-oligonucleotide covalent cross-linkages, wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or
5 nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522 may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefor. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop"
10 structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2 are used. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the transcription factor by sequestering the factor.

15 Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732 is also contemplated. Because these molecules have no free ends, they are more resistant to degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be determined using in
20 vitro expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection or transfection using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsidated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression vector. The expression vector may be any of a variety of expression vectors known in the art, including retroviral or viral vectors, vectors capable of
25 extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between $1 \times 10^{-10} \text{M}$ to $1 \times 10^{-4} \text{M}$. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use in vivo. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of
30 oligonucleotide approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., *supra*.

5 In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The extended cDNAs of the present invention (or genomic DNAs obtainable therefrom) may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with
10 a particular gene. The extended cDNAs (or genomic DNAs obtainable therefrom) of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, a portion of the extended cDNA (or genomic DNA obtainable therefrom) can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also
15 inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences from the extended cDNA or from the gene corresponding to the extended cDNA are contemplated within the scope of this invention.

EXAMPLE 60

Preparation and use of Triple Helix Probes

20 The sequences of the extended cDNAs (or genomic DNAs obtainable therefrom) are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide
25 synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

30 Treated cells are monitored for altered cell function or reduced gene expression using techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target gene corresponding to the extended cDNA from which the oligonucleotide was derived with known gene sequences that have been associated with a particular function. The cell functions can also be

predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the extended cDNA is associated with the disease using techniques described in Example 53.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced in vivo using the techniques described above and in Example 59 at a dosage calculated based on the in vitro
5 results, as described in Example 59.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. (*Science* 245:967-
10 971 (1989)).

EXAMPLE 61

Use of Extended cDNAs to Express an Encoded Protein in a Host Organism

The extended cDNAs of the present invention may also be used to express an encoded protein in a host organism to produce a beneficial effect. In such procedures, the encoded protein may be transiently expressed in the
15 host organism or stably expressed in the host organism. The encoded protein may have any of the activities described above. The encoded protein may be a protein which the host organism lacks or, alternatively, the encoded protein may augment the existing levels of the protein in the host organism.

A full length extended cDNA encoding the signal peptide and the mature protein, or an extended cDNA encoding only the mature protein is introduced into the host organism. The extended cDNA may be introduced into the host
20 organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

Alternatively, the extended cDNA may be cloned into an expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene
25 therapy, including viral or retroviral vectors.

The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells in vitro. Cells containing the expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein to produce a beneficial effect.

30

EXAMPLE 62

Use Of Signal Peptides Encoded By 5' Ests Or Sequences

Obtained Therefrom To Import Proteins Into Cells

The short core hydrophobic region (h) of signal peptides encoded by the 5'ESTS or extended cDNAs derived from the 5'ESTs of the present invention may also be used as a carrier to import a peptide or a protein of interest, so-

called cargo, into tissue culture cells (Lin *et al.*, *J. Biol. Chem.*, 270: 14225-14258 (1995); Du *et al.*, *J. Peptide Res.*, 51: 235-243 (1998); Rojas *et al.*, *Nature Biotech.*, 16: 370-375 (1998)).

When cell permeable peptides of limited size (approximately up to 25 amino acids) are to be translocated across cell membrane, chemical synthesis may be used in order to add the h region to either the C-terminus or the N-terminus to the cargo peptide of interest. Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can be genetically engineered, using techniques familiar to those skilled in the art, in order to link the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA sequence coding for a cargo polypeptide. Such genetically engineered nucleic acids are then translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then simply incubated with the cell permeable polypeptide which is then translocated across the membrane.

This method may be applied to study diverse intracellular functions and cellular processes. For instance, it has been used to probe functionally relevant domains of intracellular proteins and to examine protein-protein interactions involved in signal transduction pathways (Lin *et al.*, *supra*; Lin *et al.*, *J. Biol. Chem.*, 271: 5305-5308 (1996); Rojas *et al.*, *J. Biol. Chem.*, 271: 27456-27461 (1996); Liu *et al.*, *Proc. Natl. Acad. Sci. USA*, 93: 11819-11824 (1996); Rojas *et al.*, *Bioch. Biophys. Res. Commun.*, 234: 675-680 (1997)).

Such techniques may be used in cellular therapy to import proteins producing therapeutic effects. For instance, cells isolated from a patient may be treated with imported therapeutic proteins and then re-introduced into the host organism.

Alternatively, the h region of signal peptides of the present invention could be used in combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form triple helices, as described in examples 59 and 60 respectively, in order to inhibit processing and maturation of a target cellular RNA.

EXAMPLE 63

Reassembling & Resequencing of Clones

Full length cDNA clones obtained by the procedure described in Example 27 were double-sequenced. These sequences were assembled and the resulting consensus sequences were then reanalyzed. Open reading frames were reassigned following essentially the same process as the one described in Example 27.

After this reanalysis process a few abnormalities were revealed. The sequences presented in SEQ ID NOs: 47, 73, 79, 89, 91, 96, 126, 128, 134, and 139 are apparently unlikely to be genuine full length cDNAs. These clones are missing a stop codon and are thus more probably 3' truncated cDNA sequences. Similarly, the sequences presented in SEQ ID NOs: 45, 50, 54, 57, 73, 74, 89, 92, 95, 98, 126, 129, 130, 131 and 139 may also not be genuine full length cDNAs based on homology studies with existing protein sequences. Although both of these sequences encode a potential start methionine each could represent a 5' truncated cDNA.

In addition, SEQ ID NO: 115 was found to be an alternatively spliced transcript and the identities of some of the bases in SEQ ID NO: 131 were corrected.

Finally, after the reassignment of open reading frames for the clones, new open reading frames were chosen in some instances. For example, in the case of SEQ ID NOs: 41, 47, 50, 52, 54-56, 58, 59, 61, 74, 75, 79, 84, 89, 91, 92, 96, 98, 103, 105, 106, 126, 129, 131, and 133 the new open reading frames were no longer predicted to contain a signal peptide.

As discussed above, Table IV provides the sequence identification numbers of the extended cDNAs of the present invention, the locations of the full coding sequences in SEQ ID NOs: 40-140 and 242-377 (i.e. the nucleotides encoding both the signal peptide and the mature protein, listed under the heading FCS location in Table IV), the locations of the nucleotides in SEQ ID NOs: 40-140 and 242-377 which encode the signal peptides (listed under the heading SigPep Location in Table IV), the locations of the nucleotides in SEQ ID NOs: 40-140 and 242-377 which encode the mature proteins generated by cleavage of the signal peptides (listed under the heading Mature Polypeptide Location in Table IV), the locations in SEQ ID NOs: 40-140 and 242-377 of stop codons (listed under the heading Stop Codon Location in Table IV) the locations in SEQ ID NOs: 40-140 and 242-377 of polyA signals (listed under the heading g PolyA Signal Location in Table IV) and the locations of polyA sites (listed under the heading PolyA Site Location in Table IV).

As discussed above, Table V lists the sequence identification numbers of the polypeptides of SEQ ID NOs: 141-241 and 378-513, the locations of the amino acid residues of SEQ ID NOs: 141-241 and 378-513 in the full length polypeptide (second column), the locations of the amino acid residues of SEQ ID NOs: 141-241 and 378-513 in the signal peptides (third column), and the locations of the amino acid residues of SEQ ID NOs: 141-241 and 379-513 in the mature polypeptide created by cleaving the signal peptide from the full length polypeptide (fourth column). In Table V, and in the appended sequence listing, the first amino acid of the mature protein resulting from cleavage of the signal peptide is designated as amino acid number 1 and the first amino acid of the signal peptide is designated with the appropriate negative number, in accordance with the regulations governing sequence listings.

EXAMPLE 64

Functional Analysis of Predicted Protein Sequences

Following double-sequencing, new contigs were assembled for each of the extended cDNAs of the present invention and each was compared to known sequences available at the time of filing. These sequences originate from the following databases: Genbank (release 108 and daily releases up to October, 15, 1998), Genseq (release 32) PIR (release 53) and SwissProt (release 35). The predicted proteins of the present invention matching known proteins were further classified into 3 categories depending on the level of homology.

The first category contains proteins of the present invention exhibiting more than 70% identical amino acid residues on the whole length of the matched protein. They are clearly close homologues which most probably have the same function or a very similar function as the matched protein.

The second category contains proteins of the present invention exhibiting more remote homologies (40 to 70% over the whole protein) indicating that the protein of the present invention may have functions similar to those of the homologous protein.

The third category contains proteins exhibiting homology (90 to 100%) to a domain of a known protein

5 indicating that the matched protein and the protein of the invention may share similar features.

It should be noted that the numbering of amino acids in the protein sequences discussed in Figures 10 to 15, and Table VIII, the first methionine encountered is designated as amino acid number 1. In the appended sequence listing, the first amino acid of the mature protein resulting from cleavage of the signal peptide is designated as amino acid - number 1, and the first amino acid of the signal peptide is designated with the appropriate negative number, in
10 accordance with the regulations governing sequence listings.

In addition all of the corrected amino acid sequences (SEQ ID NOs: 141-241 and 378-513) were scanned for the presence of known protein signatures and motifs. This search was performed against the Prosite 15.0 database, using the Proscan software from the GCG package. Functional signatures and their locations are indicated in Table VIII.

15 A) Proteins which are closely related to known proteins

Protein of SEQ ID NO: 217

The protein of SEQ ID NO: 217 encoded by the extended cDNA SEQ ID NO: 116 isolated from lymphocyte shows complete identity to a human protein TFAR19 that may play a role in apoptosis (Genbank accession number AF014955, SEQ ID NO: 516) as shown by the alignment in figure 10.

20 Taken together, these data suggest that the protein of SEQ ID NO: 217 may be involved in the control of development and homeostasis. Thus, this protein may be useful in diagnosis and/or treating several types of disorders including, but not limited to, cancer, autoimmune disorders, viral infections such as AIDS, neurodegenerative disorders, osteoporosis.

25 Proteins of SEQ ID NOs: 174, 175 and 232

The proteins of SEQ ID NOs: 174, 175 and 232 encoded by the extended cDNAs SEQ ID NOs: 73, 74 and 131 respectively and isolated from lymphocytes shows complete extensive homologies to a human secreted protein (Genbank accession number W36955, SEQ ID NO: 517). As shown by the alignments of figure 11, the amino acid residues are identical to those of the 110 amino acid long matched protein except for positions 51 and 108-110 of the matched
30 protein for the protein of SEQ ID NOs: 174, for positions 48, 94 and 108-110 of the matched protein of SEQ ID NOs: 175 and for positions 94, and 108-110 of the matched protein for the protein of SEQ ID NOs: 232. Proteins of SEQ ID NOs: 174 and 232 may represent alternative forms issued from alternative use of polyadenylation signals.

Taken together, these data suggest that the proteins of SEQ ID NOs: 174, 175 and 232 may play a role in cell proliferation and/or differentiation, in immune responses and/or in haematopoiesis. Thus, this protein or part therein,

may be useful in diagnosing and treating several disorders including, but not limited to, cancer, immunological, haematological and/or inflammatory disorders. It may also be useful in modulating the immune and inflammatory responses to infectious agents and/or to suppress graft rejection .

5 Proteins of SEQ ID NO: 231

The protein of SEQ ID NO: 231 encoded by the extended cDNA SEQ ID NO: 130 shows extensive homology with the human E25 protein (Genbank accession number AF038953, SEQ ID NO: 515). As shown by the alignments in figure 12, the amino acid residues are identical except for position 159 in the 263 amino acid long matched sequence. The matched protein might be involved in the development and differentiation of haematopoietic stem/progenitor cells.

- 10 In addition, it is the human homologue of a murine protein thought to be involved in chondro-osteogenic differentiation and belonging to a novel multigene family of integral membrane proteins (Deleersnijder *et al*, *J. Biol. Chem.*, 271 : 19475-19482 (1996)).

- The protein of invention contains two short segments from positions 1 to 21 and from 100 to 120 as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, 10 : 685-686 (1994)). The first
15 transmembrane domains matches exactly those predicted for the murine E25 protein.

Taken together, these data suggest that the protein of SEQ ID NO: 231 may be involved in cellular proliferation and differentiation. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer and embryogenesis disorders.

20 Protein of SEQ ID NO: 196

- The protein of SEQ ID NO: 196 encoded by the extended cDNA SEQ ID NO: 95 shows extensive homology with the human seventransmembrane protein (Genbank accession number Y11395, SEQ ID NO: 518) and its murine homologue (Genbank accession number Y11550). As shown by the alignments in figure 13, the amino acid residues are identical except for position 174 in the 399 amino acid long human matched sequence. The matched protein potentially
25 associated to stomatin may act as a G-protein coupled receptor and is likely to be important for the signal transduction in neurons and haematopoietic cells (Mayer *et al*, *Biochem. Biophys. Acta.*, 1395 : 301-308 (1998)).

- Taken together, these data suggest that the protein of SEQ ID NOs: 196 may be involved in signal transduction. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, neurodegenerative diseases cardiovascular disorders, hypertension, renal injury and repair and septic
30 shock.

Protein of SEQ ID NO: 158

The protein of SEQ ID NOs: 158 encoded by the extended cDNA SEQ ID NO: 57 shows homology with the murine subunit 7a of the COP9 complex (Genbank accession number AF071316, SEQ ID NO: 520). As shown by the

alignments in figure 14, the amino acid residues are identical except for positions 90, 172 and 247 in the 275 amino acid long matched sequence. This complex is highly conserved between mammals and higher plants where it has been shown to act as a repressor of photomorphogenesis. All the components of the mammalian COP9 complex contain structural features also present in components of the proteasome regulatory complex and the translation initiation complex eIF3 complex, suggesting that the mammalian COP9 complex is an important cellular regulator modulating multiple signaling pathways (Wei *et al*, *Curr. Biol.*, 8 : 919-922 (1998)).

Taken together, these data suggest that the protein of SEQ ID NO: 158 may be involved in cellular signaling, probably as a subunit of the human COP9 complex. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, neurodegenerative diseases, cardiovascular disorders, hypertension, renal injury and repair and septic shock.

Protein of SEQ ID NO: 226

The protein of SEQ ID NO: 226 encoded by the extended cDNA SEQ ID NO: 125 shows homology with the bovine subunit B14.5B of the NADH-ubiquinone oxidoreductase complex (Arizmendi *et al*, *FEBS Lett.*, 313 : 80-84 (1992) and Swissprot accession -number Q02827, SEQ ID NO: 514). As shown by the alignments in figure 15, the amino acid residues are identical except for positions 3-4, 6-12, 32-34, 47, 53-55, 67 and 69-74 in the 120 amino acid long matched sequence. This complex is the first of four complexes located in the inner mitochondrial membrane and composing the mitochondrial electron transport chain. Complex I is involved in the dehydrogenation of NADH and the transportation of electrons to coenzyme Q. It is composed of 7 subunits encoded by the mitochondrial genome and 34 subunits encoded by the nuclear genome. It is also thought to play a role in the regulation of apoptosis and necrosis. Mitochondriocytopathies due to complex I deficiency are frequently encountered and affect tissues with a high energy demand such as brain (mental retardation, convulsions, movement disorders), heart (cardiomyopathy, conduction disorders), kidney (Fanconi syndrome), skeletal muscle (exercise intolerance, muscle weakness, hypotonia) and/or eye (ophthalmoplegia, ptosis, cataract and retinopathy). For a review on complex I see Smeitink *et al.*, *Hum. Mol. Gent.*, 7 : 1573-1579 (1998).

Taken together, these data suggest that the protein of SEQ ID NO: 226 may be part of the mitochondrial energy-generating system, probably as a subunit of the NADH-ubiquinone oxidoreductase complex. Thus, this protein or part therein, may be useful in diagnosing and/or treating several disorders including, but not limited to, brain disorders (mental retardation, convulsions, movement disorders), heart disorders (cardiomyopathy, conduction disorders), kidney disorders (Fanconi syndrome), skeletal muscle disorders (exercise intolerance, muscle weakness, hypotonia) and/or eye disorders ophthalmoplegia, ptosis, cataract and retinopathy).

B) Proteins which are remotely related to proteins with known functions

Proteins of SEQ ID NOs: 149, 150 and 211

The proteins of SEQ ID NOs: 149, 150 and 211 encoded by the extended cDNAs SEQ ID NOs: 48, 49 and 110 respectively and found in, skeletal muscle shows homologies with T1/ST2 ligand polypeptide of either human (Genbank accession number U41804 and Genseq accession number W09639) or rodent species (Genbank accession number U41805 and Genseq accession number W09640). These polypeptides are thought to be cytokines that bind to the ST2
5 receptor, a member of the immunoglobulin family homologous to the interleukin-1 receptor and present on some lymphoma cells. They are predicted to be cell-surface proteins containing a short transmembrane domain. (Gayle *et al*, *J. Biol. Chem.*, 271 : 5784-5789 (1996)). Proteins of SEQ ID NOs: 149, 150 and 211 may represent alternative forms issued from alternative use of polyadenylation signals.

The protein of invention contains two short transmembrane segments from positions 5 to 25 and from 195 to
10 215 as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, 10 :685-686 (1994)). The second transmembrane domain matches exactly those of the matched cell-surface protein.

Taken together, these data suggest that the protein of SEQ ID NOs: 149, 150 and 211 may act as a cytokine, thus may play a role in the regulation of cell growth and differentiation and/or in the regulation of the immune response. Thus, this protein or part therein, may be useful in diagnosing and treating several disorders including, but not limited to,
15 cancer, immunological, haematological and/or inflammatory disorders. It may also be useful in modulating the immune and inflammatory responses to infectious agents such as HIV and/or to suppress graft rejection.

Protein of SEQ ID NO: 177

The protein SEQ ID NO: 177 found in testis encoded by the extended cDNA SEQ ID NO: 76 shows homologies
20 to serine protease inhibitor proteins belonging to the pancreatic trypsin inhibitor family (Kunitz) such as the extracellular proteinase inhibitor named chelonianin (Swissprot accession number P00993). The characteristic PROSITE signature of this family is conserved in the protein of the invention (positions 69 to 87) except for a drastic change of the last cysteine residue into an arginine residue.

Taken together, these data suggest that the protein of SEQ ID NO: 177 may be a protease inhibitor, probably
25 of the Kunitz family. Thus, this protein or part therein, may be useful in diagnosing and treating several disorders including but not limited to, cancer and neurodegenerative disorders such as Alzheimer's disease.

Protein of SEQ ID NO: 146

The protein SEQ ID NO: 146 encoded by the extended cDNA SEQ ID NO: 45 shows homology to human
30 apolipoprotein L (Genbank accession number AF019225). The matched protein is a secreted high density lipoprotein associated with apoA-I-containing lipoproteins which play a key role in reverse cholesterol transport.

Taken together, these data suggest that the protein of SEQ ID NO. 146 may play a role in lipid metabolism. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to,

hyperlipidemia, hypercholesterolemia, atherosclerosis, cardiovascular disorders such as, coronary heart disease, and neurodegenerative disorders such as Alzheimer's disease or dementia.

Protein of SEQ ID NO: 163

5 The protein SEQ ED NO: 163 encoded by the extended cDNA SEQ ID NO: 62 shows homology to the yeast autophagocytosis protein AUT1 (SwissProt accession number P40344). The matched protein is required for starvation-induced non-specific bulk transport of cytoplasmic proteins to the vacuole.

 Taken together, these data suggest that the protein of SEQ ID NO: 163 may play a role in protein transport. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to,
10 autoimmune disorders and immune disorders due to dysfunction of antigen presentation.

C) Proteins homologous to a domain of a protein with known function

Protein of SEQ ID NO: 214

 The protein of SEQ ID NO: 214 encoded by the extended cDNA SEQ ID NO: 113 and expressed in adult brain
15 shows extensive homology to part of the murine SHYC protein (Genbank accession number AF072697) which is expressed in the developing and embryonic nervous system as well as along the olfactory pathway in adult brains (Köster *et al.*, *Neuroscience Letters*, 252 : 69-71 (1998)).

 Taken together, these data suggest that the protein of SEQ ID NO: 214 may play a role in nervous system development and function. Thus, this protein may be useful in diagnosing and/or treating cancer and/or brain disorders,
20 including neurodegenerative disorders such as Alzheimer's and Parkinson's diseases.

Protein of SEQ ID NO: 225

 The protein of SEQ ID NO: 225 encoded by the extended cDNA SEQ ID NO: 124 and expressed in adult prostate belong to the phosphatidylethanolainin-binding protein from which it exhibits the characteristic PROSITE
25 signature from positions 90 to 112 (see table VIII). Proteins from this widespread family, from nematodes to fly, yeast, rodent and primate species, bind hydrophobic ligands such as phospholipids and nucleotides. They are mostly expressed in brain and in testis and are thought to play a role in cell growth and/or maturation, in regulation of the sperm maturation, motility and 'in membrane remodeling. They may act either through signal transduction or through oxidoreduction reactions (for a review see Schoentgen and Jollès, *FEBS Letters*, 369 : 22-26 (1995)).

30 Taken together, these data suggest that the protein of SEQ ID NO: 225 may play a role in cell. Thus, these growth, maturation and in membrane remodeling and/or may be related to male fertility. Thus, this protein may be useful in diagnosing and/or treating cancer, neurodegenerative diseases, and/of, disorders related to male fertility and sterility.

Protein of SEQ ID NO: 153

The protein of SEQ ID NO: 153 encoded by the extended cDNA SEQ ID NO: 52 and expressed in brain exhibits homology to different integral membrane proteins. These membrane proteins include the nematode protein SRE-2 (Swissprot accession number Q09273) that belongs to the multigene SRE family of *C. elegans* receptor-like proteins and a family of tricarboxylate carriers conserved between flies and mammals. One member of this matched family is the rat tricarboxylate carrier (Genbank accession number S70011), an anion transporter localized in the inner membrane of mitochondria and involved in the biosynthesis of fatty acids and cholesterol. The protein of the invention contains a short transmembrane segments from positions 5 to 25 as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, 10 :685-686 (1994)).

Taken together, these data suggest that the protein of SEQ ID NO: 153 may play a role in signal transduction and/or in molecule transport. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, neurodegenerative diseases, immune disorders, cardiovascular disorders, hypertension, renal injury and repair and septic shock

Protein of SEQ ID NO: 213

The protein of SEQ ID NO: 213 encoded by the extended cDNA SEQ ID NO: 112 and expressed in brain exhibits homology with part of the tRNA pseudouridine 55 synthase found in *Escherichia Coli* (Swissprot accession number P09171). This bacterial protein belongs to the NAP57/CBF5/TRUB family of nucleolar proteins found in bacteria, yeasts and mammals involved in rRNA or tRNA biosynthesis, ribosomal subunit assembly and/or centromere/microtubule binding.

Taken together, these data suggest that the protein of SEQ ID NO: 213 may play a role in rRNA or tRNA biogenesis and function. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, hearing loss or disorders linked to chromosomal instability such as dyskeratosis.

Protein of SEQ ID NO: 240

The protein of SEQ ID NO: 240 encoded by the extended cDNA SEQ ID NO: 139 and expressed in brain exhibits homology with a family of eukaryotic cell surface antigens containing 4 transmembrane domains. The PROSITE signature for this family is conserved in the protein of the invention except for a substitution of an alanine residue in place of any of the following hydrophobic residues : leucine, valine, isoleucine or methionine (positions 21 to 36).

The protein of the invention contains three short transmembrane segments from positions 6 to 26, 32 to 52 and from 56 to 76 as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, 10 : 685-686 (1994)). These transmembrane domains match the last three transmembrane domains of the matched protein family.

Taken together, these data suggest that the protein of SEQ ID NO: 240 may play a role in immunological and/or inflammatory responses, probably as a cell surface antigen. Thus, this protein or part therein, may be useful in diagnosing and treating several disorders including, but not limited to, cancer, immunological, haematological and/or

inflammatory disorders. It may also be useful in modulating the immune and inflammatory responses to infectious agents and/or to suppress graft rejection.

Protein of SEQ ID NO: 239

5 The protein of SEQ ID NO: 239 encoded by the extended cDNA SEQ ID NO: 138 exhibits homology with a conserved region in a family of NA⁺/H⁺ exchanger conserved in yeast, nematode and mammals. These cation/proton exchangers are integral membrane proteins with 5 transmembrane segments involved in intracellular pH regulation, maintenance of cell volume, reabsorption of sodium across specialized epithelia, vectorial transport and are also thought to play a role in signal transduction and especially in the induction of cell proliferation and in the induction of apoptosis.

10 The protein of invention contains four short transmembrane segments from positions 21 to 41, 48 to 68 and from 131 to 151 as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, 10 : 685-686 (1994)). The third and fourth transmembrane domains match the fourth and fifth transmembrane segments of the matched family of proteins.

 Taken together, these data suggest that the protein of SEQ ID NO: 239 may play a role in membrane
15 permeability and/or in signal transduction. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, neurodegenerative diseases, cardiovascular disorders, hypertension, renal injury and repair, septic shock as well as disorders of membrane permeability such as diarrhea.

Protein of SEQ ID NO: 200

20 The protein of SEQ ID NO: 200 encoded by the extended cDNA SEQ ED NO: 99 and expressed in brain exhibits extensive homology to the N-terminus of cell division cycle protein 23 (Genbank accession number AF053977) and also to a lesser extent to its homologue in *Saccharomyces cerevisiae*. The matched protein is required for chromosome segregation and is part of the anaphase-promoting complex necessary for cell cycle progression to mitosis.

 Taken together, these data suggest that the protein of SEQ ID NO: 200 may play a role in cellular mitosis.
25 Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer and leukemia.

Protein of SEQ ID NO: 230

 The protein of SEQ ID NO: 230 encoded by the extended cDNA SEQ ID NO: 129 exhibits extensive homology to
30 the C-terminus of the eta subunit of T-complex polypeptide 1 conserved from yeasts to mammals, and even complete identity with the last 54 amino acid residues of the human protein (Genbank accession number AF026292). The matched protein is a chaperonin which assists the folding of actins and tubulins in eukaryotic cells upon ATP hydrolysis.

 Taken together, these data suggest that the protein of SEQ ID NO: 230 may play a role in the folding, transport, assembly and degradation of proteins. Thus, this protein may be useful in diagnosing and/or treating several

types of disorders including, but not limited to, cancer, cardiovascular disorders, immune disorders, neurodegenerative disorders, osteoporosis and arthritis.

Protein of SEQ ID NO: 167

5 The protein of SEQ ID NO: 167 encoded by the extended cDNA SEQ ID NO: 66 exhibits homology to a monkey pepsinogen A-4 precursor (Swissprot accession number P27678) and to related members of the aspartyl protease family. The matched protein belongs to a family of widely distributed proteolytic enzymes known to exist in vertebrate, fungi, plants, retroviruses and some plant viruses.

 Taken together, these data suggest that the protein of SEQ ID NO: 167 may play a role in the degradation of
10 proteins. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, autoimmune disorders and immune disorders due to dysfunction of antigen presentation.

Protein of SEQ ID NO: 179

 The protein of SEQ ID NO: 179 encoded by the extended cDNA SEQ ID NO: 78 found in testis exhibits
15 homology to part of mammalian colipase precursors. Colipases are secreted cofactors for pancreatic lipases that allow the lipase to anchor at the water-lipid interface. Colipase plays a crucial role in the intestinal digestion and absorption of dietary fats. The 5 cysteines characteristic for this protein family are conserved in the protein of the invention although the colipase PROSITE signature is not.

 Taken together, these data suggest that the protein of SEQ ID NO: 179 may play a role in the lipid metabolism
20 and/or in male fertility. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, hyperlipidemia, hypercholesterolemia, atherosclerosis, cardiovascular disorders such as coronary heart disease, and neurodegenerative disorders such as Alzheimer's disease or dementia, and disorders linked to male fertility.

25 Protein of SEQ ID NO: 227

 The protein of SEQ ID NO: 227 encoded by the extended cDNA SEQ ID NO: 126 exhibits extensive homology to the ATP binding region of a whole family of serine/threonine protein kinases belonging to the CDC2/CDC28 subfamily. The PROSITE signature characteristic for this domain is present in the protein of the invention from positions 10 to 34.

 Taken together, these data suggest that the protein of SEQ ID NO: 158 may bind ATP, and even be a protein
30 kinase. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, neurodegenerative diseases, cardiovascular disorders, hypertension, renal injury and repair and septic shock.

Although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims.

5 As discussed above, the extended cDNAs of the present invention or portions thereof can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to
10 compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or
15 potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit
20 another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other
25 protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing
30 such methods include without limitation "Molecular Cloning; A Laboratory Manual", 2d ed., Cole Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology; Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a

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nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

SEQUENCE LISTING FREE TEXT

The following free text appears in the accompanying Sequence Listing:

In vitro transcription product

oligonucleotide

5 promoter

transcription start site

Von Heijne matrix

Score

matinspector prediction

10 name

TABLE I

SEQ ID NO. in Present application	Provisional Application Disclosing Sequence	SEQ ID NO. in provisional application
40	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	51
41	U.S. Provisional Patent Application Serial No. 60/081,563, filed Apr. 13, 1998	72
42	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	52
43	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	78
44	U.S. Provisional Patent Application Serial No. 60/081,563, filed Apr. 13, 1998	73
45	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	41
46	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	67
47	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	82
48	U.S. Provisional Patent Application Serial No. 60/081,563, filed Apr. 13, 1998	80
49	U.S. Provisional Patent Application Serial No. 60/081,563, filed Apr. 13, 1998	81
50	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	53
51	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	54
52	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	195
53	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	44
54	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	46
55	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	68
56	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	48
57	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	55
58	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	49
59	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	50
60	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	97
61	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	51
62	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	69
63	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	49
64	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	199
65	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	53
66	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	57
67	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	54
68	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	55
69	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	58
70	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	59

CONT. TABLE I

71	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	60
72	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	112
73	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	52
74	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	59
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77	U.S. Provisional Patent Application Serial No. 60/081,563, filed Apr. 13, 1998	75
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79	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	61
80	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	130
81	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	65
82	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	54
83	U.S. Provisional Patent Application Serial No. 60/081,563, filed Apr. 13, 1998	78
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98	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	62
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105	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	64
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110	U.S. Provisional Patent Application Serial No. 60/081,563, filed Apr. 13, 1998	82
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113	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	46
114	U.S. Provisional Patent Application Serial No. 60/074,121, filed Feb. 9, 1998	47
115	U.S. Provisional Patent Application Serial No. 60/066,677, filed Nov. 13, 1997	53
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129	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	48
130	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	51
131	U.S. Provisional Patent Application Serial No. 60/066,677, filed Nov. 13, 1997	50
132	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	56
133	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	57
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140	U.S. Provisional Patent Application Serial No. 60/096,116, filed Aug. 10, 1998	67
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248	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	81
249	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	82
250	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	83
251	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	84
252	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	85
253	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	86
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365	U.S. Provisional Patent Application Serial No. 60/069,957, filed Dec. 17, 1997	1998
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TABLE II : Parameters used for each step of EST analysis

Step	Search Characteristics			Selection Characteristics	
	Program	Strand	Parameters	Identity (%)	Length (bp)
Miscellaneous	Blastn	both	S=61 X=16	90	17
tRNA	Fasta	both	.	80	60
rRNA	Blastn	both	S=108	80	40
mtRNA	Blastn	both	S=108	80	40
Procaryotic	Blastn	both	S=144	90	40
Fungal	Blastn	both	S=144	90	40
Alu	fasta*	both	.	70	40
L1	Blastn	both	S=72	70	40
Repeats	Blastn	both	S=72	70	40
Promoters	Blastn	top	S=54 X=16	90	15 _⊥
Vertebrate	fasta*	both	S=108	90	30
ESTs	Blastn	both	S=108 X=16	90	30
Proteins	blastx _η	top	E=0.001	.	.

* use "Quick Fast" Database Scanner

⊥ alignment further constrained to begin closer than 10bp to EST(5' end

5 _η using BLOSUM62 substitution matrix

TABLE III: Parameters used for each step of extended cDNA analysis

Step	Search characteristics		Selection characteristics			
	Program	Strand	Parameters	Identity (%)	Length (bp)	Comments
miscellaneous*	FASTA	both	.	90	15	
tRNA*	FASTA	both	.	80	90	
rRNA*	BLASTN	both	S-108	80	40	
mtRNA*	BLASTN	both	S-108	80	40	
Procaryotic [†]	BLASTN	both	S-144	90	40	
Fungal*	BLASTN	both	S-144	90	40	
Alu*	BLASTN	both	S-72	70	40	
L1*	BLASTN	both	S-72	70	40	max 5 matches, masking
Repeats*	BLASTN	both	S-72	70	40	max 5 matches, masking
PolyA	BLAST2N	top	W-6,S-10,E-1000	90	8	masking
Polyadenylation signal		top	AATAAA allowing 1 mismatch			in the last 20 nucleotides preceding the 5' end of the polyA
Vertebrate*	BLASTN then FASTA	both	.	90 then 70	30	first BLASTN and then FASTA on matching sequences
ESTs*	BLAST2N	both	.	90	30	
Geneseq	BLASTN	both	W-8, B-10	90	30	
ORF	BLASTP	top	W-8, B-10	.	.	on ORF proteins, max 10 matches
Proteins*	BLASTX	top	E-0.001	70	30	

* steps common to EST analysis and using the same algorithms and parameters

5 * steps also used in EST analysis but with different algorithms and/or parameters

TABLE IV

Id	FCS Location	SigPep Location	Mature Polypeptide Location	Stop Codon Location	PolyA Signal Location	PolyA Site Location
40	7 through 471	7 through 99	100 through 471	472	537 through 542	554 through 568
41	168 through 332	-	168 through 332	333	557 through 562	-
42	51 through 251	51 through 110	111 through 251	252	849 through 854	882 through 895
43	20 through 613	20 through 82	83 through 613	614	-	-
44	12 through 416	12 through 86	87 through 416	417	425 through 430	445 through 458
45	276 through 1040	276 through 485	486 through 1040	1041	-	2024 through 2036
46	443 through 619	443 through 589	590 through 619	620	-	1267 through 1276
47	206 through 747	-	206 through 747	-	-	-
48	36 through 521	36 through 104	105 through 521	522	528 through 533	548 through 561
49	36 through 395	36 through 104	105 through 395	396	599 through 604	619 through 632
50	21 through 41	-	21 through 41	42	328 through 333	357 through 370
51	35 through 631	35 through 160	161 through 631	632	901 through 906	979 through 994
52	271 through 399	-	271 through 399	400	-	-
53	103 through 252	103 through 213	214 through 252	253	-	588 through 597
54	2 through 460	-	2 through 460	461	713 through 718	735 through 748
55	31 through 231	-	31 through 231	232	769 through 774	690 through 703
56	305 through 565	-	305 through 565	566	694 through 699	713 through 725
57	124 through 873	124 through 378	379 through 873	874	1673 through 1678	1694 through 1705
58	135 through 206	-	135 through 206	207	850 through 855	1056 through 1069
59	135 through 818	-	135 through 818	819	909 through 914	1071 through 1084
60	33 through 290	33 through 92	93 through 290	291	-	-
61	485 through 616	-	485 through 616	617	-	669 through 682
62	54 through 995	54 through 227	228 through 995	996	1130 through 1135	1181 through 1191
63	657 through 923	657 through 896	897 through 923	924	957 through 962	974 through 1008
64	18 through 311	18 through 62	63 through 311	312	-	-
65	151 through 426	151 through 258	259 through 426	427	505 through 510	527 through 538
66	10 through 1062	10 through 57	58 through 1062	1063	1710 through 1715	1735 through 1747
67	78 through 491	78 through 218	219 through 491	492	1652 through 1657	1673 through 1686
68	69 through 371	69 through 287	288 through 371	372	510 through 515	530 through 542
69	2 through 757	2 through 205	206 through 757	758	-	1160 through 1174
70	2 through 1051	2 through 205	206 through 1051	1052	1248 through 1253	1272 through 1285
71	2 through 1171	2 through 205	206 through 1171	1172	1368 through 1373	1386 through 1398
72	42 through 611	42 through 287	288 through 611	612	787 through 792	808 through 821
73	62 through 916	62 through 757	758 through 916	-	-	904 through 916
74	62 through 520	-	62 through 520	521	1124 through 1129	1141 through 1153
75	21 through 167	-	21 through 167	168	-	-
76	22 through 318	22 through 93	94 through 318	319	497 through 502	516 through 526
77	8 through 292	8 through 118	119 through 292	293	317 through 322	339 through 352
78	16 through 378	16 through 84	85 through 378	379	502 through 507	522 through 542

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81	47 through 541	47 through 220	221 through 541	542	-	597 through 605
82	46 through 285	46 through 150	151 through 285	286	364 through 369	385 through 396
83	22 through 240	22 through 84	85 through 240	241	397 through 402	421 through 432
84	89 through 382	-	89 through 382	383	-	408 through 420
85	80 through 415	80 through 142	143 through 415	416	471 through 476	488 through 501
86	152 through 361	152 through 283	284 through 361	362	-	-
87	32 through 307	32 through 70	71 through 307	308	1240 through 1245	1261 through 1272
88	114 through 734	114 through 239	240 through 734	735	768 through 773	793 through 804
89	199 through 802	-	199 through 802	-	780 through 785	791 through 802
90	38 through 1174	38 through 148	149 through 1174	1175	1452 through 1457	1478 through 1490
91	26 through 361	-	26 through 361	-	-	350 through 361
92	3 through 131	-	3 through 131	132	-	591 through 605
93	33 through 185	33 through 80	81 through 185	186	570 through 575	586 through 591
94	184 through 915	184 through 237	238 through 915	916	1119 through 1124	1139 through 1150
95	58 through 1116	58 through 159	160 through 1116	1117	1486 through 1491	1504 through 1513
96	327 through 417	-	327 through 417	-	-	404 through 417
97	63 through 398	63 through 206	207 through 398	399	-	-
98	2 through 163	-	2 through 163	164	488 through 493	511 through 522
99	13 through 465	13 through 75	76 through 465	466	-	-
100	20 through 703	20 through 94	95 through 703	704	1000 through 1005	1023 through 1041
101	103 through 294	103 through 243	244 through 294	295	-	-
102	81 through 518	81 through 173	174 through 518	519	-	-
103	66 through 326	-	66 through 326	327	1066 through 1071	1087 through 1098
104	170 through 289	170 through 250	251 through 289	290	-	-
105	36 through 497	-	36 through 497	498	650 through 655	663 through 685
106	18 through 320	-	18 through 320	321	539 through 544	542 through 554
107	71 through 1438	71 through 136	137 through 1438	1439	1644 through 1649	1665 through 1678
108	25 through 318	25 through 75	76 through 318	319	452 through 457	482 through 494
109	84 through 332	84 through 170	171 through 332	333	-	702 through 714
110	32 through 718	32 through 100	101 through 718	719	770 through 775	793 through 805
111	26 through 481	26 through 88	89 through 481	482	755 through 760	775 through 787
112	26 through 562	26 through 187	188 through 562	563	-	-
113	4 through 810	4 through 279	280 through 810	811	858 through 863	881 through 893
114	55 through 459	55 through 120	121 through 459	460	1444 through 1449	1462 through 1475
115	48 through 248	48 through 161	162 through 248	249	283 through 288	308 through 321
116	25 through 399	25 through 186	187 through 399	400	-	-
117	10 through 1137	10 through 72	73 through 1137	1138	1144 through 1149	1162 through 1173
118	72 through 704	72 through 161	162 through 704	705	772 through 777	-
119	44 through 505	44 through 223	224 through 505	506	-	-
120	25 through 393	25 through 150	151 through 393	394	734 through 739	757 through 770

CONT. TABLE IV

121	58 through 1095	58 through 114	115 through 1095	1096	-	1202 through 1213
122	31 through 660	31 through 90	91 through 660	661	1288 through 1293	1307 through 1318
123	31 through 582	31 through 90	91 through 582	583	816 through 821	840 through 853
124	15 through 695	15 through 80	81 through 695	696	795 through 800	814 through 826
125	74 through 295	74 through 196	197 through 295	296	545 through 550	561 through 571
126	440 through 659	-	440 through 659	-	601 through 606	-
127	38 through 283	38 through 85	86 through 283	284	257 through 262	-
128	121 through 477	121 through 288	289 through 477	-	-	-
129	2 through 163	-	2 through 163	164	292 through 297	310 through 323
130	46 through 675	46 through 87	88 through 675	676	1364 through 1369	1383 through 1392
131	62 through 385	-	62 through 385	386	974 through 979	987 through 999
132	422 through 550	422 through 475	476 through 550	551	-	714 through 725
133	124 through 231	-	124 through 231	232	-	387 through 400
134	131 through 1053	131 through 169	170 through 1053	-	1019 through 1024	-
135	86 through 403	86 through 181	182 through 403	404	1097 through 1102	1117 through 1128
136	37 through 162	37 through 93	94 through 162	163	224 through 229	243 through 254
137	31 through 381	31 through 90	91 through 381	382	-	875 through 886
138	46 through 579	46 through 156	157 through 579	580	-	-
139	92 through 471	92 through 172	173 through 471	-	454 through 459	458 through 471
140	154 through 675	154 through 498	499 through 675	676	819 through 824	838 through 849
242	18 through 173	18 through 77	78 through 173	174	864 through 869	882 through 893
243	17 through 595	17 through 85	86 through 595	596	820 through 825	840 through 851
244	89 through 334	89 through 130	131 through 334	335	462 through 467	484 through 495
245	21 through 614	21 through 83	84 through 614	615	849 through 854	873 through 884
246	94 through 573	94 through 258	259 through 573	574	862 through 867	886 through 897
247	74 through 397	74 through 127	128 through 397	398	472 through 477	507 through 518
248	51 through 242	51 through 116	117 through 242	243	319 through 324	339 through 350
249	111 through 191	111 through 155	156 through 191	192	965 through 970	986 through 996
250	45 through 602	45 through 107	108 through 602	603	828 through 833	850 through 860
251	24 through 560	24 through 101	102 through 560	561	563 through 568	583 through 593
252	109 through 558	109 through 273	274 through 558	559	-	1104 through 1114
253	128 through 835	128 through 220	221 through 835	836	1145 through 1150	1170 through 1181
254	59 through 505	59 through 358	359 through 505	506	1042 through 1047	1062 through 1073
255	1 through 207	1 through 147	148 through 207	208	784 through 789	807 through 818
256	12 through 734	12 through 101	102 through 734	735	914 through 919	961 through 971
257	378 through 518	378 through 467	468 through 518	519	607 through 612	628 through 640
258	110 through 304	110 through 193	194 through 304	305	708 through 713	732 through 743
259	201 through 419	201 through 272	273 through 419	420	601 through 606	627 through 637
260	123 through 302	123 through 176	177 through 302	303	1279 through 1284	1301 through 1312
261	98 through 673	98 through 376	377 through 673	674	-	1025 through 1035
262	17 through 463	17 through 232	233 through 463	464	657 through 662	684 through 696
263	263 through 481	263 through 322	323 through 481	482	-	858 through 868

CONT. TABLE IV

264	42 through 299	42 through 101	102 through 299	300	-	762 through 775
265	198 through 431	198 through 260	261 through 431	432	-	1064 through 1074
266	279 through 473	279 through 362	363 through 473	474	944 through 949	970 through 981
267	12 through 644	12 through 92	93 through 644	645	1002 through 1007	1020 through 1031
268	91 through 459	91 through 330	331 through 459	460	-	1271 through 1281
269	70 through 327	70 through 147	148 through 327	328	1741 through 1746	1763 through 1774
270	12 through 497	12 through 104	105 through 497	498	935 through 940	955 through 967
271	90 through 383	90 through 200	201 through 383	384	609 through 614	632 through 643
272	332 through 541	332 through 376	377 through 541	542	739 through 744	761 through 773
273	43 through 222	43 through 177	178 through 222	223	530 through 535	555 through 566
274	115 through 231	115 through 180	181 through 231	232	419 through 424	445 through 455
275	232 through 384	232 through 300	301 through 384	385	650 through 655	662 through 673
276	143 through 427	143 through 286	287 through 427	428	606 through 611	628 through 639
277	284 through 463	294 through 379	380 through 463	464	-	762 through 772
278	162 through 671	162 through 398	399 through 671	672	805 through 810	830 through 840
279	63 through 632	63 through 308	309 through 632	633	808 through 813	829 through 840
280	21 through 362	21 through 200	201 through 362	363	821 through 826	838 through 849
281	21 through 503	21 through 344	345 through 503	504	1305 through 1310	1330 through 1341
282	1 through 201	1 through 63	64 through 201	202	637 through 642	660 through 671
283	39 through 1034	39 through 134	135 through 1034	1035	1566 through 1571	1587 through 1597
284	69 through 263	69 through 125	126 through 263	264	1173 through 1178	1196 through 1205
285	115 through 285	115 through 204	205 through 285	286	505 through 510	525 through 536
286	90 through 344	90 through 140	141 through 344	345	500 through 505	515 through 527
287	57 through 311	57 through 107	108 through 311	312	467 through 472	482 through 493
288	96 through 302	96 through 182	183 through 302	303	-	501 through 514
289	161 through 526	161 through 328	329 through 526	527	-	799 through 811
290	210 through 332	210 through 299	300 through 332	333	594 through 599	613 through 625
291	212 through 361	212 through 319	320 through 361	362	650 through 655	673 through 684
292	75 through 482	75 through 128	129 through 482	483	595 through 600	618 through 627
293	50 through 631	50 through 244	245 through 631	632	777 through 782	801 through 812
294	154 through 576	154 through 360	361 through 576	577	737 through 742	763 through 775
295	154 through 897	154 through 360	361 through 897	898	1017 through 1022	1044 through 1054
296	146 through 292	146 through 253	254 through 292	293	395 through 400	433 through 444
297	126 through 383	126 through 167	168 through 383	384	726 through 731	743 through 754
298	66 through 497	66 through 239	240 through 497	498	594 through 599	618 through 629
299	49 through 411	49 through 96	97 through 411	412	732 through 737	750 through 763
300	49 through 534	49 through 96	97 through 534	535	593 through 598	612 through 623
301	86 through 415	86 through 145	146 through 415	416	540 through 545	560 through 571
302	56 through 268	56 through 100	101 through 268	269	584 through 589	601 through 612
303	32 through 328	32 through 103	104 through 328	329	508 through 513	528 through 539
304	21 through 527	21 through 95	96 through 527	528	921 through 926	953 through 963
305	147 through 647	147 through 374	375 through 647	648	-	668 through 681

CONT. TABLE IV

306	262 through 471	262 through 306	307 through 471	472	663 through 668	682 through 693
307	74 through 1216	74 through 172	173 through 1216	1217	1627 through 1632	1640 through 1652
308	48 through 164	48 through 89	90 through 164	165	482 through 487	505 through 517
309	185 through 334	185 through 295	296 through 334	335	355 through 360	392 through 405
310	195 through 347	195 through 272	273 through 347	348	1037 through 1042	1071 through 1082
311	90 through 815	90 through 179	180 through 815	816	883 through 888	905 through 916
312	52 through 513	52 through 231	232 through 513	514	553 through 558	572 through 583
313	172 through 438	172 through 354	355 through 438	439	682 through 687	685 through 697
314	148 through 366	148 through 225	226 through 366	367	770 through 775	792 through 803
315	175 through 336	175 through 276	277 through 336	337	-	812 through 823
316	191 through 553	191 through 304	305 through 553	554	766 through 771	804 through 817
317	106 through 603	106 through 216	217 through 603	604	-	1102 through 1112
318	47 through 586	47 through 124	125 through 586	587	1583 through 1588	1614 through 1623
319	99 through 371	99 through 290	291 through 371	372	491 through 496	513 through 524
320	44 through 814	44 through 112	113 through 814	815	-	978 through 989
321	3 through 581	3 through 182	183 through 581	582	-	1006 through 1016
322	107 through 427	107 through 190	191 through 427	428	499 through 504	516 through 529
323	45 through 407	45 through 83	84 through 407	408	1008 through 1013	1032 through 1042
324	201 through 332	201 through 251	252 through 332	333	-	869 through 880
325	217 through 543	217 through 255	256 through 543	544	-	1206 through 1217
326	18 through 446	18 through 140	141 through 446	447	930 through 935	948 through 959
327	29 through 724	29 through 118	119 through 724	725	886 through 891	910 through 920
328	404 through 586	404 through 466	467 through 586	587	1304 through 1309	1334 through 1344
329	331 through 432	331 through 387	388 through 432	433	548 through 553	573 through 585
330	59 through 703	59 through 220	221 through 703	704	886 through 891	903 through 914
331	672 through 752	672 through 722	723 through 752	753	-	1150 through 1161
332	57 through 311	57 through 128	129 through 311	312	332 through 337	351 through 363
333	80 through 232	80 through 127	128 through 232	233	617 through 622	634 through 645
334	91 through 291	91 through 219	220 through 291	292	367 through 372	389 through 400
335	196 through 384	196 through 240	241 through 384	385	461 through 466	485 through 496
336	54 through 590	54 through 227	228 through 590	591	-	955 through 965
337	133 through 846	133 through 345	346 through 846	847	-	890 through 901
338	138 through 671	138 through 248	249 through 671	672	1319 through 1324	1338 through 1347
339	124 through 411	124 through 186	187 through 411	412	948 through 953	971 through 983
340	372 through 494	372 through 443	444 through 494	495	708 through 713	732 through 745
341	112 through 450	112 through 192	193 through 450	451	1053 through 1058	1095 through 1106
342	117 through 866	117 through 170	171 through 866	867	1159 through 1164	1178 through 1190
343	13 through 465	13 through 75	76 through 465	466	1035 through 1040	1060 through 1070
344	2 through 718	2 through 76	77 through 718	719	1170 through 1175	1203 through 1213
345	86 through 709	86 through 361	362 through 709	710	943 through 948	963 through 973
346	63 through 320	63 through 179	180 through 320	321	771 through 776	799 through 810
347	299 through 418	299 through 379	380 through 418	419	739 through 744	762 through 771

CONT. TABLE IV

348	186 through 380	186 through 233	234 through 380	381	383 through 388	396 through 409
349	69 through 458	69 through 233	234 through 458	459	564 through 569	602 through 613
350	12 through 638	12 through 263	264 through 638	639	951 through 956	975 through 985
351	282 through 389	282 through 332	333 through 389	390	1413 through 1418	1437 through 1447
352	208 through 339	208 through 294	295 through 339	340	-	1631 through 1641
353	69 through 557	69 through 224	225 through 557	558	849 through 854	870 through 883
354	134 through 325	134 through 274	275 through 325	326	-	718 through 729
355	78 through 731	78 through 227	228 through 731	732	-	1002 through 1013
356	46 through 693	46 through 90	91 through 693	694	937 through 942	962 through 973
357	126 through 527	126 through 182	183 through 527	528	834 through 839	856 through 867
358	66 through 320	66 through 113	114 through 320	321	490 through 495	508 through 519
359	73 through 948	73 through 159	160 through 948	949	-	1016 through 1028
360	69 through 434	69 through 236	237 through 434	435	419 through 424	441 through 452
361	628 through 804	628 through 711	712 through 804	805	-	864 through 875
362	70 through 366	70 through 108	109 through 366	367	496 through 501	521 through 531
363	70 through 366	70 through 108	109 through 366	367	-	1233 through 1244
364	111 through 434	111 through 185	186 through 434	435	-	618 through 631
365	19 through 567	19 through 63	64 through 567	568	749 through 754	771 through 781
366	19 through 312	19 through 63	64 through 312	313	896 through 901	921 through 931
367	64 through 612	64 through 234	235 through 612	613	-	839 through 849
368	39 through 458	39 through 80	81 through 458	459	613 through 618	633 through 644
369	9 through 185	9 through 50	51 through 185	186	-	906 through 918
370	14 through 316	14 through 121	122 through 316	317	442 through 447	458 through 471
371	70 through 1092	70 through 234	235 through 1092	1093	1475 through 1480	1493 through 1504
372	274 through 597	274 through 399	400 through 597	598	731 through 736	754 through 765
373	230 through 469	230 through 307	308 through 469	470	1004 through 1009	1027 through 1040
374	72 through 545	72 through 203	204 through 545	546	-	1151 through 1162
375	36 through 425	36 through 119	120 through 425	426	1215 through 1220	1240 through 1250
376	155 through 751	155 through 340	341 through 751	752	912 through 917	937 through 947
377	46 through 585	46 through 120	121 through 585	586	584 through 589	606 through 619

TABLE V

Id	Full Length Polypeptide Location	Signal Peptide Location	Mature Polypeptide Location
141	-31 through 124	-31 through -1	1 through 124
142	1 through 55	-	1 through 55
143	-20 through 47	-20 through -1	1 through 47
144	-21 through 177	-21 through -1	1 through 177
145	-25 through 110	-25 through -1	1 through 110
146	-70 through 185	-70 through -1	1 through 185
147	-49 through 10	-49 through -1	1 through 10
148	1 through 180	-	1 through 180
149	-23 through 139	-23 through -1	1 through 139
150	-23 through 97	-23 through -1	1 through 97
151	1 through 7	-	1 through 7
152	-42 through 157	-42 through -1	1 through 157
153	1 through 43	-	1 through 43
154	-37 through 13	-37 through -1	1 through 13
155	1 through 153	-	1 through 153
156	1 through 67	-	1 through 67
157	1 through 87	-	1 through 87
158	-85 through 165	-85 through -1	1 through 165
159	1 through 24	-	1 through 24
160	1 through 228	-	1 through 228
161	-20 through 66	-20 through -1	1 through 66
162	1 through 44	-	1 through 44
163	-58 through 256	-58 through -1	1 through 256
164	-80 through 9	-80 through -1	1 through 9
165	-15 through 83	-15 through -1	1 through 83
166	-36 through 56	-36 through -1	1 through 56
167	-16 through 335	-16 through -1	1 through 335
168	-47 through 91	-47 through -1	1 through 91
169	-73 through 28	-73 through -1	1 through 28
170	-68 through 184	-68 through -1	1 through 184
171	-68 through 282	-68 through -1	1 through 282
172	-68 through 322	-68 through -1	1 through 322
173	-82 through 108	-82 through -1	1 through 108
174	-232 through 53	-232 through -1	1 through 53
175	1 through 153	-	1 through 153
176	1 through 49	-	1 through 49
177	-24 through 75	-24 through -1	1 through 75
178	-37 through 58	-37 through -1	1 through 58
179	-23 through 98	-23 through -1	1 through 98
180	1 through 59	-	1 through 59
181	-14 through 72	-14 through -1	1 through 72
182	-58 through 107	-58 through -1	1 through 107
183	-35 through 45	-35 through -1	1 through 45
184	-21 through 52	-21 through -1	1 through 52
185	1 through 98	-	1 through 98
186	-21 through 91	-21 through -1	1 through 91
187	-44 through 26	-44 through -1	1 through 26
188	-13 through 79	-13 through -1	1 through 79
189	-42 through 165	-42 through -1	1 through 165
190	1 through 201	-	1 through 201

CONT. TABLE V

191	-37 through 342	-37 through -1	1 through 342
192	1 through 112	-	1 through 112
193	1 through 43	-	1 through 43
194	-16 through 35	-16 through -1	1 through 35
195	-18 through 226	-18 through -1	1 through 226
196	-34 through 319	-34 through -1	1 through 319
197	1 through 30	-	1 through 30
198	-48 through 64	-48 through -1	1 through 64
199	1 through 54	-	1 through 54
200	-21 through 130	-21 through -1	1 through 130
201	-25 through 203	-25 through -1	1 through 203
202	-47 through 17	-47 through -1	1 through 17
203	-31 through 115	-31 through -1	1 through 115
204	1 through 87	-	1 through 87
205	-27 through 13	-27 through -1	1 through 13
206	1 through 154	-	1 through 154
207	1 through 101	-	1 through 101
208	-22 through 434	-22 through -1	1 through 434
209	-17 through 81	-17 through -1	1 through 81
210	-29 through 54	-29 through -1	1 through 54
211	-23 through 206	-23 through -1	1 through 206
212	-21 through 131	-21 through -1	1 through 131
213	-54 through 125	-54 through -1	1 through 125
214	-92 through 177	-92 through -1	1 through 177
215	-22 through 113	-22 through -1	1 through 113
216	-38 through 29	-38 through -1	1 through 29
217	-54 through 71	-54 through -1	1 through 71
218	-21 through 355	-21 through -1	1 through 355
219	-30 through 181	-30 through -1	1 through 181
220	-60 through 94	-60 through -1	1 through 94
221	-42 through 81	-42 through -1	1 through 81
222	-19 through 327	-19 through -1	1 through 327
223	-20 through 190	-20 through -1	1 through 190
224	-20 through 164	-20 through -1	1 through 164
225	-22 through 205	-22 through -1	1 through 205
226	-41 through 33	-41 through -1	1 through 33
227	1 through 73	-	1 through 73
228	-16 through 66	-16 through -1	1 through 66
229	-56 through 63	-56 through -1	1 through 63
230	1 through 54	-	1 through 54
231	-14 through 196	-14 through -1	1 through 196
232	1 through 108	-	1 through 108
233	-18 through 25	-18 through -1	1 through 25
234	1 through 36	-	1 through 36
235	-13 through 294	-13 through -1	1 through 294
236	-32 through 74	-32 through -1	1 through 74
237	-19 through 23	-19 through -1	1 through 23
238	-20 through 97	-20 through -1	1 through 97
239	-37 through 141	-37 through -1	1 through 141
240	-27 through 99	-27 through -1	1 through 99
241	-115 through 59	-115 through -1	1 through 59
378	-20 through 32	-20 through -1	1 through 32
379	-23 through 170	-23 through -1	1 through 170
380	-14 through 68	-14 through -1	1 through 68

CONT. TABLE V

381	-21 through 177	-21 through -1	1 through 177
382	-55 through 105	-55 through -1	1 through 105
383	-18 through 90	-18 through -1	1 through 90
384	-22 through 42	-22 through -1	1 through 42
385	-15 through 12	-15 through -1	1 through 12
386	-21 through 165	-21 through -1	1 through 165
387	-26 through 153	-26 through -1	1 through 153
388	-55 through 95	-55 through -1	1 through 95
389	-31 through 205	-31 through -1	1 through 205
390	-100 through 49	-100 through -1	1 through 49
391	-49 through 20	-49 through -1	1 through 20
392	-30 through 211	-30 through -1	1 through 211
393	-30 through 17	-30 through -1	1 through 17
394	-28 through 37	-28 through -1	1 through 37
395	-24 through 49	-24 through -1	1 through 49
396	-18 through 42	-18 through -1	1 through 42
397	-93 through 99	-93 through -1	1 through 99
398	-72 through 77	-72 through -1	1 through 77
399	-20 through 53	-20 through -1	1 through 53
400	-20 through 66	-20 through -1	1 through 66
401	-21 through 57	-21 through -1	1 through 57
402	-28 through 37	-28 through -1	1 through 37
403	-27 through 184	-27 through -1	1 through 184
404	-80 through 43	-80 through -1	1 through 43
405	-26 through 60	-26 through -1	1 through 60
406	-31 through 131	-31 through -1	1 through 131
407	-37 through 61	-37 through -1	1 through 61
408	-15 through 55	-15 through -1	1 through 55
409	-45 through 15	-45 through -1	1 through 15
410	-22 through 17	-22 through -1	1 through 17
411	-23 through 28	-23 through -1	1 through 28
412	-48 through 47	-48 through -1	1 through 47
413	-32 through 28	-32 through -1	1 through 28
414	-79 through 91	-79 through -1	1 through 91
415	-82 through 108	-82 through -1	1 through 108
416	-60 through 54	-60 through -1	1 through 54
417	-108 through 53	-108 through -1	1 through 53
418	-21 through 46	-21 through -1	1 through 46
419	-32 through 300	-32 through -1	1 through 300
420	-19 through 46	-19 through -1	1 through 46
422	-30 through 27	-30 through -1	1 through 27
423	-17 through 68	-17 through -1	1 through 68
424	-17 through 68	-17 through -1	1 through 68
425	-29 through 40	-29 through -1	1 through 40
426	-56 through 66	-56 through -1	1 through 66
427	-30 through 11	-30 through -1	1 through 11
428	-36 through 14	-36 through -1	1 through 14
429	-18 through 118	-18 through -1	1 through 118
430	-65 through 129	-65 through -1	1 through 129
431	-69 through 72	-69 through -1	1 through 72
432	-69 through 179	-69 through -1	1 through 179
433	-36 through 13	-36 through -1	1 through 13
434	-14 through 72	-14 through -1	1 through 72
435	-58 through 86	-58 through -1	1 through 86

CONT. TABLE V

436	-16 through 105	-16 through -1	1 through 105
437	-16 through 146	-16 through -1	1 through 146
438	-20 through 90	-20 through -1	1 through 90
439	-15 through 56	-15 through -1	1 through 56
440	-24 through 75	-24 through -1	1 through 75
441	-25 through 144	-25 through -1	1 through 144
442	-76 through 91	-76 through -1	1 through 91
443	-15 through 55	-15 through -1	1 through 55
444	-33 through 348	-33 through -1	1 through 348
445	-14 through 25	-14 through -1	1 through 25
446	-37 through 13	-37 through -1	1 through 13
447	-26 through 25	-26 through -1	1 through 25
448	-30 through 212	-30 through -1	1 through 212
449	-60 through 94	-60 through -1	1 through 94
450	-61 through 28	-61 through -1	1 through 28
451	-26 through 47	-26 through -1	1 through 47
452	-34 through 20	-34 through -1	1 through 20
453	-38 through 83	-38 through -1	1 through 83
454	-37 through 129	-37 through -1	1 through 129
455	-26 through 154	-26 through -1	1 through 154
456	-64 through 27	-64 through -1	1 through 27
457	-23 through 234	-23 through -1	1 through 234
458	-60 through 133	-60 through -1	1 through 133
459	-28 through 79	-28 through -1	1 through 79
460	-13 through 108	-13 through -1	1 through 108
461	-17 through 27	-17 through -1	1 through 27
462	-13 through 96	-13 through -1	1 through 96
463	-41 through 102	-41 through -1	1 through 102
464	-30 through 202	-30 through -1	1 through 202
465	-21 through 40	-21 through -1	1 through 40
466	-19 through 15	-19 through -1	1 through 15
467	-54 through 161	-54 through -1	1 through 161
468	-17 through 10	-17 through -1	1 through 10
469	-24 through 61	-24 through -1	1 through 61
470	-16 through 35	-16 through -1	1 through 35
471	-43 through 24	-43 through -1	1 through 24
472	-15 through 48	-15 through -1	1 through 48
473	-58 through 121	-58 through -1	1 through 121
474	-71 through 167	-71 through -1	1 through 167
475	-37 through 141	-37 through -1	1 through 141
476	-21 through 75	-21 through -1	1 through 75
477	-24 through 17	-24 through -1	1 through 17
478	-27 through 86	-27 through -1	1 through 86
479	-18 through 232	-18 through -1	1 through 232
480	-21 through 130	-21 through -1	1 through 130
481	-25 through 214	-25 through -1	1 through 214
482	-92 through 116	-92 through -1	1 through 116
483	-39 through 47	-39 through -1	1 through 47
484	-27 through 13	-27 through -1	1 through 13
485	-16 through 49	-16 through -1	1 through 49
486	-55 through 75	-55 through -1	1 through 75
487	-84 through 125	-84 through -1	1 through 125
488	-17 through 19	-17 through -1	1 through 19
489	-29 through 15	-29 through -1	1 through 15

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490	-52 through 111	-52 through -1	1 through 111
491	-47 through 17	-47 through -1	1 through 17
492	-50 through 168	-50 through -1	1 through 168
493	-15 through 201	-15 through -1	1 through 201
494	-19 through 115	-19 through -1	1 through 115
495	-16 through 69	-16 through -1	1 through 69
496	-29 through 263	-29 through -1	1 through 263
497	-56 through 66	-56 through -1	1 through 66
498	-28 through 31	-28 through -1	1 through 31
499	-13 through 86	-13 through -1	1 through 86
500	-13 through 86	-13 through -1	1 through 86
501	-25 through 83	-25 through -1	1 through 83
502	-15 through 168	-15 through -1	1 through 168
503	-15 through 83	-15 through -1	1 through 83
504	-57 through 126	-57 through -1	1 through 126
505	-14 through 126	-14 through -1	1 through 126
506	-14 through 45	-14 through -1	1 through 45
507	-36 through 65	-36 through -1	1 through 65
508	-55 through 286	-55 through -1	1 through 286
509	-42 through 66	-42 through -1	1 through 66
510	-26 through 54	-26 through -1	1 through 54
511	-44 through 114	-44 through -1	1 through 114
512	-28 through 102	-28 through -1	1 through 102
513	-62 through 137	-62 through -1	1 through 137
514	-25 through 155	-25 through -1	1 through 155

TABLE VI

Id	Collection refs	Deposit Name
40	ATCC # 98921	SignalTag 121-144
41	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
42	ATCC # 98921	SignalTag 121-144
43	ATCC # 98920	SignalTag 67-90
44	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
45	ATCC # 98920	SignalTag 67-90
46	ATCC # 98923	SignalTag 44-66
47	ATCC # 98920	SignalTag 67-90
48	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
49	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
50	ATCC # 98921	SignalTag 121-144
51	ATCC # 98921	SignalTag 121-144
52	ATCC # 98920	SignalTag 67-90
53	ATCC # 98923	SignalTag 44-66
54	ATCC # 98920	SignalTag 67-90
55	ATCC # 98920	SignalTag 67-90
56	ATCC # 98920	SignalTag 67-90
57	ATCC # 98921	SignalTag 121-144
58	ATCC # 98920	SignalTag 67-90
59	ATCC # 98920	SignalTag 67-90
60	ATCC # 98920	SignalTag 67-90
61	ATCC # 98923	SignalTag 44-66
62	ATCC # 98923	SignalTag 44-66
63	ATCC # 98923	SignalTag 44-66
64	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
65	ATCC # 98923	SignalTag 44-66
66	ATCC # 98921	SignalTag 121-144
67	ATCC # 98920	SignalTag 67-90
68	ATCC # 98920	SignalTag 67-90
69	ATCC # 98921	SignalTag 121-144
70	ATCC # 98921	SignalTag 121-144
71	ATCC # 98921	SignalTag 121-144
72	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
73	ATCC # 98923	SignalTag 44-66

74	ATCC # 98923	SignalTag 44-66
75	ATCC # 98920	SignalTag 67-90
76	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
77	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
78	ATCC # 98921	SignalTag 121-144
79	ATCC # 98923	SignalTag 44-66
80	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
81	ATCC # 98921	SignalTag 121-144
82	ATCC # 98920	SignalTag 67-90
83	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
84	ATCC # 98923	SignalTag 44-66
85	ATCC # 98923	SignalTag 44-66
86	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
87	ATCC # 98923	SignalTag 44-66
88	ATCC # 98923	SignalTag 44-66
89	ATCC # 98923	SignalTag 44-66
90	ATCC # 98923	SignalTag 44-66
91	ATCC # 98923	SignalTag 44-66
92	ATCC # 98920	SignalTag 67-90
93	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
94	ATCC # 98923	SignalTag 44-66
95	ATCC # 98923	SignalTag 44-66
96	ATCC # 98920	SignalTag 67-90
97	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
98	ATCC # 98921	SignalTag 121-144
99	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
100	ATCC # 98921	SignalTag 121-144
101	ATCC # 98920	SignalTag 67-90
102	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
103	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
104	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
105	ATCC # 98921	SignalTag 121-144
106	ATCC # 98920	SignalTag 67-90
107	ATCC # 98920	SignalTag 67-90
108	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
109	ATCC # 98923	SignalTag 44-66
110	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120

111	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
112	ATCC # 98920	SignalTag 67-90
113	ATCC # 98920	SignalTag 67-90
114	ATCC # 98923	SignalTag 44-66
115	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
116	ATCC # 98920	SignalTag 67-90
117	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
118	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
119	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
120	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
121	ATCC # 98923	SignalTag 44-66
122	ATCC # 98920	SignalTag 67-90
123	ATCC # 98920	SignalTag 67-90
124	ATCC # 98922	SignalTag 91-94, 96, 97, 99-107, 109-112 et 114-120
125	ECACC # 98121506	SignalTag 11121998
126	ECACC # 98121506	SignalTag 11121998
127	ECACC # 98121506	SignalTag 11121998
128	ECACC # 98121506	SignalTag 11121998
129	ECACC # 98121506	SignalTag 11121998
130	ECACC # 98121506	SignalTag 11121998
131	ECACC # 98121506	SignalTag 11121998
132	ECACC # 98121506	SignalTag 11121998
133	ECACC # 98121506	SignalTag 11121998
134	ECACC # 98121506	SignalTag 11121998
135	ECACC # 98121506	SignalTag 11121998
136	ECACC # 98121506	SignalTag 11121998
137	ECACC # 98121506	SignalTag 11121998
138	ECACC # 98121506	SignalTag 11121998
139	ECACC # 98121506	SignalTag 11121998
140	ECACC # 98121506	SignalTag 11121998

TABLE VII

Internal designation number	SEQ ID NO	Type of sequence
20-5-2-C3-CL0_4	40	DNA
20-8-4-A11-CL2_6	41	DNA
21-1-4-F2-CL11_1	42	DNA
22-11-2-H9-CL1_1	43	DNA
25-7-3-D4-CL0_2	44	DNA
26-27-3-D7-CL0_1	45	DNA
26-35-4-H9-CL1_1	46	DNA
26-45-2-C4-CL2_6	47	DNA
27-1-2-B3-CL0_1	48	DNA
27-1-2-B3-CL0_2	49	DNA
27-19-3-G7-CL11_2	50	DNA
33-10-4-E2-CL13_4	51	DNA
33-10-4-H2-CL2_2	52	DNA
33-110-4-A5-CL1_1	53	DNA
33-13-1-C1-CL1_1	54	DNA
33-30-2-A6-CL0_1	55	DNA
33-35-4-F4-CL1_2	56	DNA
33-35-4-G1-CL1_2	57	DNA
33-36-3-E2-CL1_1	58	DNA
33-36-3-E2-CL1_2	59	DNA
33-36-3-F2-CL2_2	60	DNA
33-4-2-G5-CL2_1	61	DNA
33-49-1-H4-CL1_1	62	DNA
33-66-2-B10-CL4_1	63	DNA
33-97-4-G8-CL2_2	64	DNA
33-98-4-C1-CL1_3	65	DNA
47-14-1-C3-CL0_5	66	DNA
47-15-1-E11-CL0_1	67	DNA
47-15-1-H8-CL0_2	68	DNA
48-1-1-H7-CL0_1	69	DNA
48-1-1-H7-CL0_4	70	DNA
48-1-1-H7-CL0_5	71	DNA
48-3-1-H9-CL0_6	72	DNA
48-54-1-G9-CL2_1	73	DNA

48-54-1-G9-CL3_1	74	DNA
48-74-H2-CL2_2	75	DNA
51-11-3-D5-CL1_3	76	DNA
51-11-3-G9-CL0_1	77	DNA
51-15-4-A12-CL11_3	78	DNA
51-17-4-A4-CL3_1	79	DNA
51-2-3-F10-CL1_5	80	DNA
51-2-4-F5-CL11_2	81	DNA
51-27-4-F2-CL0_2	82	DNA
51-34-3-F8-CL0_2	83	DNA
57-1-4-E2-CL1_2	84	DNA
57-19-2-G8-CL2_1	85	DNA
57-27-3-G10-CL2_2	86	DNA
58-33-3-B4-CL1_2	87	DNA
58-34-3-C9-CL1_2	88	DNA
58-4-4-G2-CL2_1	89	DNA
58-48-1-G3-CL2_4	90	DNA
58-6-1-H4-CL1_1	91	DNA
60-12-1-E11-CL1_2	92	DNA
65-4-4-H3-CL1_1	93	DNA
74-5-1-E4-CL1_2	94	DNA
76-13-3-A9-CL1_2	95	DNA
76-16-1-D6-CL1_1	96	DNA
76-28-3-A12-CL1_5	97	DNA
76-42-2-F3-CL0_1	98	DNA
77-16-4-G3-CL1_3	99	DNA
77-39-4-H4-CL11_4	100	DNA
78-24-3-H4-CL2_1	101	DNA
78-27-3-D1-CL1_6	102	DNA
78-28-3-D2-CL0_2	103	DNA
78-7-1-G5-CL2_6	104	DNA
84-3-1-G10-CL11_6	105	DNA
58-48-4-E2-CL0_1	106	DNA
23-12-2-G6-CL1_2	107	DNA
25-8-4-B12-CL0_5	108	DNA
26-44-3-C5-CL2_1	109	DNA
27-1-2-B3-CL0_3	110	DNA

30-12-3-G5-CLO_1	111	DNA
33-106-2-F10-CL1_3	112	DNA
33-28-4-D1-CLO_1	113	DNA
33-31-3-C8-CL2_1	114	DNA
48-24-1-D2-CL3_2	115	DNA
48-46-4-A11-CL1_4	116	DNA
51-1-4-C1-CLO_2	117	DNA
51-39-3-H2-CL1_2	118	DNA
51-42-3-F9-CL1_1	119	DNA
51-5-3-G2-CLO_4	120	DNA
57-18-4-H5-CL2_1	121	DNA
76-23-3-G8-CL1_1	122	DNA
76-23-3-G8-CL1_3	123	DNA
78-8-3-E6-CLO_1	124	DNA
19-10-1-C2-CL1_3	125	DNA
33-11-1-B11-CL1_2	126	DNA
33-113-2-B8-CL1_2	127	DNA
33-19-1-C11-CL1_1	128	DNA
33-61-2-F6-CLO_2	129	DNA
47-4-4-C6-CL2_2	130	DNA
48-54-1-G9-CL1_1	131	DNA
51-43-3-G3-CLO_1	132	DNA
55-1-3-D11-CLO_1	133	DNA
58-14-2-D3-CL1_2	134	DNA
58-35-2-B6-CL2_3	135	DNA
76-18-1-F6-CL1_1	136	DNA
76-23-3-G8-CL2_2	137	DNA
76-30-3-B7-CL1_1	138	DNA
78-21-3-G7-CL2_1	139	DNA
58-45-4-B11-CL13_2	140	DNA
20-5-2-C3-CLO_4	141	PRT
20-8-4-A11-CL2_6	142	PRT
21-1-4-F2-CL11_1	143	PRT
22-11-2-H9-CL1_1	144	PRT
25-7-3-D4-CLO_2	145	PRT
26-27-3-D7-CLO_1	146	PRT
26-35-4-H9-CL1_1	147	PRT

26-45-2-C4-CL2_6	148	PRT
27-1-2-B3-CLO_1	149	PRT
27-1-2-B3-CLO_2	150	PRT
27-19-3-G7-CL11_2	151	PRT
33-10-4-E2-CL13_4	152	PRT
33-10-4-H2-CL2_2	153	PRT
33-110-4-A5-CL1_1	154	PRT
33-13-1-C1-CL1_1	155	PRT
33-30-2-A6-CLO_1	156	PRT
33-35-4-F4-CL1_2	157	PRT
33-35-4-G1-CL1_2	158	PRT
33-36-3-E2-CL1_1	159	PRT
33-36-3-E2-CL1_2	160	PRT
33-36-3-F2-CL2_2	161	PRT
33-4-2-G5-CL2_1	162	PRT
33-49-1-H4-CL1_1	163	PRT
33-66-2-B10-CL4_1	164	PRT
33-97-4-G8-CL2_2	165	PRT
33-98-4-C1-CL1_3	166	PRT
47-14-1-C3-CLO_5	167	PRT
47-15-1-E11-CLO_1	168	PRT
47-15-1-H8-CLO_2	169	PRT
48-1-1-H7-CLO_1	170	PRT
48-1-1-H7-CLO_4	171	PRT
48-1-1-H7-CLO_5	172	PRT
48-3-1-H9-CLO_6	173	PRT
48-54-1-G9-CL2_1	174	PRT
48-54-1-G9-CL3_1	175	PRT
48-7-4-H2-CL2_2	176	PRT
51-11-3-D5-CL1_3	177	PRT
51-11-3-G9-CLO_1	178	PRT
51-15-4-A12-CL11_3	179	PRT
51-17-4-A4-CL3_1	180	PRT
51-2-3-F10-CL1_5	181	PRT
51-2-4-F5-CL11_2	182	PRT
51-27-4-F2-CLO_2	183	PRT
51-34-3-F8-CLO_2	184	PRT

57-1-4-E2-CL1_2	185	PRT
57-19-2-G8-CL2_1	186	PRT
57-27-3-G10-CL2_2	187	PRT
58-33-3-B4-CL1_2	188	PRT
58-34-3-C9-CL1_2	189	PRT
58-4-4-G2-CL2_1	190	PRT
58-48-1-G3-CL2_4	191	PRT
58-6-1-H4-CL1_1	192	PRT
60-12-1-E11-CL1_2	193	PRT
65-4-4-H3-CL1_1	194	PRT
74-5-1-E4-CL1_2	195	PRT
76-13-3-A9-CL1_2	196	PRT
76-16-1-D6-CL1_1	197	PRT
76-28-3-A12-CL1_5	198	PRT
76-42-2-F3-CLO_1	199	PRT
77-16-4-G3-CL1_3	200	PRT
77-39-4-H4-CL11_4	201	PRT
78-24-3-H4-CL2_1	202	PRT
78-27-3-D1-CL1_6	203	PRT
78-28-3-D2-CLO_2	204	PRT
78-7-1-G5-CL2_6	205	PRT
84-3-1-G10-CL11_6	206	PRT
58-48-4-E2-CLO_1	207	PRT
23-12-2-G6-CL1_2	208	PRT
25-8-4-B12-CLO_5	209	PRT
26-44-3-C5-CL2_1	210	PRT
27-1-2-B3-CLO_3	211	PRT
30-12-3-G5-CLO_1	212	PRT
33-106-2-F10-CL1_3	213	PRT
33-28-4-D1-CLO_1	214	PRT
33-31-3-C8-CL2_1	215	PRT
48-24-1-D2-CL3_2	216	PRT
48-46-4-A11-CL1_4	217	PRT
51-1-4-C1-CLO_2	218	PRT
51-39-3-H2-CL1_2	219	PRT
51-42-3-F9-CL1_1	220	PRT
51-5-3-G2-CLO_4	221	PRT

57-18-4-H5-CL2_1	222	PRT
76-23-3-G8-CL1_1	223	PRT
76-23-3-G8-CL1_3	224	PRT
78-8-3-E6-CLO_1	225	PRT
19-10-1-C2-CL1_3	226	PRT
33-11-1-B11-CL1_2	227	PRT
33-113-2-B8-CL1_2	228	PRT
33-19-1-C11-CL1_1	229	PRT
33-61-2-F6-CLO_2	230	PRT
47-4-4-C6-CL2_2	231	PRT
48-54-1-G9-CL1_1	232	PRT
51-43-3-G3-CLO_1	233	PRT
55-1-3-D11-CLO_1	234	PRT
58-14-2-D3-CL1_2	235	PRT
58-35-2-B6-CL2_3	236	PRT
76-18-1-F6-CL1_1	237	PRT
76-23-3-G8-CL2_2	238	PRT
76-30-3-B7-CL1_1	239	PRT
78-21-3-G7-CL2_1	240	PRT
58-45-4-B11-CL13_2	241	PRT
20-6-1-D11-FL2	242	DNA
20-8-4-A11-FL2	243	DNA
22-6-2-C1-FL2	244	DNA
22-11-2-H9-FL1	245	DNA
23-8-3-B1-FL1	246	DNA
24-3-3-C6-FL1	247	DNA
24-4-1-H3-FL1	248	DNA
26-45-2-C4-FL2	249	DNA
26-48-1-H10-FL1	250	DNA
26-49-1-A5-FL2	251	DNA
30-6-4-E3-FL3	252	DNA
33-6-1-G11-FL1	253	DNA
33-8-1-A3-FL2	254	DNA
33-11-3-C6-FL1	255	DNA
33-14-4-E1-FL1	256	DNA
33-21-2-D5-FL1	257	DNA
33-26-4-E10-FL1	258	DNA

33-27-1-E11-FL1	259	DNA
33-28-4-D1-FL1	260	DNA
33-28-4-E2-FL2	261	DNA
33-30-4-C4-FL1	262	DNA
33-35-4-F4-FL1	263	DNA
33-36-3-F2-FL2	264	DNA
33-52-4-F9-FL2	265	DNA
33-52-4-H3-FL1	266	DNA
33-59-1-B7-FL1	267	DNA
33-71-1-A8-FL1	268	DNA
33-72-2-B2-FL1	269	DNA
33-105-2-C3-FL1	270	DNA
33-107-4-C3-FL1	271	DNA
33-110-2-G4-FL1	272	DNA
47-7-4-D2-FL2	273	DNA
47-10-2-G12-FL1	274	DNA
47-14-3-D8-FL1	275	DNA
47-18-3-C2-FL1	276	DNA
47-18-3-G5-FL2	277	DNA
47-18-4-E3-FL2	278	DNA
48-3-1-H9-FL3	279	DNA
48-4-2-H3-FL1	280	DNA
48-6-1-C9-FL1	281	DNA
48-7-4-H2-FL2	282	DNA
48-8-1-D8-FL3	283	DNA
48-13-3-H8-FL1	284	DNA
48-19-3-A7-FL1	285	DNA
48-19-3-G1-FL1	286	DNA
48-25-4-D8-FL1	287	DNA
48-21-4-H4-FL1	288	DNA
48-26-3-B8-FL2	289	DNA
48-29-1-E2-FL1	290	DNA
48-31-3-F7-FL1	291	DNA
48-47-3-A5-FL1	292	DNA
51-1-1-G12-FL1	293	DNA
51-1-4-E9-FL3	294	DNA
51-1-4-E9-FL2	295	DNA

51-2-1-E10-FL1	296	DNA
51-2-3-F10-FL1	297	DNA
51-2-4-F5-FL1	298	DNA
51-3-3-B10-FL2	299	DNA
51-3-3-B10-FL3	300	DNA
51-7-3-G3-FL1	301	DNA
51-10-3-D11-FL1	302	DNA
51-11-3-D5-FL1	303	DNA
51-13-1-F7-FL3	304	DNA
51-15-4-H10-FL1	305	DNA
51-17-4-A4-FL1	306	DNA
51-18-1-C3-FL1	307	DNA
51-25-3-F3-FL1	308	DNA
51-27-1-E8-FL1	309	DNA
51-28-2-G1-FL2	310	DNA
51-39-3-H2-FL1	311	DNA
51-42-3-F9-FL1	312	DNA
51-44-4-H4-FL1	313	DNA
55-1-3-H10-FL1	314	DNA
55-5-4-A6-FL1	315	DNA
58-26-3-D1-FL1	316	DNA
57-18-1-D5-FL1	317	DNA
57-27-3-A11-FL1	318	DNA
57-27-3-G10-FL2	319	DNA
58-10-3-D12-FL1	320	DNA
58-11-1-G10-FL1	321	DNA
58-11-2-G8-FL2	322	DNA
58-36-3-A9-FL2	323	DNA
58-38-1-A2-FL2	324	DNA
58-38-1-E5-FL1	325	DNA
58-44-2-B3-FL3	326	DNA
58-45-3-H11-FL1	327	DNA
58-53-2-B12-FL2	328	DNA
59-9-4-A10-FL1	329	DNA
60-16-3-A6-FL1	330	DNA
60-17-3-G8-FL2	331	DNA
62-5-4-B10-FL1	332	DNA

65-4-4-H3-FL1	333	DNA
74-3-1-B9-FL1	334	DNA
76-4-1-G5-FL1	335	DNA
76-7-3-A12-FL1	336	DNA
76-16-4-C9-FL3	337	DNA
76-30-3-B7-FL1	338	DNA
77-5-1-C2-FL1	339	DNA
77-5-4-E7-FL1	340	DNA
77-11-1-A3-FL1	341	DNA
77-16-3-D7-FL1	342	DNA
77-16-4-G3-FL1	343	DNA
77-25-1-A6-FL1	344	DNA
77-26-2-F2-FL3	345	DNA
78-6-2-E3-FL2	346	DNA
78-7-1-G5-FL2	347	DNA
78-16-2-C2-FL1	348	DNA
78-18-3-B4-FL3	349	DNA
78-20-1-G11-FL1	350	DNA
78-22-3-E10-FL1	351	DNA
78-24-2-B8-FL1	352	DNA
78-24-3-A8-FL1	353	DNA
78-24-3-H4-FL2	354	DNA
78-25-1-F11-FL1	355	DNA
78-26-1-B5-FL1	356	DNA
78-27-3-D1-FL1	357	DNA
78-29-1-B2-FL1	358	DNA
78-29-4-B6-FL1	359	DNA
14-1-3-E6-FL1	360	DNA
30-9-1-G8-FL2	361	DNA
33-10-4-H2-FL2	362	DNA
33-10-4-H2-FL1	363	DNA
74-10-3-C9-FL2	364	DNA
33-97-4-G8-FL3	365	DNA
33-97-4-G8-FL2	366	DNA
33-104-4-H4-FL1	367	DNA
47-2-3-B3-FL1	368	DNA
47-37-4-G11-FL1	369	DNA

57-25-1-F10-FL2	370	DNA
58-19-3-D3-FL1	371	DNA
58-34-3-C9-FL2	372	DNA
58-48-4-E2-FL2	373	DNA
76-21-1-C4-FL1	374	DNA
78-26-2-H7-FL1	375	DNA
77-20-2-E11-FL1	376	DNA
47-1-3-F7-FL2	377	DNA
20-6-1-D11-FL2	378	PRT
20-8-4-A11-FL2	379	PRT
22-6-2-C1-FL2	380	PRT
22-11-2-H9-FL1	381	PRT
23-8-3-B1-FL1	382	PRT
24-3-3-C6-FL1	383	PRT
24-4-1-H3-FL1	384	PRT
26-45-2-C4-FL2	385	PRT
26-48-1-H10-FL1	386	PRT
26-49-1-A5-FL2	387	PRT
30-6-4-E3-FL3	388	PRT
33-6-1-G11-FL1	389	PRT
33-8-1-A3-FL2	390	PRT
33-11-3-C6-FL1	391	PRT
33-14-4-E1-FL1	392	PRT
33-21-2-D5-FL1	393	PRT
33-26-4-E10-FL1	394	PRT
33-27-1-E11-FL1	395	PRT
33-28-4-D1-FL1	396	PRT
33-28-4-E2-FL2	397	PRT
33-30-4-C4-FL1	398	PRT
33-35-4-F4-FL1	399	PRT
33-36-3-F2-FL2	400	PRT
33-52-4-F9-FL2	401	PRT
33-52-4-H3-FL1	402	PRT
33-59-1-B7-FL1	403	PRT
33-71-1-A8-FL1	404	PRT
33-72-2-B2-FL1	405	PRT
33-105-2-C3-FL1	406	PRT

33-107-4-C3-FL1	407	PRT
33-110-2-G4-FL1	408	PRT
47-7-4-D2-FL2	409	PRT
47-10-2-G12-FL1	410	PRT
47-14-3-D8-FL1	411	PRT
47-18-3-C2-FL1	412	PRT
47-18-3-G5-FL2	413	PRT
47-18-4-E3-FL2	414	PRT
48-3-1-H9-FL3	415	PRT
48-4-2-H3-FL1	416	PRT
48-6-1-C9-FL1	417	PRT
48-7-4-H2-FL2	418	PRT
48-8-1-D8-FL3	419	PRT
48-13-3-H8-FL1	420	PRT
48-19-3-A7-FL1	421	PRT
48-19-3-G1-FL1	422	PRT
48-25-4-D8-FL1	423	PRT
48-21-4-H4-FL1	424	PRT
48-26-3-B8-FL2	425	PRT
48-29-1-E2-FL1	426	PRT
48-31-3-F7-FL1	427	PRT
48-47-3-A5-FL1	428	PRT
51-1-1-G12-FL1	429	PRT
51-1-4-E9-FL3	430	PRT
51-1-4-E9-FL2	431	PRT
51-2-1-E10-FL1	432	PRT
51-2-3-F10-FL1	433	PRT
51-2-4-F5-FL1	434	PRT
51-3-3-B10-FL2	435	PRT
51-3-3-B10-FL3	436	PRT
51-7-3-G3-FL1	437	PRT
51-10-3-D11-FL1	438	PRT
51-11-3-D5-FL1	439	PRT
51-13-1-F7-FL3	440	PRT
51-15-4-H10-FL1	441	PRT
51-17-4-A4-FL1	442	PRT
51-18-1-C3-FL1	443	PRT

51-25-3-F3-FL1	444	PRT
51-27-1-E8-FL1	445	PRT
51-28-2-G1-FL2	446	PRT
51-39-3-H2-FL1	447	PRT
51-42-3-F9-FL1	448	PRT
51-44-4-H4-FL1	449	PRT
55-1-3-H10-FL1	450	PRT
55-5-4-A6-FL1	451	PRT
58-26-3-D1-FL1	452	PRT
57-18-1-D5-FL1	453	PRT
57-27-3-A11-FL1	454	PRT
57-27-3-G10-FL2	455	PRT
58-10-3-D12-FL1	456	PRT
58-11-1-G10-FL1	457	PRT
58-11-2-G8-FL2	458	PRT
58-36-3-A9-FL2	459	PRT
58-38-1-A2-FL2	460	PRT
58-38-1-E5-FL1	461	PRT
58-44-2-B3-FL3	462	PRT
58-45-3-H11-FL1	463	PRT
58-53-2-B12-FL2	464	PRT
59-9-4-A10-FL1	465	PRT
60-16-3-A6-FL1	466	PRT
60-17-3-G8-FL2	467	PRT
62-5-4-B10-FL1	468	PRT
65-4-4-H3-FL1	469	PRT
74-3-1-B9-FL1	470	PRT
76-4-1-G5-FL1	471	PRT
76-7-3-A12-FL1	472	PRT
76-16-4-C9-FL3	473	PRT
76-30-3-B7-FL1	474	PRT
77-5-1-C2-FL1	475	PRT
77-5-4-E7-FL1	476	PRT
77-11-1-A3-FL1	477	PRT
77-16-3-D7-FL1	478	PRT
77-16-4-G3-FL1	479	PRT
77-25-1-A6-FL1	480	PRT

77-26-2-F2-FL3	481	PRT
78-6-2-E3-FL2	482	PRT
78-7-1-G5-FL2	483	PRT
78-16-2-C2-FL1	484	PRT
78-18-3-B4-FL3	485	PRT
78-20-1-G11-FL1	486	PRT
78-22-3-E10-FL1	487	PRT
78-24-2-B8-FL1	488	PRT
78-24-3-A8-FL1	489	PRT
78-24-3-H4-FL2	490	PRT
78-25-1-F11-FL1	491	PRT
78-26-1-B5-FL1	492	PRT
78-27-3-D1-FL1	493	PRT
78-29-1-B2-FL1	494	PRT
78-29-4-B6-FL1	495	PRT
14-1-3-E6-FL1	496	PRT
30-9-1-G8-FL2	497	PRT
33-10-4-H2-FL2	498	PRT
33-10-4-H2-FL1	499	PRT
74-10-3-C9-FL2	500	PRT
33-97-4-G8-FL3	501	PRT
33-97-4-G8-FL2	502	PRT
33-104-4-H4-FL1	503	PRT
47-2-3-B3-FL1	504	PRT
47-37-4-G11-FL1	505	PRT
57-25-1-F10-FL2	506	PRT
58-19-3-D3-FL1	507	PRT
58-34-3-C9-FL2	508	PRT
58-48-4-E2-FL2	509	PRT
76-21-1-C4-FL1	510	PRT
78-26-2-H7-FL1	511	PRT
77-20-2-E11-FL1	512	PRT
47-1-3-F7-FL2	513	PRT

TABLE VIII

ID	Locations	PROSITE Signature Name
195	110-121	Aldehyde dehydrogenases cys-teine active site
221	28-37	ATP synthase alpha and beta subunits signature
223	171-181	Regulator of chromosome condensation (RCC1) signature 2
225	90-112	Phosphatidylethanolamine-binding protein family signature
226	10-34	Protein kinases ATP-binding region signature

WHAT IS CLAIMED IS:

1. A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 40-140 and 242-377 or a sequence complementary thereto.
2. A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of
5 SEQ ID NOs: 40-140 and 242-377 or one of the sequences complementary thereto.
3. A purified or isolated nucleic acid comprising the full coding sequences of one of SEQ ID NOs: 40, 42-44, 46, 48, 49, 51, 53, 60, 62-72, 76-78, 80-83, 85-88, 90, 93, 94, 97, 99-102, 104, 107-125, 127, 132, 135-138, 140 and 242-377 wherein the full coding sequence comprises the sequence encoding signal peptide and the sequence encoding mature protein.
- 10 4. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 40-44, 46, 48, 49, 51-53, 55, 56, 58-72, 75-78, 80-88, 90, 93, 94, 97, 99-125, 127, 132, 133, 135-138, 140, and 242-377 which encode a mature protein.
5. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 40, 42-46, 48, 49, 51, 53, 57, 60, 62-73, 76-78, 80-83, 85-88, 90, 93-95, 97, 99-102, 104, 107-125, 127, 128, 130, 132, 134-140
15 and 242-377 which encode the signal peptide.
6. A purified or isolated nucleic acid encoding a polypeptide having the sequence of one of the sequences of SEQ ID NOs: 141-241 and 378-513.
7. A purified or isolated nucleic acid encoding a polypeptide having the sequence of a mature protein included in one of the sequences of SEQ ID NOs: 141-145, 147, 149, 150, 152-154, 156, 157, 159-172, 176-179, 181-
20 189, 191, 194, 195, 198, 200-226, 228, 233, 234, 236-239, 241 and 378-513.
8. A purified or isolated nucleic acid encoding a polypeptide having the sequence of a signal peptide included in one of the sequences of SEQ ID NOs: 141, 143-147, 149, 150, 152, 154, 158, 161, 163-174, 177-179, 181-184, 186-189, 191, 194-196, 198, 200-203, 205, 208-226, 228, 229, 231, 233, 235-241, and 378-513.
9. A purified or isolated protein comprising the sequence of one of SEQ ID NOs: 141-241 and 378-513.
- 25 10. A purified or isolated polypeptide comprising at least 10 consecutive amino acids of one of the sequences of SEQ ID NOs: 141-241 and 378-513.
11. An isolated or purified polypeptide comprising a signal peptide of one of the polypeptides of SEQ ID NOs: 141, 143-147, 149, 150, 152, 154, 158, 161, 163-174, 177-179, 181-184, 186-189, 191, 194-196, 198, 200-203, 205, 208-226, 228, 229, 231, 233, 235-241, and 378-513.
- 30 12. An isolated or purified polypeptide comprising a mature protein of one of the polypeptides of SEQ ID NOs: 141-145, 147, 149, 150, 152-154, 156, 157, 159-172, 176-179, 181-189, 191, 194, 195, 198, 200-226, 228, 233, 234, 236-239, 241 and 378-513.
13. A method of making a protein comprising one of the sequences of SEQ ID NO: 141-241 and 378-513, comprising the steps of:

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obtaining a cDNA comprising one of the sequences of sequence of SEQ ID NO: 40-140 and 242-377;
inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter; and
introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said
cDNA.

- 5 14. The method of Claim 13, further comprising the step of isolating said protein.
15. A protein obtainable by the method of Claim 14.
16. A host cell containing a recombinant nucleic acid of Claim 1.
17. A purified or isolated antibody capable of specifically binding to a protein having the sequence of one
 of SEQ ID NOs: 141-241 and 378-513.
- 10 18. In an array of polynucleotides of at least 15 nucleotides in length, the improvement comprising
 inclusion in said array of at least one of the sequences of SEQ ID NOs: 40-140 and 242-377, or one of the sequences
 complementary to the sequences of SEQ ID NOs: 40-140 and 242-377, or a fragment thereof of at least 15 consecutive
 nucleotides.
19. A purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent
15 conditions to the sequence of one of SEQ ID NOs: 40-140 and 242-377 or a sequence complementary to one of the
 sequences of SEQ ID NOs: 40-140 and 242-377.
20. A purified or isolated antibody capable of binding to a polypeptide comprising at least 10 consecutive
 amino acids of the sequence of one of SEQ ID NOs: 141-241 and 378-513.

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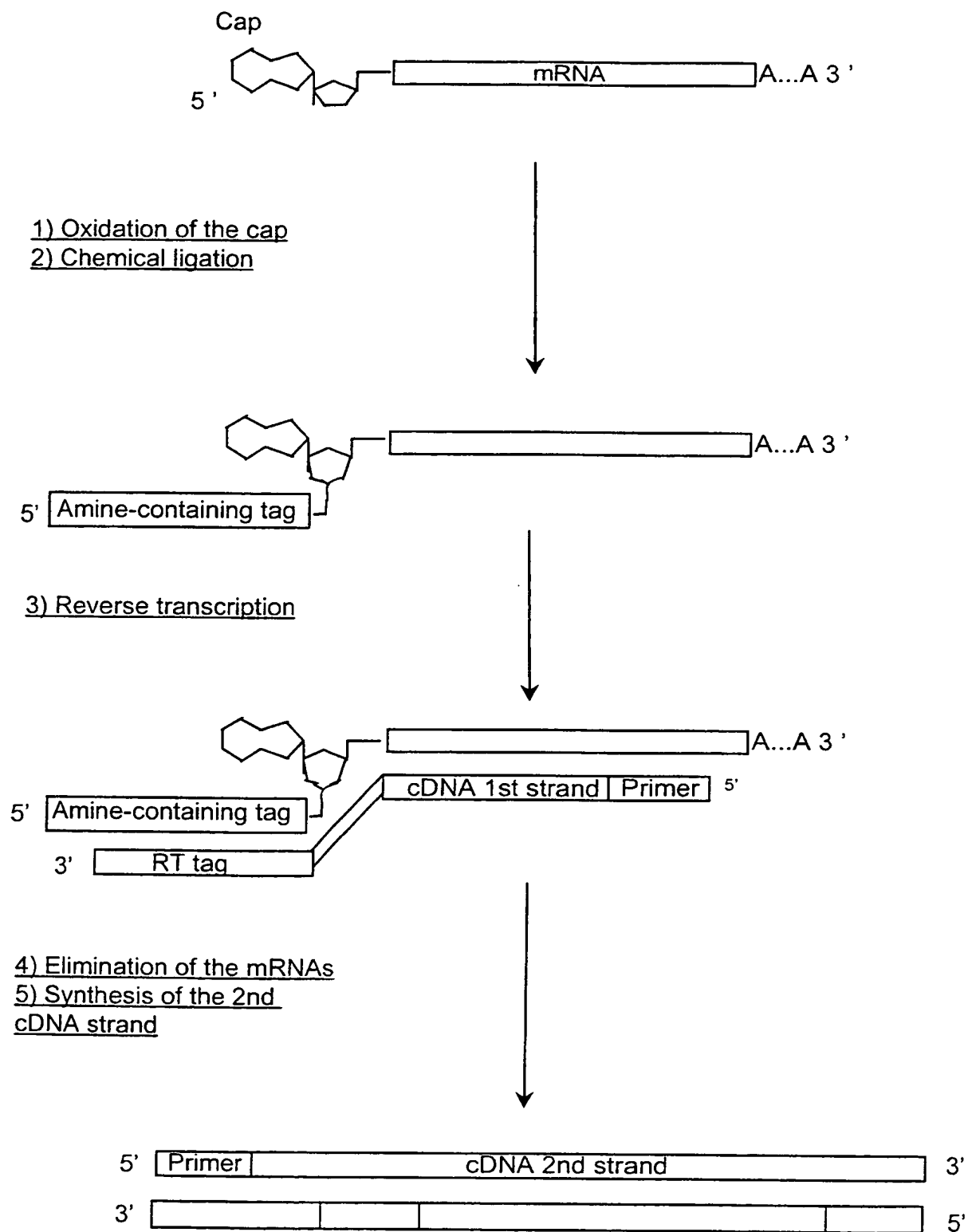


Figure 1

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3,5	0,121	0,036	0,467	0,664
4	0,096	0,06	0,519	0,708
4,5	0,078	0,079	0,565	0,745
5	0,062	0,098	0,615	0,782
5,5	0,05	0,127	0,659	0,813
6	0,04	0,163	0,694	0,836
6,5	0,033	0,202	0,725	0,855
7	0,025	0,248	0,763	0,878
7,5	0,021	0,304	0,78	0,889
8	0,015	0,368	0,816	0,909
8,5	0,012	0,418	0,836	0,92
9	0,009	0,512	0,856	0,93
9,5	0,007	0,581	0,863	0,934
10	0,006	0,679	0,835	0,919

FIGURE 2

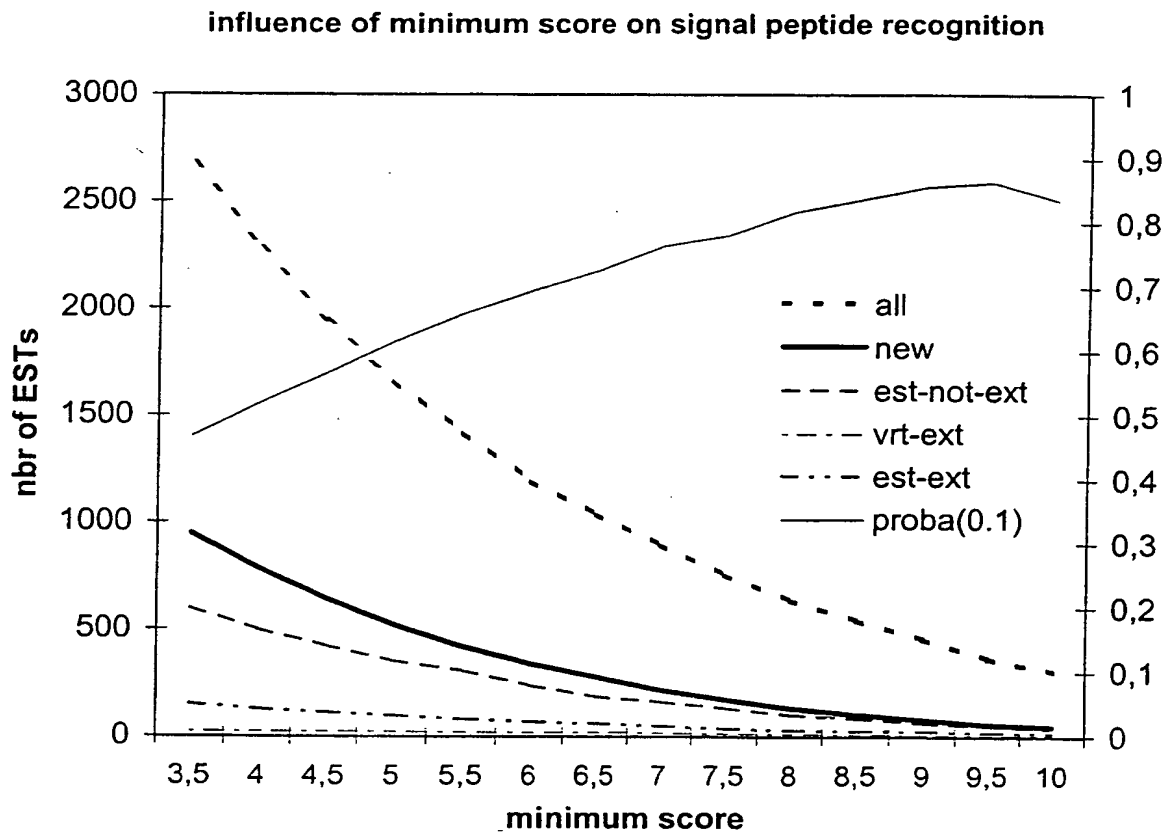


FIGURE 3

Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3,5	2674	947	599	23	150
4	2278	784	499	23	126
4,5	1943	647	425	22	112
5	1657	523	353	21	96
5,5	1417	419	307	19	80
6	1190	340	238	18	68
6,5	1035	280	186	18	60
7	893	219	161	15	48
7,5	753	173	132	12	36
8	636	133	101	11	29
8,5	543	104	83	8	26
9	456	81	63	6	24
9,5	364	57	48	6	18
10	303	47	35	6	15

FIGURE 4

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Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	16	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Surrenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	55	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

FIGURE 5

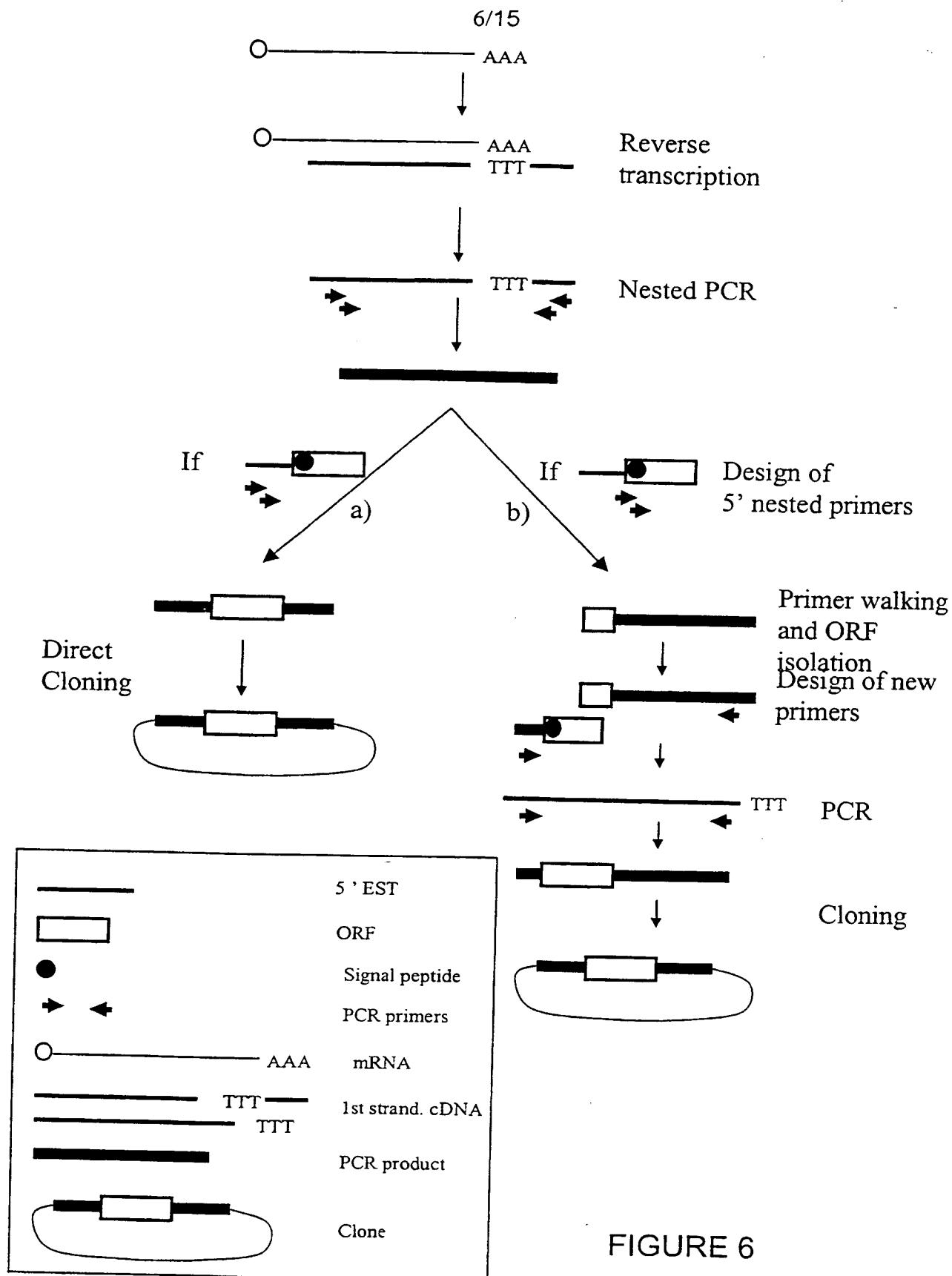
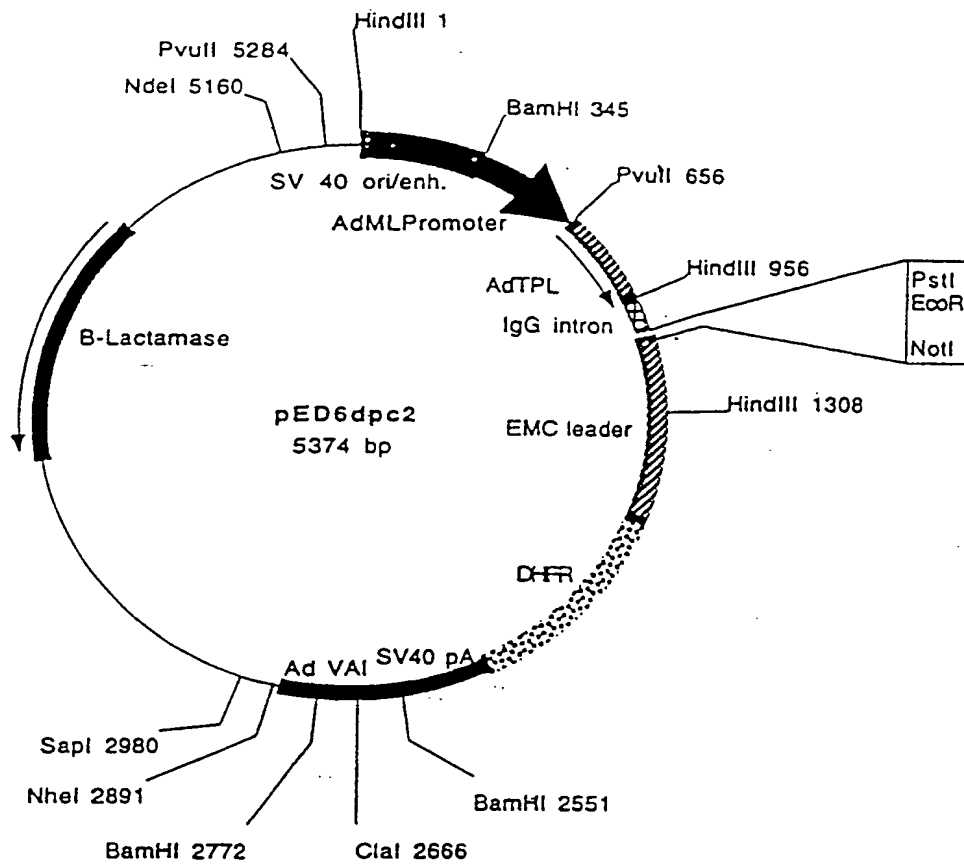


FIGURE 6

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Plasmid name: pED6dpc2

Plasmid size: 5374 bp

FIGURE 7

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Description of promoters structure isolated from SignalTag 5 'ESTs

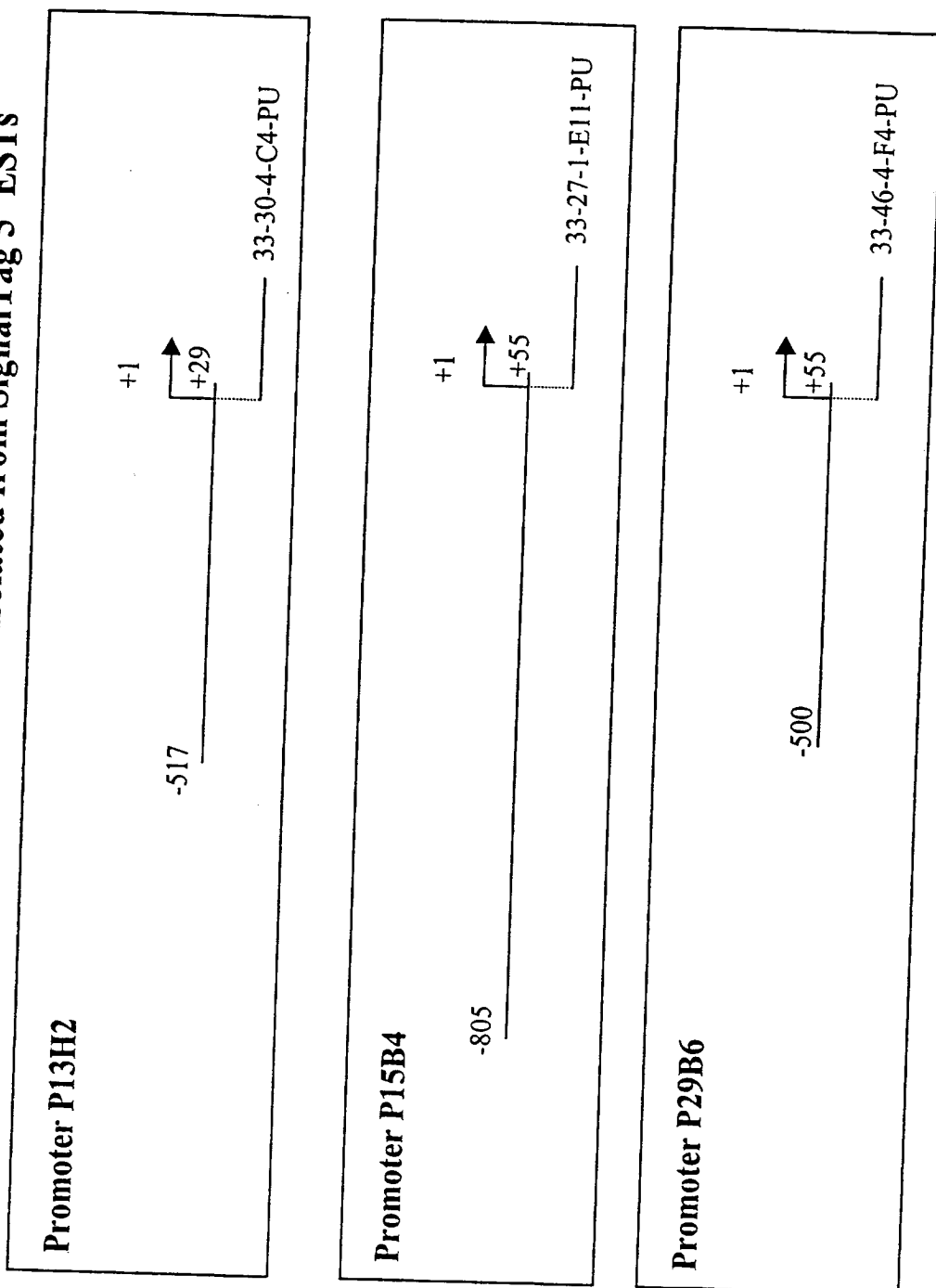


FIGURE 8

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Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences

Promoter sequence P13H2 (546 bp):

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.983	9	TGTCAGTTG
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAATTAG
S8_01	-425	+	0.966	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-364	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHAE47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETAE47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETAITF2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC
IK2_01	-126	+	0.985	12	AGTTGGGAATTCC
CREL_01	-123	+	0.962	10	TGGGAATTCC
GATA1_02	-96	+	0.950	14	TCAGTGATATGGCA
SRY_02	-41	-	0.951	12	TAAAACAAAACA
E2F_02	-33	+	0.957	8	TTAGCGC
MZF1_01	-5	-	0.975	8	TGAGGGGA

Promoter sequence P15B4 (861bp) :

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q6	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCTTGGA
STAT_01	-673	-	0.951	9	TTCCAGGA
MZF1_01	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTTCC
MZF1_01	-424	+	0.986	8	AGAGGGGA
SRY_02	-398	-	0.955	12	GAAAACAAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTCC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.986	8	AGAGGGGA

Promoter sequence P29B6 (555 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	CAGCACGTGAGT
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT
CETS1P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGGTCTC

Figure 9

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100.0% identity in 125 aa overlap

```
          10      20      30      40      50      60
SEQ ID NO: 217 MADEELEALRRQRLAELQAKHGDPGDAAQQEAKHREAEMRNSILAQVLDQSARARLSNLA
               X::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ ID NO: 516 MADEELEALRRQRLAELQAKHGDPGDAAQQEAKHREAEMRNSILAQVLDQSARARLSNLA
               10      20      30      40      50      60

          70      80      90     100     110     120
SEQ ID NO: 217 LVKPEKTKAVENYLIQMARYGQLSEKVSEQGLIEILKKVSQQTEKTTTVKFNRRKVMDS
               :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ ID NO: 516 LVKPEKTKAVENYLIQMARYGQLSEKVSEQGLIEILKKVSQQTEKTTTVKFNRRKVMDS
               70      80      90     100     110     120
```

```
SEQ ID NO: 217 EDDDY
               ::::X
SEQ ID NO: 516 EDDDY
```

FIGURE 10

11/15

CLUSTAL W(1.5) multiple sequence alignment

```
SEQ ID NO: 517      MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
SEQ ID NO: 232      -----MGCVFQSTEDKCIFKIDWTLS
SEQ ID NO: 174      -----MGCVFQSTEDKRIFKIDWTLS
SEQ ID NO: 175      -----MGCVFQSTVDKCIFKIDWTLS
                      ***** ** *****

SEQ ID NO: 517      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDNLCDGSLLLQDVQDVE-----
SEQ ID NO: 232      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTYICEIRL
SEQ ID NO: 174      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDNLCDGSLLLQDVQEQADQGTYICEIRL
SEQ ID NO: 175      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTYICEIRL
                      *****

SEQ ID NO: 517      -----
SEQ ID NO: 232      KGESQVFKKAVVLHVLPEEPKGTQMLT-----
SEQ ID NO: 174      KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE
SEQ ID NO: 175      KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGR--RAK

SEQ ID NO: 517      -----
SEQ ID NO: 232      -----
SEQ ID NO: 174      IVFRYYHKLMSAEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGN
SEQ ID NO: 175      VTRRKHHCVREGSG-----

SEQ ID NO: 517      -----
SEQ ID NO: 232      -----
SEQ ID NO: 174      LVFKKTIIVLHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTC
SEQ ID NO: 175      -----

SEQ ID NO: 517      -----
SEQ ID NO: 232      -----
SEQ ID NO: 174      GNKSSVNSTVLVKNTKKTNP
SEQ ID NO: 175      -----
```

FIGURE 11

12/15

99.6% identity in 225 aa overlap

```

      10      20      30      40      50      60
SEQ ID NO: 515 PTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQEKEGSSGRCMLTLLGLSFILAGLI
SEQ ID NO: 231                               LRVATQEKEGSSGRCMLTLLGLSFILAGLI
                                         10      20      30

      70      80      90     100     110     120
SEQ ID NO: 515 VGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDV
SEQ ID NO: 231 VGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDV
                      40      50      60      70      80      90

     130     140     150     160     170     180
SEQ ID NO: 515 PVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLAGSRY
SEQ ID NO: 231 PVPSFSDSDPAAIHDFEKGMTAYLDLLLGCYLMPLNTSIVMPPKNLVELFGKLAGSRY
                      100     110     120     130     140     150

     190     200     210     220     230     240
SEQ ID NO: 515 LPQTYVVREDLVAVEEIRDVSNLGFIFYQLCNRKSFRLRRRDLLLGFNKRAIDKCWKIR
SEQ ID NO: 231 LPQTYVVREDLVAVEEIRDVSNLGFIFYQLCNRKSFRLRRRDLLLGFNKRAIDKCWKIR
                      160     170     180     190     200     210

     250     260
SEQ ID NO: 515 HFPNEFIVETKICQE
SEQ ID NO: 231 HFPNEFIVETKICQE
                      220
```

FIGURE 12

13/15

99.7% identity in 353 aa overlap

```

                                10      20      30
SEQ ID NO:196                MERGLKSADPRDGTGYTGWAGIAVLYLHLY
                                :
SEQ ID NO:518 LAEGYFDAAGRLTPEFSQRLTNKIRELLQQMERGLKSADPRDGTGYTGWAGIAVLYLHLY
                   20      30      40      50      60      70

                   40      50      60      70      80      90
SEQ ID NO:196 DVFGDPAYLQLAHGYVKQSLNCLTKRSITFLCGDAGPLAVAAVLYHKMNNEKQAEDCITR
                   :
SEQ ID NO:518 DVFGDPAYLQLAHGYVKQSLNCLTKRSITFLCGDAGPLAVAAVLYHKMNNEKQAEDCITR
                   80      90      100     110     120     130

                   100     110     120     130     140     150
SEQ ID NO:196 LIHLNKIDPHAPNEMLYGRIGYIYALLFVNKNFGVEKTPQSHIQICETILTSGENLARK
                   :
SEQ ID NO:518 LIHLNKIDPHAPNEMLYGRIGYIYALLFVNKNFGVEKIPQSHIQICETILTSGENLARK
                   140     150     160     170     180     190

                   160     170     180     190     200     210
SEQ ID NO:196 RNFTAKSPLMYEWYQEYYVGAAGLAGIYIYLLMQPSLQVSQGKLHSLVKPSVDYVCQLKF
                   :
SEQ ID NO:518 RNFTAKSPLMYEWYQEYYVGAAGLAGIYIYLLMQPSLQVSQGKLHSLVKPSVDYVCQLKF
                   200     210     220     230     240     250

                   220     230     240     250     260     270
SEQ ID NO:196 PSGNYPPCIGDNRDLLVHWCHGAPGVIYMLIQAYKVFREEKYLCDAYQCADVIWQYGLLK
                   :
SEQ ID NO:518 PSGNYPPCIGDNRDLLVHWCHGAPGVIYMLIQAYKVFREEKYLCDAYQCADVIWQYGLLK
                   260     270     280     290     300     310

                   280     290     300     310     320     330
SEQ ID NO:196 KGYGLCHGSAGNAYAFLLTYNLTQDMKYLYRACKFAEWCLEYGEHGCRTPDTPFSLFEGM
                   :
SEQ ID NO:518 KGYGLCHGSAGNAYAFLLTYNLTQDMKYLYRACKFAEWCLEYGEHGCRTPDTPFSLFEGM
                   320     330     340     350     360     370

                   340     350
SEQ ID NO:196 AGTIYFLADLLVPTKARFPAPFEL
                   :
SEQ ID NO:518 AGTIYFLADLLVPTKARFPAPFEL
                   380     390
```

FIGURE 13

14/15

98.5% identity in 194 aa overlap

```

          90      100      110      120      130      140
SEQ ID NO:519 ARNLPPLTDAQKNKLRHLSVVTLAAKVKCIPYAVLLEALALRNVRQLEDLVIEAVYADVL
               :
SEQ ID NO:158 ARNLPPLTEAQKNKLRHLSVVTLAAKVKCIPYAVLLEALALRNVRQLEDLVIEAVYADVL
          60      70      80      90      100      110

          150      160      170      180      190      200
SEQ ID NO:519 RGSLDQRNQRLEVDYSIGRDIQRQDLSAIAQTLQEWCVGCEVVLSGIEEQVSRANQHKEQ
               :
SEQ ID NO:158 RGSLDQRNQRLEVDYSIGRDIQRQDLSAIAQTLQEWCVGCEVVLSGIEEQVSRANQHKEQ
          120      130      140      150      160      170

          210      220      230      240      250      260
SEQ ID NO:519 QLGLKQQIESEVANLKKTIKVTAAAAAATSQDPEQHLTELREPASGTNQRQPSKKASKG
               :
SEQ ID NO:158 QLGLKQQIESEVANLKKTIKVTAAAAAATSQDPEQHLTELREPAPGTNQRQPSKKASKG
          180      190      200      210      220      230

          270
SEQ ID NO:519 KGLRGSAKIWSKSN
               :
SEQ ID NO:158 KGLRGSAKIWSKSN
          240      250

```

88.7% identity in 62 aa overlap

```

          10      20      30      40      50      60
SEQ ID NO:519 MSAEVKVTGQNQEQLLLAKSAKGAALATLIHQVLEAPGVYVFGELLDMPNVRELAESDF
               :
SEQ ID NO:158 MSAEVKVTGQNQEQLLLAKSAKGAALATLIHQVLEAPGVYVFGELLDMPNVRELXARNL
          10      20      30      40      50      60

SEQ ID NO:519 AS
               .X
SEQ ID NO:158 PP

```

FIGURE 14

15/15

68.9% identity in 74 aa overlap

```

                10      20      30      40      50
SEQ ID NO:226  MIARRNPVPLRFLPDEARSLPPPKLTDPRLLYIGFLGYCSGLIDNLIARRRPIATAGLHR
                .....
SEQ ID NO:514  MMTGRQGRATFQFLPDEARSLPPPKLTDPRLAFVGFLGYCSGLIDNAIRRRPVLLAGLHR
                10      20      30      40      50      60

                60      70
SEQ ID NO:226  QLLYITAFFLLDIIL
                .....
SEQ ID NO:514  QLLYITSFVFGYLLKRQDYMAYVRDHDMSYIKSHPEDFPEKDKKTYGEVFEEFHPVR
                70      80      90      100     110     120
```

FIGURE 15

<110> Dumas Milne Edwards, Jean-Baptiste
Duclert, Aymeric
Bougueleret, Lydie

<120> Extended cDNAs for Secreted Proteins

<130> GENSET.019A

<160> 519

<170> Patent.pm

<210> 1

<211> 47

<212> RNA

<213> Artificial Sequence

<220>

<221> In vitro transcription product

<221> modified_base

<222> (1)...(1)

<223> m7g

<400> 1

ngcauccuac ucccauccaa uuccacccua acuccuccca ucuccac

47

<210> 2

<211> 46

<212> RNA

<213> Artificial Sequence

<220>

<223> In vitro transcription product

<400> 2

gcauccuacu cccauccaau uccacccuaa cuccucccau cuccac

46

<210> 3

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> In vitro transcription product

<400> 3

atcaagaatt cgcacgagac catta

25

<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 4

taatggtctc gtgcgaattc ttgat

25

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 5

ccgacaagac caacgtcaag gccgc

25

<210> 6

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 6

tcaccagcag gcagtggctt aggag

25

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 7

agtgattcct gctactttgg atggc

25

<210> 8

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 8

gcttggtcctt gttctggagt ttaga

25

<210> 9

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 9
tccagaatgg gagacaagcc aattt

25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 10
agggaggagg aaacagcgtg agtcc

25

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 11
atgggaaagg aaaagactca tatca

25

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 12
agcagcaaca atcaggacag cacag

25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 13
atcaagaatt cgcacgagac catta

25

<210> 14
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 14
atcggttgaga ctcgtaccag cagagtcacg agagagacta cacggtactg gttttttttt 60
tttttvn 67

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 15
ccagcagagt cacgagagag actacacgg 29

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide

<400> 16
cacgagagag actacacggt actgg 25

<210> 17
<211> 526
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> complement(261..376)
<223> blastn

<221> misc_feature
<222> complement(380..486)
<223> blastn

<221> misc_feature
<222> complement(110..145)
<223> blastn

<221> misc_feature
<222> complement(196..229)
<223> blastn

<221> sig_peptide
 <222> 90..140
 <223> Von Heijne matrix

<400> 17

```

aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca      60
gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc      113
                               Met Lys Lys Val Leu Leu Leu Ile
                               -15                               -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag      161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                               -5                               5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr      209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
                               10                               15                               20
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att      257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
                               25                               30                               35
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata      305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40                               45                               50                               55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa      354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
                               60                               65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat      414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta      474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa      526

```

<210> 18
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17
 <223> Von Heijne matrix
 score 8.2
 seq LLLITAILAVAVG/FP

<400> 18
 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 1 5 10 15
 Gly

<210> 19
 <211> 822
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 260..464
 <223> blastn

<221> misc_feature
 <222> 118..184

<223> blastn

<221> misc_feature

<222> 56..113

<223> blastn

<221> misc_feature

<222> 454..485

<223> blastn

<221> misc_feature

<222> 118..545

<223> blastn

<221> misc_feature

<222> 65..369

<223> blastn

<221> misc_feature

<222> 61..399

<223> blastn

<221> misc_feature

<222> 408..458

<223> blastn

<221> misc_feature

<222> 60..399

<223> blastn

<221> misc_feature

<222> 393..432

<223> blastn

<221> sig_peptide

<222> 346..408

<223> Von Heijne matrix

<400> 19

```
actcctttta gcataggggc ttcggcgcca gcggccagcg ctagtcggtc tggtaagtgc      60
ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc      120
ctcaaacggc ctagtgcttc gcgcttcgag agaaaatcag cggctctaatt aattcctctg      180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca      240
cgttcctggt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                   Met Trp Trp Phe
                                   -20
```

```
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
-15                               -10                               -5
```

```
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
1                               5                               10                               15
```

```
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
20                               25                               30
```

```
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
35                               40                               45
```

```
aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaa      602
Lys
```

```
ctcttcaraa acatgtcttt acaagcatat ctcttgatt gctttctaca ctgttgaatt      662
```

```

gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg 722
gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw 782
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa 822

```

```

<210> 20
<211> 21
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..21
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTSA/AF

```

```

<400> 20
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
1           5           10          15
Ile Trp Thr Ser Ala
      20

```

```

<210> 21
<211> 405
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> complement(103..398)
<223> blastn

```

```

<221> sig_peptide
<222> 185..295
<223> Von Heijne matrix

```

```

<400> 21
atcaccttct tctccatcct tstctgggcc agtccccarc ccagtccttc tcctgacctg 60
ccagagccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct 120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
      Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
      -35 -30 -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
      -20 -15 -10
ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg 325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
      -5 1 5 10
cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc 374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaaa a 405

```

```

<210> 22
<211> 37
<212> PRT

```

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..37

<223> Von Heijne matrix
score 5.9
seq LSYASSALSPCLT/AP

<400> 22

Met	Val	Leu	Thr	Thr	Leu	Pro	Leu	Pro	Ser	Ala	Asn	Ser	Pro	Val	Asn
1				5				10					15		
Met	Pro	Thr	Thr	Gly	Pro	Asn	Ser	Leu	Ser	Tyr	Ala	Ser	Ser	Ala	Leu
			20					25					30		
Ser	Pro	Cys	Leu	Thr											
			35												

<210> 23

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 149..331

<223> blastn

<221> misc_feature

<222> 328..485

<223> blastn

<221> misc_feature

<222> complement(182..496)

<223> blastn

<221> sig_peptide

<222> 196..240

<223> Von Heijne matrix

<400> 23

aaaaaattgg	tcccagtttt	caccctgccg	cagggctggc	tggggagggc	agcggtttag	60
attagccgtg	gcctaggccg	tttaacgggg	tgacacgagc	ntgcagggcc	gagtccaagg	120
cccggagata	ggaccaaccg	tcaggaatgc	gaggaatggt	tttcttcgga	ctctatcgag	180
gcacacagac	agacc atg	ggg att	ctg tct	aca gtg	aca gcc tta	231
	Met Gly	Ile Leu	Ser Thr	Val Thr	Ala Leu	Thr Phe
	-15		-10		-5	
gcc ara	gcc ctg	gac ggc	tgc aga	aat ggc	att gcc	cac cct
Ala Xaa	Ala Leu	Asp Gly	Cys Arg	Asn Gly	Ile Ala	His Pro
	1		5		10	
gag aag	cac aga	ctc gag	aaa tgt	agg gaa	ctc gag	asc asc
Glu Lys	His Arg	Leu Glu	Lys Cys	Arg Glu	Leu Glu	Xaa Xaa
	15		20		25	
gcc cca	gga tca	acc cas	cac cga	aga aaa	aca acc	aga aga
Ala Pro	Gly Ser	Thr Xaa	His Arg	Arg Arg	Lys Thr	Thr Arg
	30		35		40	
tct tca	gcc tgaaatgaak	cgggatcaa	atggttgctg	atcaragccc		424
Ser Ser	Ala					
atatttaaat	tgaaaaagtc	aaattgasca	ttattaaata	aagcttggtt	aatatgtctc	484
aaacaaaaaa	aa					496

<210> 24
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..15
 <223> Von Heijne matrix
 score 5.5
 seq ILSTVTALTFAXA/LD

<400> 24
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
 1 5 10 15

<210> 25
 <211> 623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix

<400> 25
 aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgctc atg gag agg 57
 Met Glu Arg
 -15
 ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
 Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
 -10 -5 1
 tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
 Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
 5 10 15
 gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
 Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
 20 25 30 35
 caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta 249
 Gln Val Cys Ile Ser Asn Glu Val Val Ser Phe Lys Trp Ser Val
 40 45 50
 cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac 297
 Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
 55 60 65
 atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc 345
 Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
 70 75 80
 agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag 393
 Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
 85 90 95
 gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg 441
 Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
 100 105 110 115
 agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc 489
 Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
 120 125 130
 ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga 534

Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
 135 140 145
 taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa 594
 taaactctca tgcccccaaa aaaaaaaaaa 623

<210> 26
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16
 <223> Von Heijne matrix
 score 10.1
 seq LVLTLCTLPLAVA/SA

<400> 26
 Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
 1 5 10 15

<210> 27
 <211> 848
 <212> DNA
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 32..73
 <223> Von Heijne matrix

<400> 27
 aacttttgcc tgtgttttcc accctgaaag a atg ttg tgg ctg ctc ttt ttt 52
 Met Leu Trp Leu Leu Phe Phe
 -10
 ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat 100
 Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
 -5 1 5
 gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca 148
 Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
 10 15 20 25
 tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct 196
 Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
 30 35 40
 ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat 244
 Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
 45 50 55
 gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt 292
 Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
 60 65 70
 aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca 340
 Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
 75 80 85
 gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat 388
 Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
 90 95 100 105
 gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc 436
 Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro

```

      110      115      120
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt 484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe
      125      130      135
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg 532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp
      140      145      150
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa 580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu
      155      160      165
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat 628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp
      170      175      180      185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag 676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu
      190      195      200
gat gag agg ctg acc cct ctc tgaagggctg ttgttctgct tcctcaaraa 727
Asp Glu Arg Leu Thr Pro Leu
      205
attaaacatt tggttctgtg tgactgctga gcacccctgaa ataccaagag cagatcatat 787
wttttggttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa 847
c 848

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<210> 28
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 <213> Homo sapiens

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 score 10.7
 seq LWLLFFLVTAIHA/EL

<400> 28
 Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
 1 5 10

<210> 29
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 29
 gggaagatgg agatagtatt gcctg

25

<210> 30
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 30
ctgccatgta catgatagag agattc

26

<210> 31
<211> 546
<212> DNA
<213> Homo sapiens

<220>
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<222> 1..517

<221> transcription start site
<222> 518

<221> protein_bind
<222> 17..25
<223> matinspector prediction
name CMYB_01
score 0.983
sequence tgtcagttg

<221> protein_bind
<222> complement(18..27)
<223> matinspector prediction
name MYOD_Q6
score 0.961
sequence cccaactgac

<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

<221> protein_bind
<222> 94..104
<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag

<221> protein_bind
<222> complement(129..139)
<223> matinspector prediction
name DELTAEF1_01
score 0.960
sequence gcacacctcag

<221> protein_bind
<222> complement(155..165)
<223> matinspector prediction
name GATA_C
score 0.964
sequence agataaatcca

<221> protein_bind

<222> 170..178
<223> matinspector prediction
name CMYB_01
score 0.958
sequence cttcagttg

<221> protein_bind
<222> 176..189
<223> matinspector prediction
name GATA1_02
score 0.959
sequence ttgtagataggaca

<221> protein_bind
<222> 180..190
<223> matinspector prediction
name GATA_C
score 0.953
sequence agataggacat

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1ALPHA47_01
score 0.973
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1BETA47_01
score 0.983
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1BETAITF2_01
score 0.978
sequence cataacagatggtaag

<221> protein_bind
<222> complement(287..296)
<223> matinspector prediction
name MYOD_Q6
score 0.954
sequence accatctgtt

<221> protein_bind
<222> complement(302..314)
<223> matinspector prediction
name GATA1_04
score 0.953
sequence tcaagataaagta

<221> protein_bind
<222> 393..405
<223> matinspector prediction
name IK1_01
score 0.963
sequence agttgggaattcc

<221> protein_bind
 <222> 393..404
 <223> matinspector prediction
 name IK2_01
 score 0.985
 sequence agttgggaattc

<221> protein_bind
 <222> 396..405
 <223> matinspector prediction
 name CREL_01
 score 0.962
 sequence tgggaattcc

<221> protein_bind
 <222> 423..436
 <223> matinspector prediction
 name GATA1_02
 score 0.950
 sequence tcagtgatatggca

<221> protein_bind
 <222> complement(478..489)
 <223> matinspector prediction
 name SRY_02
 score 0.951
 sequence taaaacaaaaca

<221> protein_bind
 <222> 486..493
 <223> matinspector prediction
 name E2F_02
 score 0.957
 sequence tttagcgc

<221> protein_bind
 <222> complement(514..521)
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 name MZF1_01
 score 0.975
 sequence tgagggga

<400> 31
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 tcttgatttg cctgctaatt ctattatttc tgggaactaaa ttagtttgat ggttctatta 120
 gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
 gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
 atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300
 atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta 360
 gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
 catcagtgat atggcaaata tgggactaag ggtagtgtatc agaggggttaa aattgtgtgt 480
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 cttcat 546

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<223> Oligonucleotide

<400> 32

gtaccaggga ctgtgaccat tgc

23

<210> 33

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 33

ctgtgaccat tgctcccaag agag

24

<210> 34

<211> 861

<212> DNA

<213> Homo sapiens

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<221> promoter

<222> 1..806

<221> transcription start site

<222> 807

<221> protein_bind

<222> complement(60..70)

<223> matinspector prediction

name NFY_Q6

score 0.956

sequence ggaccaatcat

<221> protein_bind

<222> 70..77

<223> matinspector prediction

name MZF1_01

score 0.962

sequence cctgggga

<221> protein_bind

<222> 124..132

<223> matinspector prediction

name CMYB_01

score 0.994

sequence tgaccgttg

<221> protein_bind

<222> complement(126..134)

<223> matinspector prediction

name VMYB_02

score 0.985

sequence tccaacggt

<221> protein_bind

<222> 135..143

<223> matinspector prediction
name STAT_01
score 0.968
sequence ttcctggaa

<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
name STAT_01
score 0.951
sequence ttccaggaa

<221> protein_bind
<222> complement(252..259)
<223> matinspector prediction
name MZF1_01
score 0.956
sequence ttggggga

<221> protein_bind
<222> 357..368
<223> matinspector prediction
name IK2_01
score 0.965
sequence gaatgggatttc

<221> protein_bind
<222> 384..391
<223> matinspector prediction
name MZF1_01
score 0.986
sequence agagggga

<221> protein_bind
<222> complement(410..421)
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name SRY_02
score 0.955
sequence gaaaacaaaaca

<221> protein_bind
<222> 592..599
<223> matinspector prediction
name MZF1_01
score 0.960
sequence gaagggga

<221> protein_bind
<222> 618..627
<223> matinspector prediction
name MYOD_Q6
score 0.981
sequence agcatctgcc

<221> protein_bind
<222> 632..642
<223> matinspector prediction
name DELTAEF1_01
score 0.958
sequence tcccaccttcc

<221> protein_bind

<222> complement(813..823)
 <223> matinspector prediction
 name S8_01
 score 0.992
 sequence gaggcaattat

<221> protein_bind
 <222> complement(824..831)
 <223> matinspector prediction
 name MZF1_01
 score 0.986
 sequence agagggga

<400> 34
 tactataggg cacgctggt cgacggccgg gctgttctgg agcagagggc atgtcagtaa 60
 tgattggtcc ctggggaagg tctggctggc tccagcacag tgaggcattt aggtatctct 120
 cggtgaccgt tggattcctg gaagcagtag ctgttctggt tggatctggt agggacaggg 180
 ctcaagagggc taggcacgag ggaaggtcag aggagaaggs aggsarggcc cagtgagarg 240
 ggagcatgcc tcccccaac cctggcttsc ycttggyam agggcgkty tgggmacttr 300
 aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcacia tagcctgaat 360
 gggatttcag gttagncagg gtgagagggg aggtctctctg gcttagtttt gttttgtttt 420
 ccaaataaag gtaacttgct ccttctgct acgggccttg gtcttggett gtcctcacc 480
 agtcggaact cctaccact ttcaggagag tggtttttagg cccgtggggc tgttctgttc 540
 caagcagtgt gagaacatgg ctggtagagg ctctagctgt gtgcggggcc tgaaggggag 600
 tgggttctcg cccaaagagc atctgcccac tcccacett ccttctccc accagaagct 660
 tgcctgagct gtttgacaa aaatccaaac cccacttggc tactctggcc tggcttcagc 720
 ttggaaccca atacctaggc ttacaggcca tcctgagcca ggggcctctg gaaattctct 780
 tcctgatggt cctttagggt tgggcacaaa atataattgc ctctcccctc tcccattttc 840
 tctcttgga gcaatggtca c 861

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 <211> 20
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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 35
 ctgggatgga aggcacgga 20

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 36
 gagaccacac agctagacaa 20

<210> 37
 <211> 555
 <212> DNA
 <213> Homo sapiens

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<222> 1..500

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<222> 501

<221> protein_bind
<222> 191..206
<223> matinspector prediction
 name ARNT_01
 score 0.964
 sequence ggactcacgtgctgct

<221> protein_bind
<222> 193..204
<223> matinspector prediction
 name NMYC_01
 score 0.965
 sequence actcacgtgctg

<221> protein_bind
<222> 193..204
<223> matinspector prediction
 name USF_01
 score 0.985
 sequence actcacgtgctg

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
 name USF_01
 score 0.985
 sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
 name NMYC_01
 score 0.956
 sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
 name MYCMAX_02
 score 0.972
 sequence cagcacgtgagt

<221> protein_bind
<222> 195..202
<223> matinspector prediction
 name USF_C
 score 0.997
 sequence tcacgtgc

<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
 name USF_C
 score 0.991

sequence gcacgtga

<221> protein_bind
 <222> complement(210..217)
 <223> matinspector prediction
 name MZF1_01
 score 0.968
 sequence catgggga

<221> protein_bind
 <222> 397..410
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 name ELK1_02
 score 0.963
 sequence ctctccggaagcct

<221> protein_bind
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 name CETS1P54_01
 score 0.974
 sequence tccggaagcc

<221> protein_bind
 <222> complement(460..470)
 <223> matinspector prediction
 name AP1_Q4
 score 0.963
 sequence agtgactgaac

<221> protein_bind
 <222> complement(460..470)
 <223> matinspector prediction
 name AP1FJ_Q2
 score 0.961
 sequence agtgactgaac

<221> protein_bind
 <222> 547..555
 <223> matinspector prediction
 name PADS_C
 score 1.000
 sequence tgtggtctc

<400> 37
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 aggacagcat ttgtkacatc tgggtctactg caccttccct ctgccgtgca cttggccttt 120
 kawaagctca gcaccggtgc ccatcacagg gccggcagca cacacatccc attactcaga 180
 aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta 240
 gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaattcc aagtgattgt 300
 cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag 360
 gttgctctgc ccattggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc 420
 cgtgtcttct gctgtctccc gctcacatcc cacacttggtg ttcagtcact gagttacaga 480
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 tagctgtgtg gtctc 555

<210> 38
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 38

ggccatacac ttgagtgac

19

<210> 39

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 39

atatagacaa acgcacacc

19

<210> 40

<211> 568

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 7..471

<221> sig_peptide

<222> 7..99

<223> Von Heijne matrix

score 6.9

seq LLLVPSALSLLLA/LL

<221> polyA_signal

<222> 537..542

<221> polyA_site

<222> 554..568

<400> 40

gggacc atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro

48

-30 -25 -20
ctg tcg aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc
Leu Ser Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu

96

-15 -10 -5
gcc ctc ctc ctg cct cac tgc cag aag ccc ttt gtg tat gac ctt cac
Ala Leu Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His

144

1 5 10 15
gca gtc aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata
Ala Val Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile

192

20 25 30
att tgc ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat
Ile Cys Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr

240

35 40 45
aat ttt agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc
Asn Phe Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser

288

50 55 60

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ttt ttg ctg ggt acc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc      336
Phe Leu Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu
   65                               70                               75
att gaa gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg      384
Ile Glu Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu
   80                               85                               90                               95
cct tct gga tta atc ttt tgt tgt gct ttt tgc tct gag act aaa ctc      432
Pro Ser Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu
                   100                               105                               110
ttc tta tca aga caa gct atg gca gag aac ttt tcc atc taataaattt      481
Phe Leu Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
                   115                               120
aagagtagat tcatctgtat ggttgagagt aggctctgac tatgtatatg tgtataataa      541
acctacatat ccaaaaaaaaa aaaaaaa      568

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<210> 41
 <211> 569
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 168..332

<221> polyA_signal
 <222> 557..562

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gatacggcgc ccagcggggg cagaaagcaa cattgaatgc agaagaa atg gcg gac      176
                                   Met Ala Asp
                                   1
ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cgc atg tat tat      224
Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg Met Tyr Tyr
   5                               10                               15
aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg gga      272
Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly
   20                               25                               30                               35
aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa aag      320
Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys
                   40                               45                               50
aag agg agc aac taggagtcca ctctgaccca gccagagtcc aggtttccac      372
Lys Arg Ser Asn
                   55
aggaagcaga tggagctcct ttcacagggg ctctgagaaa aactggagcc gatctcaaga      432
agccccacat cttcctaagg ggccccatgg cctgtttggg ggcagggtag gtccctggggc      492
actgtggggc gctgctgc tgatgtgggc tctaggccag cttgttgta cgtacgtggt      552
gtgaaataaa gcccaag      569

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<210> 42
 <211> 895
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 51..251

<221> sig_peptide
 <222> 51..110
 <223> Von Heijne matrix
 score 5.3
 seq ALIFGGFISLIGA/AF

<221> polyA_signal
 <222> 849..854

<221> polyA_site
 <222> 882..895

<400> 42
 ccgagagtgc cgggscggtcg gcgggtcagg gcagcccggg gcctgacgcc atg tcc 56
 Met Ser
 -20
 cgg aac ctg cgc acc gcg ctc att ttc ggc ggc ttc atc tcc ctg atc 104
 Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile
 -15 -10 -5
 ggc gcc gcc ttc tat ccc atc tac ttc cgg ccc cta atg aga ttg gag 152
 Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg Leu Glu
 1 5 10
 gag tac aag aag gaa caa gct ata aat cgg gct gga att gtt caa gag 200
 Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val Gln Glu
 15 20 25 30
 gat gtg cag cca cca ggg tta aaa gtg tgg tct gat cca ttt ggc agg 248
 Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe Gly Arg
 35 40 45
 aaa tgagagggct gtcacagct ctgattaaga aaggagattt cttcatgctt 301
 Lys
 tcgattctgc atgggggtaca gccagtcacc tcaccagaga atgacggctg gagaagaaaa 361
 ctctgtaata ccataaataa gagggtctgt aataaaagac tgtgcacaag gattaatatt 421
 tcccttctta agtatcaaaa gaactctgga acaaattata ccattaggaa ggttttcatg 481
 attcagttga ttttccaaaa atgaagctat ctcaaccagc tgggtttgga ggagcaatct 541
 gcttattatt ctgtcggttac cacttactca agcgagctgt gatatgaata caagcaacca 601
 gtgggctcgg gaaggtccgg gtctcttctg ccattctcca gataagagat ttcagtaaaa 661
 aactgccatg ctgagctgcc ttatagagct cttcgaaaat gttcgagttg ataaagctct 721
 ttgaggacaa ggtacttcgt gcacctcatg ctgaagattg caccatgttg gaagataaat 781
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 gtgaaaaaat agacattaag atgatttatt tccactttgc aaaaaaaaaa aaaa 895

<210> 43
 <211> 691
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..613

<221> sig_peptide
 <222> 20..82
 <223> Von Heijne matrix
 score 10
 seq LWALAMVTRPASA/AP

<400> 43
 ataccttaga ccctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc 52
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala

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-20          -15
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca      100
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro
-10          -5          1          5
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg      148
Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu
          10          15          20
cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga tgg      196
Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Trp
          25          30          35
ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa      244
Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
          40          45          50
ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt      292
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu
55          60          65          70
cgg gca agc ctg ttg gag act cag atg gag gag gat att ctg cag ctg      340
Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu
          75          80          85
cag gca gag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca cag      388
Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln
          90          95          100
aag gtg cta cgg gac agc gtg cag cgg cta gaa gtc cag ctg agg agc      436
Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser
          105          110          115
gcc tgg ctg ggc cct gcc tac cga gaa ttt gag gtc tta aag gct cac      484
Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His
          120          125          130
gct gac aag cag agc cac atc cta tgg gcc ctc aca ggc cac gtg cag      532
Ala Asp Lys Gln Ser His Ile Leu Trp Ala Leu Thr Gly His Val Gln
          135          140          145          150
cgg cag agg cgg gag atg gtg gca cag cag cat cgg ctg cga cag atc      580
Arg Gln Arg Arg Glu Met Val Ala Gln Gln His Arg Leu Arg Gln Ile
          155          160          165
cag gag aga ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac      633
Gln Glu Arg Leu His Thr Ala Ala Leu Pro Ala
          170          175
tgaggaccaa tcatgtctgca aggaacactt ccacgccccg tgaggcccct gtgcaggg      691

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<210> 44
<211> 458
<212> DNA
<213> Homo sapiens

<220>
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<222> 12..416

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<222> 12..86
<223> Von Heijne matrix
      score 4
      seq LVVMVPLVGLIHL/GW

<221> polyA_signal
<222> 425..430

<221> polyA_site
<222> 445..458

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<400> 44
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      Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu
      -25                -20                -15
gtt gtt atg gtc cct tta gtt ggg ctc ata cat ttg ggg tgg tac aga      98
Val Val Met Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg
      -10                -5                1
atc aaa agc agc cct gtt ttc caa ata cct aaa aac gac gac att cct      146
Ile Lys Ser Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro
      5                10                15                20
gag caa gat agt ctg gga ctt tca aat ctt cag aag agc caa atc cag      194
Glu Gln Asp Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln
      25                30                35
ggg aag nta gca ggc ttg caa tct tca ggt aaa gaa gca gct ttg aat      242
Gly Lys Xaa Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn
      40                45                50
ctg agc ttc ata tcg aaa gaa gag atg aaa aat acc agt tgg att aga      290
Leu Ser Phe Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg
      55                60                65
aag aac tgg ctt ctt gta gct ggg ata tct ttc ata ggt gac cat ctt      338
Lys Asn Trp Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu
      70                75                80
gga aca tac ttt ttg cag agg tct gca aag cag tct gta aaa ttt cag      386
Gly Thr Tyr Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln
      85                90                95                100
tct caa agc aaa caa aag agt att gaa gag tgaagtaaaa taaatatttg      436
Ser Gln Ser Lys Gln Lys Ser Ile Glu Glu
      105                110
gaattactaa aaaaaaaaaa aa      458

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<210> 45
<211> 2036
<212> DNA
<213> Homo sapiens

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<221> sig_peptide
<222> 276..485
<223> Von Heijne matrix
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      seq SVIGVMLAPFTAG/LS

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<221> polyA_site
<222> 2024..2036

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tggttgga gttccaagaa aagaaacgct tcaccgaaga agtcattgaa tacttccaga      120
agaaagttag cccagtgcat ctgaaaatcc tgctgactag cgatgaagcc tggaagagat      180
tcgtgcgtgt ggctggattg cccaggggaag aagcagatgc tctctatgaa gctctgaaga      240
atcttacacc atatgtggct attgaggaca aagac atg cag caa aaa gaa cag      293
      Met Gln Gln Lys Glu Gln
      -70                -65
cag ttt agg gag tgg ttt ttg aaa gag ttt cct caa atc aga tgg aag      341
Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile Arg Trp Lys
      -60                -55                -50
att cag gag tcc ata gaa agg ctt cgt gtc att gca aat gag att gaa      389

```

Ile	Gln	Glu	Ser	Ile	Glu	Arg	Leu	Arg	Val	Ile	Ala	Asn	Glu	Ile	Glu		
			-45				-40					-35					
aag	gtc	cac	aga	ggc	tgc	gtc	atc	gcc	aat	gtg	gtg	tct	ggc	tcc	act	437	
Lys	Val	His	Arg	Gly	Cys	Val	Ile	Ala	Asn	Val	Val	Ser	Gly	Ser	Thr		
		-30					-25					-20					
ggc	atc	ctg	tct	gtc	att	ggc	gtt	atg	ttg	gca	cca	ttt	aca	gca	ggg	485	
Gly	Ile	Leu	Ser	Val	Ile	Gly	Val	Met	Leu	Ala	Pro	Phe	Thr	Ala	Gly		
	-15					-10					-5						
ctg	agc	ctg	agc	att	act	gca	gct	ggg	gta	ggg	ctg	gga	ata	gca	tct	533	
Leu	Ser	Leu	Ser	Ile	Thr	Ala	Ala	Gly	Val	Gly	Leu	Gly	Ile	Ala	Ser		
1			5						10					15			
gcc	acg	gct	ggg	atc	gcc	tcc	agc	atc	gtg	gag	aac	aca	tac	aca	agg	581	
Ala	Thr	Ala	Gly	Ile	Ala	Ser	Ser	Ile	Val	Glu	Asn	Thr	Tyr	Thr	Arg		
		20					25					30					
tca	gca	gaa	ctc	aca	gcc	agc	agg	ctg	act	gca	acc	agc	act	gac	caa	629	
Ser	Ala	Glu	Leu	Thr	Ala	Ser	Arg	Leu	Thr	Ala	Thr	Ser	Thr	Asp	Gln		
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ttg	gag	gca	tta	agg	gac	att	ctg	cat	gac	atc	aca	ccc	aat	gtg	ctt	677	
Leu	Glu	Ala	Leu	Arg	Asp	Ile	Leu	His	Asp	Ile	Thr	Pro	Asn	Val	Leu		
	50					55					60						
tcc	ttt	gca	ctt	gat	ttt	gac	gaa	gcc	aca	aaa	atg	att	gcg	aat	gat	725	
Ser	Phe	Ala	Leu	Asp	Phe	Asp	Glu	Ala	Thr	Lys	Met	Ile	Ala	Asn	Asp		
65					70					75				80			
gtc	cat	aca	ctc	agg	aga	tct	aaa	gcc	act	ggt	gga	cgc	cct	ttg	att	773	
Val	His	Thr	Leu	Arg	Arg	Ser	Lys	Ala	Thr	Val	Gly	Arg	Pro	Leu	Ile		
			85							90				95			
gct	tgg	cga	tat	gta	cct	ata	aat	gtt	gtt	gag	aca	ctg	aga	aca	cgt	821	
Ala	Trp	Arg	Tyr	Val	Pro	Ile	Asn	Val	Val	Glu	Thr	Leu	Arg	Thr	Arg		
			100						105					110			
ggg	gcc	ccc	acc	cgg	ata	gtg	aga	aaa	gta	gcc	cgg	aac	ctg	ggc	aag	869	
Gly	Ala	Pro	Thr	Arg	Ile	Val	Arg	Lys	Val	Ala	Arg	Asn	Leu	Gly	Lys		
		115					120					125					
gcc	act	tca	ggt	gtc	ctc	gtt	gtg	ctg	gat	gta	gtc	aac	ctt	gtg	caa	917	
Ala	Thr	Ser	Gly	Val	Leu	Val	Val	Leu	Asp	Val	Val	Asn	Leu	Val	Gln		
		130					135					140					
gac	tca	ctg	gac	ttg	cac	aag	ggg	gaa	aaa	tcc	gag	tct	gct	gag	ttg	965	
Asp	Ser	Leu	Asp	Leu	His	Lys	Gly	Glu	Lys	Ser	Glu	Ser	Ala	Glu	Leu		
		145				150				155				160			
ctg	agg	cag	tgg	gct	cag	gag	ctg	gag	gag	aat	ctc	aat	gag	ctc	acc	1013	
Leu	Arg	Gln	Trp	Ala	Gln	Glu	Leu	Glu	Glu	Asn	Leu	Asn	Glu	Leu	Thr		
			165						170				175				
cat	atc	cat	cag	agt	cta	aaa	gca	ggc	taggccaat	tggtgcggga						1060	
His	Ile	His	Gln	Ser	Leu	Lys	Ala	Gly									
			180					185									
agtcagggac	cccaaacgga	gggactggct	gaagccatgg	cagaagaacg	tggtattgtga											1120	
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tcctgggtg	tgccatctt	ctatggctga	gactgtagg	atgaaataaa	ccccagctc											1660	
ccatagtgtc	cccaggctta	ttagggaagag	gaaattccc	cctaataaa	tttggctaga											1720	
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acctcattag	caattttaat	ttctccccgg	tcctgtggctc	ctgtgatctc	acctgcctc											1840	
cacttgctt	gtgatattct	attaccttgt	gaagtaggtg	atctttgtga	cccacaccct											1900	
attcatacac	tccctcccct	tttggaagtc	cctaataaaa	acttgcctgg	tttgcagctt											1960	
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ttcaaaaaaa	aaaaaa															2036	

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 <213> Homo sapiens

 <220>
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 <222> 443..619

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 <222> 443..589
 <223> Von Heijne matrix
 score 7
 seq LICVVCLYIVCRC/GS

 <221> polyA_site
 <222> 1267..1276

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 tgtaaataat tggtagaaaa attctactct gctgtggaat taccaagata atatagacca 180
 gaaactagct gatcaaatta atgatctcca acaaactgta atgtggctag gggatcatat 240
 agttagttta gaatatagaa tgcgggttaca atgtgattga aatacctctg atttttgcat 300
 tactcctcat ctgtgtaatg aaacagagca tgagtgggaa aaagttaaga gatattttaa 360
 aggtcatact agaaatttat ctttggatat tgcaaaagcta aaggaacaag tatttcaagc 420
 ccctcagata catctgacac ta atg cca gga act gaa gtg ctt gaa gga gct 472
 Met Pro Gly Thr Glu Val Leu Glu Gly Ala
 -45 -40
 aca gac gga tta gca gct att aac ctg cta aaa tgg atc aag aca ctt 520
 Thr Asp Gly Leu Ala Ala Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu
 -35 -30 -25
 gga ggc tct gtg att tca atg att gtg ctt tta atc tgt gtt gtt tgt 568
 Gly Gly Ser Val Ile Ser Met Ile Val Leu Leu Ile Cys Val Val Cys
 -20 -15 -10
 ctt tat ata gtc tgt aga tgc gga agc cac ctc tgg aga gaa agc cac 616
 Leu Tyr Ile Val Cys Arg Cys Gly Ser His Leu Trp Arg Glu Ser His
 -5 1 5
 cac tgagagcaag caatgatagc tgtggcggtt ttgcaaaaag aaaagggaga 669
 His
 10
 caagcgccca gctatagtta ccaataaagc atggtactgg tattaataata ggcattgtgt 729
 ctgttccaat ggaacagaat agagaacca gaaacaaagc caaatattta cagccaactg 789
 atctctgaca aagcaaacaa aaacataaag tgggggaaagg acaccctatt ccacaaatag 849
 tgcagggata attggcaagc cacatgtaga aaaatgaagc tggatcctcg tctctcactt 909
 tatacaaaaa tcaactcaaa atgggtcaaa gtcttaactc taagacctga aaccataaca 969
 attctagaaa ataacattgg aaaaactcct ctagacattg gtttaggcaa aaagttcatg 1029
 accaagaacc caaaagcaaa tgcaataaaa aggaagataa atagatggga cctaattaag 1089
 ctgaaaagct tctgcatagc aaaaggaata atcagcagag caaacagaca acccacaggg 1149
 tgggagaaaa tatttgcaag ctatgtatct gacaatggac taatatccag aatctacaag 1209
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 aaaaaaa 1276

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<220>

<221> CDS

<222> 206..745

<400> 47

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tgGCCagttt tatgaatggc ttcctgtgtc taatgaccct gacaacccat gttcactcaa      120
gtGCCaagcc aaaggaacaa ccctggttgt tgaactagca cctaagggtct tagatggtag      180
gcgttgctat acagaatctt tggat atg tgc atc agt ggt tta tgc caa att      232
                               Met Cys Ile Ser Gly Leu Cys Gln Ile
                               1       5

ggt ggc tgc gat cac cag ctg gga agc acc gtc aag gaa gat aac tgt      280
Val Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys
10                               15       20       25

ggg gtc tgc aac gga gat ggg tcc acc tgc cgg ctg gtc cga ggg cag      328
Gly Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln
                               30       35       40

tat aaa tcc cag ctc tcc gca acc aaa tgc gat gat act gtg gtt gca      376
Tyr Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala
                               45       50       55

att ccc tat gga agt aga cat att cgc ctt gtc tta aaa ggt cct gat      424
Ile Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp
60                               65       70

cac tta tat ctg gaa acc aaa acc ctc cag ggg act aaa ggt gaa aac      472
His Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn
75                               80       85

agt ctc agc tcc aca gga act ttc ctt gtg gac aat tct agt gtg gac      520
Ser Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp
90                               95       100       105

ttc cag aaa ttt cca gac aaa gag ata ctg aga atg gct gga cca ctc      568
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu
110                               115       120

aca gca gat ttc att gtc aag att cgt aac tgc ggc tcc gct gac agt      616
Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser
125                               130       135

aca gtc cag ttc atc ttc tat caa ccc atc atc cac cga tgg agg gag      664
Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu
140                               145       150

acg gat ttc ttt cct tgc tca gca acc tgt gga gga ggt tat cag ctg      712
Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu
155                               160       165

aca tgc gct gag tgc tac gat ctg agg agc aac cg      747
Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn
170                               175       180

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<210> 48

<211> 561

<212> DNA

<213> Homo sapiens

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<222> 36..521

<221> sig_peptide

<222> 36..104

<223> Von Heijne matrix

score 7.4

seq VLLLAALPPVLLP/GA

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<222> 528..533

<221> polyA_site
<222> 548..561

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Met Gly Asp Lys Ile Trp
-20
ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg 101
Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu
-15 -10 -5
cct ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt 149
Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe
1 5 10 15
acc ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg 197
Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu
20 25 30
aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta 245
Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu
35 40 45
gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt 293
Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe
50 55 60
gaa caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt 341
Glu Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly
65 70 75
gat tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag 389
Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys
80 85 90 95
gtg att ttc ttt gaa tta atc ccg gat aat atg gga gaa cag gca caa 437
Val Ile Phe Phe Glu Leu Ile Pro Asp Asn Met Gly Glu Gln Ala Gln
100 105 110
gaa caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat 485
Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp
115 120 125
atg aaa ctg gaa gac atc ctg gtc agt atg gtc ttc taataaaata 531
Met Lys Leu Glu Asp Ile Leu Val Ser Met Val Phe
130 135
aaaattatta acagccaaaa aaaaaaaaaa 561

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<211> 632
<212> DNA
<213> Homo sapiens

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<222> 36..395

<221> sig_peptide
<222> 36..104
<223> Von Heijne matrix
score 7.4
seq VLLLAALPPVLLP/GA

<221> polyA_signal
<222> 599..604

<221> polyA_site

<222> 619..632

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-20

ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg 101
 Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu

-15

-10

-5

cct ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt 149
 Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe

1

5

10

15

acc ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg 197
 Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu

20

25

30

aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta 245
 Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu

35

40

45

gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt 293
 Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe

50

55

60

gaa caa aga aaa tca gat gga gtt cac acg tgt ata aga agt aaa aat 341
 Glu Gln Arg Lys Ser Asp Gly Val His Thr Cys Ile Arg Ser Lys Asn

65

70

75

ggg cca ggc act gcg gtt cac gcc tat aat ccc agc act ttc cga ggc 389
 Gly Pro Gly Thr Ala Val His Ala Tyr Asn Pro Ser Thr Phe Arg Gly

80

85

90

95

caa gtg tagagactga agttggtgat tacatgttct gctttgacaa tacattcagc 445
 Gln Val

accatttctg agaaggtgat tttctttgaa ttaatcctgg ataatatggg agaacaggca 505

caaggacaag aagattggaa gaaatatatt actggcacag atatattgga tatgaaactg 565

gaagacatcc tggtcagtat ggtcttctaa taaaataaaa attattaaca gccaaaaaaa 625

aaaaaaa 632

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<211> 370

<212> DNA

<213> Homo sapiens

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<222> 21..41

<221> polyA_signal

<222> 328..333

<221> polyA_site

<222> 357..370

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 Met Val Glu Met Thr Gly Val

1

5

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taggagaagg gcatgctcag gccagcccat tagcccagga ggaggacaag aaacacacgg 171

agcagacaca agccacctca ccaaccacgc caaggctgtc ctgaattagc aaccctgaca 231

cgtgtgagca agtccaacgg acaccggaag atccacctag tcaagcccaa ccaagactgg 291

cagagctgcc aagctgacca cttaaggcgc atgaggaata aacactcgtt gctgcatgcc 351

attgcaaaaa aaaaaaaaaa 370

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 <222> 35..631

<221> sig_peptide
 <222> 35..160
 <223> Von Heijne matrix
 score 8.6
 seq ASLFLLLSLTVFS/IV

<221> polyA_signal
 <222> 901..906

<221> polyA_site
 <222> 979..994

<400> 51
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 Met Asp Gly Gln Lys Lys Asn
 -40
 tgg aag gac aag gtt gtt gac ctc ctg tac tgg aga gac att aag aag 103
 Trp Lys Asp Lys Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys
 -35 -30 -25 -20
 act gga gtg gtg ttt ggt gcc agc cta ttc ctg ctg ctt tca ttg aca 151
 Thr Gly Val Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr
 -15 -10 -5
 gta ttc agc att gtg agc gta aca gcc tac att gcc ttg gcc ctg ctc 199
 Val Phe Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu
 1 5 10
 tct gtg acc atc agc ttt agg ata tac aag ggt gtg atc caa gct atc 247
 Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile
 15 20 25
 cag aaa tca gat gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa 295
 Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu
 30 35 40 45
 gtt gct ata tct gag gag ttg gtt cag aag tac agt aat tct gct ctt 343
 Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu
 50 55 60
 ggt cat gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt 391
 Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
 65 70 75
 gat gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt 439
 Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
 80 85 90
 acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg gct 487
 Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Ile Leu Ala
 95 100 105
 ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat cag gca 535
 Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His Gln Ala
 110 115 120 125
 cag ata gat cat tat cta gta ctt gca aat aag aat gtt aaa gat gct 583
 Gln Ile Asp His Tyr Leu Val Leu Ala Asn Lys Asn Val Lys Asp Ala
 130 135 140
 atg gct aaa atc caa gca aaa atc cct gga ttg aag cgc aaa gct gaa 631

Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu
 145 150 155
 tgaaaaacgcc caaaataatt agtaggagtt catcttttaa ggggatattc atttgattat 691
 acggggggagg gtcaggggaag aacgaacctt gacgttgcag tgcagtttca cagatcgttg 751
 ttagatctttt attttttagcc atgcactgtt gtgaggaaaa attacctgtc ttgactgcca 811
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 tttttcctat ctatctgagg cactgggtgga ataaaaaacc tgtatatatt actttgttgc 931
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 aaa 994

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 gtcactgaga gacgtctcag agaggctgtg cagctgctgg aggactataa gcatgggacc 180
 ctgcgcccgg ggggtcaccaa tgaacagctc tggagtgcac agaaaatcaa gcaggctatt 240
 ctacatccgg acaccaatga gaagatcttc atg cca ttt aga atg tca ggt tat 294
 Met Pro Phe Arg Met Ser Gly Tyr
 1 5
 att cct ttt ggg acg cca att gta agt gtt acc ttc aaa gga ttt cct 342
 Ile Pro Phe Gly Thr Pro Ile Val Ser Val Thr Phe Lys Gly Phe Pro
 10 15 20
 ttt cta aaa aat tat ttt aaa tgt cta act tta tgt tat tgc tca cgg 390
 Phe Leu Lys Asn Tyr Phe Lys Cys Leu Thr Leu Cys Tyr Cys Ser Arg
 25 30 35 40
 gta ttt gac tgaattgttg att 412
 Val Phe Asp

<210> 53
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 103..252

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 <223> Von Heijne matrix
 score 3.9
 seq PGPSLRLFSGSQA/SV

<221> polyA_site
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 Met Glu Trp Ala

-35

gga aag cag cgg gac ttt cag gta agg gca gct ccg ggc tgg gat cat	162
Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro Gly Trp Asp His	
-30 -25 -20	
ttg gcc tcc ttt cct ggc cct tct ctc cgg ctg ttt tct ggg agt cag	210
Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe Ser Gly Ser Gln	
-15 -10 -5	
gcg agt gtc tgt agt ctc tgc tgc ggg ttt ggg gct cag gaa	252
Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala Gln Glu	
1 5 10	
tgatgtcatg ctccaacagt tggattctat tagcttaagg aggagggaaa cagccaattt	312
tcttgacttt gcaaactctag ctgatctcac tcttgctgaa tctgaggtgt ttagacttca	372
ctctaaaaag catcatttta cttttattta gcacaaaggc acaggatatt ttacaggaa	432
gaatctttta tatggaaaaa tctgagttaa catcactccc gtggtgtttg tagttcttac	492
agggaaactc cagtgccttt tgagccgctt gttcgtccta gtgaacactg tctgttttgt	552
ctcttggtgc tgctatgtct gacctgtaat gggagaaaaa aagaa	597

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<221> polyA_signal
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<221> polyA_site
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Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala	
1 5 10 15	
cat gtc cac cta cct gaa aat gtt cgc agc cag tct cct ggc cat gtg	97
His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val	
20 25 30	
cgc agg ggc aga agt ggt gca cag gta cta ccg acc gga cct gat gag	145
Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu	
35 40 45	
aaa cag gtt gag aag agt gaa gtt gat ttc tca aag tca cat agc tta	193
Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu	
50 55 60	
gtg aga cga ttt gag gat ctg aag ccc aag ctt tct gtt tgc aaa act	241
Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr	
65 70 75 80	
gga tca caa gtc ttt cgg tgc gag aac tgg aag gtc tgg gca gag tgc	289
Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser	
85 90 95	
agc aga gga gac cat gat gac tgc cta gac ttg tgc tca gtg ctg tgt	337
Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys	
100 105 110	
tgg gga gaa ctg cta cgg aca ata cct gaa att cca cca aag cgt gga	385
Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly	
115 120 125	
gaa ctc aaa acg gag ctt ttg gga ctg aaa gaa aga aaa cac aaa cct	433
Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro	
130 135 140	

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caa gtt tct caa cag gag gaa ctt aaa taactatgcc aagaattctg      480
Gln Val Ser Gln Gln Glu Leu Lys
145                      150
tgaataatat aagtcttaaa tatgtatttc ttaatttatt gcatcaaact acttgtcctt      540
aagcacttag tctaattgcta actgcaagag gaggtgctca gtggatgttt agccgatacg      600
ttgaaattta attacggttt gattgatatt tcttgaaaac cgccaaagca catatcatca      660
aaccatttca tgaatatggt ttggaagatg tttagtcttg aatataatgc gaaatagaat      720
atttghtaagt ctacaaaaaa aaaaaaaaaa                                748

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<210> 55
 <211> 703
 <212> DNA
 <213> Homo sapiens

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 <222> 31..231

<221> polyA_signal
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<221> polyA_site
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                                1           5
ctc agc cct gct aag ctg atg atg ctg act ata gga gat gtt att aaa      102
Leu Ser Pro Ala Lys Leu Met Met Leu Thr Ile Gly Asp Val Ile Lys
10           15           20
caa ctg att gaa gcc cac gag cag ggg aaa gac atc gat cta aat aag      150
Gln Leu Ile Glu Ala His Glu Gln Gly Lys Asp Ile Asp Leu Asn Lys
25           30           35           40
gtg aga acc aag aca gct gcc aaa tat ggc ctt tct gcc cag ccc cgc      198
Val Arg Thr Lys Thr Ala Ala Lys Tyr Gly Leu Ser Ala Gln Pro Arg
45           50           55
ctg gtg gat atc att gct gcc gtc cct cct gag tagctgggat tacaggcacc      251
Leu Val Asp Ile Ile Ala Ala Val Pro Pro Glu
60           65
cgccgctgcc aatttttgta tttttagtag ggatgggggt ttcaccatat tggtcaggct      311
gggtctcgaac tcctgacctc aggtgatcaa cccaccttgg cctccctaaa tgccgggatt      371
acaggcatga gccaccgctc cgggcctttg attttttaag gtggattttg gttgttataa      431
atggagaaag gtaagagttc aagttcaacc cgtgtgtgaa agcaaaaaca tggaaaacag      491
gattggcttc ttcaaaggct cctctttaga aactgcctct ttgaaatttc gaggtaatct      551
actttggaga ctctgcctgg agagggtcag ttcctaagtt aaaagcatcg cttaaccttg      611
gctcctgtgg cattttacaa aggtttaaag gaattgattc ctctgaaagg gcctgaaaat      671
aaaaagtctt taacatacaa aaaaaaaaaa aa                                703

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<210> 56
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 <212> DNA
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 <222> 305..565

<221> polyA_signal
<222> 694..699

<221> polyA_site
<222> 713..725

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tgagttggat ccagggtctag ctgctgttga cctcccccact cccacgctgc cctcctgcct      180
gcagccatga cgcccctgct caccctgatc ctggtgggtcc tcatgggctt acctctggcc      240
caggccttgg actgccacgt gtgaggacta caaatccctc caggatatca ttgccatcct      300
gggt atg gat gaa ctt tct gag gaa gac aag ttg acc gtg tcc cgt gca      349
  Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala
    1          5          10          15
cgg aaa ata cag cgt ttc ttg tct cag cca ttc cag gtt gct gag gtc      397
Arg Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val
          20          25          30
ttc aca ggt cat atg ggg aag ctg gta ccc ctg aag gag acc atc aaa      445
Phe Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys
          35          40          45
gga ttc cag cag att ttg gca ggt gaa tat gac cat ctc cca gaa cag      493
Gly Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln
          50          55          60
gcc ttc tat atg gtg gga ccc att gaa gaa gct gtg gca aaa gct gat      541
Ala Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp
          65          70          75
aag ctg gct gaa gag cat tca tcg tgaggggtct ttgtcctctg tactgtctct      595
Lys Leu Ala Glu Glu His Ser Ser
          80          85
ctccttgccc ctaacccaaa aagcttcatt tttctgtgta ggctgcacaa ggccttgat      655
tgaagatata ttctttctga acagtattta aggtttccaa taaagtgtac acccctcaaa      715
aaaaaaaaaa                                     725

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<210> 57
<211> 1705
<212> DNA
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<222> 124..873

<221> sig_peptide
<222> 124..378
<223> Von Heijne matrix
score 3.6
seq HLSVVTAAKVVC/IP

<221> polyA_signal
<222> 1673..1678

<221> polyA_site
<222> 1694..1705

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cccgagagc ctgaccagag ctctggacat cctgagccca agtccccac actcagtgca      120
gtg atg agt gcg gaa gtg aag gtg aca ggg cag aac cag gag caa ttt      168
  Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe

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-85	-80	-75	
ctg ctc cta gcc aag tgc gcc aag ggg gca gcg ctg gcc aca ctc atc			216
Leu Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile			
-70	-65	-60	-55
cat cag gtg ctg gag gcc cct ggt gtc tac gtg ttt gga gaa ctg ctg			264
His Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu			
-50	-45	-40	
gac atg ccc aat gtt aga gag ctg naa gcc cgg aat ctt cct cca cta			312
Asp Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu			
-35	-30	-25	
aca gag gct cag aag aat aag ctt cga cac ctc tca gtt gtc acc ctg			360
Thr Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu			
-20	-15	-10	
gct gct aaa gta aag tgt atc cca tat gca gtg ttg ctg gag gct ctt			408
Ala Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu			
-5	1	5	10
gcc ctg cgt aat gtg cgg cag ctg gaa gac ctt gtg att gag gct gtg			456
Ala Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val			
15	20	25	
tat gct gac gtg ctt cgt ggc tcc ctg gac cag cgc aac cag cgg ctc			504
Tyr Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu			
30	35	40	
gag gtt gac tac agc atc ggg cgg gac atc cag cgc cag gac ctc agt			552
Glu Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser			
45	50	55	
gcc att gcc cga acc ctg cag gaa tgg tgt gtg ggc tgt gag gtc gtg			600
Ala Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val			
60	65	70	
ctg tca ggc att gag gag cag gtg agc cgt gcc aac caa cac aag gag			648
Leu Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu			
75	80	85	90
cag cag ctg ggc ctg aag cag cag att gag agt gag gtt gcc aac ctt			696
Gln Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu			
95	100	105	
aaa aaa acc att aaa gtt acg acg gca gca gca gcc gca gcc aca tct			744
Lys Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Ala Ala Thr Ser			
110	115	120	
cag gac cct gag caa cac ctg act gag ctg agg gaa cca gct cct ggc			792
Gln Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly			
125	130	135	
acc aac cag cgc cag ccc agc aag aaa gcc tca aag ggc aag ggg ctc			840
Thr Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu			
140	145	150	
cga ggg agc gcc aag att tgg tcc aag tgc aat tgaaagaact gtcgtttcct			893
Arg Gly Ser Ala Lys Ile Trp Ser Lys Ser Asn			
155	160	165	
ccctggggat gtgggggtccc agctgcctgc ctgcctctta ggagtccctca gagagccttc			953
tgtgcccctg gccagctgat aatcctaggt tcatgaccct tcacctcccc taaccccaaa			1013
catagatcac accttctcta gggaggagtc aaatgtaggt catgtttttg ttgggtacttt			1073
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gcatgcctga tccccagttc ctatacccta cccctgacct attgagcagc ctctgaagag			1313
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cgtttcttaa catgttgaga gatgattctt tcttgccct ggccatctcg ggaagcttga			1553
tggcaatcct ggaagggttt aatctccttt tgtgagtttg gtggggaagg gaagggtata			1613
tagattatat taaaaaaaaa aagggtatata tgcatatatc tatatataat atgacgcaga			1673
aataaatcta tgagaaatcc aaaaaaaaaa aa			1705

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 <222> 135..206

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<221> polyA_site
 <222> 1056..1069

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 agtgggaaag ggaa atg ccg acc aat tgc gct gcg gcg ggc tgt gcc act 170
 Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr
 1 5 10
 acc tac aac aag cac att aac atc agc ttc cac agg taacctgggc 216
 Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg
 15 20
 agggagtggg ggtgacggaa actggagttc ctattgtggc tatcgcttgt gtggaaggaa 276
 caggaggatt ctgctaattc taataacttt ccagctggg agcagggaag catcgatatgt 336
 cctttgtgtt tctcaaactc gcccaattgt tctctgcttt cggggaagct ttactcattt 396
 tctaaaagaa atccaagtac tgtttgggtca ttacccttta gtaaaaaaaaa gtaacaggag 456
 gatatcgtaa ttttctactg ttttattcct ctggttagacc gggccttgac atgaatgacg 516
 ccgtaagggg gaaagagatc ttcccaatca gcaatcacccg taaaagcctg ctgtgttccc 576
 gttaaaatta ggaaattctc actagatgaa ttgacatggg aggcatttag atttctaata 636
 gtcacatagt aattctgcgg aggaattgag tcactcttga tagccatgga attaagcgat 696
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 cttctctgca agtgcctgcc acgtgcccga agaaaagaca cattaaaaag ttaagtgaca 936
 ccagtcctga ttttatatat tttatatacc taacaacgta tatgttagta tgtagaaatt 996
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 aaaaaaaaaaaa aaa 1069

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 agtgggaaag ggaa atg ccg acc aat tgc gct gcg gcg ggc tgt gcc act 170

	Met	Pro	Thr	Asn	Cys	Ala	Ala	Ala	Gly	Cys	Ala	Thr	
	1				5					10			
acc tac aac aag cac att aac atc agc ttc cac agg ttt cct ttg gat													218
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp													
	15				20					25			
cct aaa aga aga aaa gaa tgg gtt cgc ctg gtt agg cgc aaa aat ttt													266
Pro Lys Arg Arg Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe													
	30				35					40			
gtg cca gga aaa cac act ttt ctt tgt tca aag cac ttt gaa gcc tcc													314
Val Pro Gly Lys His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser													
	45				50					55			60
tgt ttt gac cta aca gga caa act cga cga ctt aaa atg gat gct gtt													362
Cys Phe Asp Leu Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val													
	65									70			75
cca acc att ttt gat ttt tgt acc cat ata aag tct atg aaa ctc aag													410
Pro Thr Ile Phe Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys													
	80									85			90
tca agg aat ctt ttg aag aaa aac aac agt tgt tct cca gct gga cca													458
Ser Arg Asn Leu Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro													
	95									100			105
tct agt tta aaa tca aac att agt agt cag caa gta cta ctt gaa cac													506
Ser Ser Leu Lys Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His													
	110									115			120
agc tat gcc ttt agg aat cct atg gag gca aaa aag agg atc att aaa													554
Ser Tyr Ala Phe Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys													
	125									130			135
ctg gaa aaa gaa ata gca agc tta aga aga aaa atg aaa act tgc cta													602
Leu Glu Lys Glu Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu													
	145									150			155
caa aag gaa cgc aga gca act cga aga tgg atc aaa gcc atg tgt ttg													650
Gln Lys Glu Arg Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu													
	160									165			170
gta aag aat tta gaa gca aat agt gta tta cct aaa ggt aca tca gaa													698
Val Lys Asn Leu Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu													
	175									180			185
cac atg tta cca act gcc tta agc agt ctt cct ttg gaa gat ttt aag													746
His Met Leu Pro Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys													
	190									195			200
atc ctt gaa caa gat caa caa gat aaa aca ctg cta agt cta aat cta													794
Ile Leu Glu Gln Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu													
	205									210			215
aaa cag acc aag agt acc ttc att taaatttagc ttgcacagag cttgatgcct													848
Lys Gln Thr Lys Ser Thr Phe Ile													
	225												
atccttcatt cttttcagaa gtaaagataa ttatggcact tatgccaaaa ttcattatctt													908
aataaagttt tacttgaagt aacattactg aatttgtgaa gacttgatta caaaagaata													968
aaaaacttca tatggaaatt ttatttgaaa atgagtggaa gcgccttaca ttagaattac													1028
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<210> 60
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..290

<221> sig_peptide
 <222> 33..92

<223> Von Heijne matrix
score 5.4
seq WFWHSSALGLVLA/PP

<400> 60
aatggtaggc cttcatgtga gccagttact ac atg aat ctt cat ttc cca cag 53
Met Asn Leu His Phe Pro Gln
-20 -15
tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca cct ttc 101
Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro Pro Phe
-10 -5 1
tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt agg cta 149
Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys Arg Leu
5 10 15
tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc tgt tta 197
Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr Cys Leu
20 25 30 35
tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa aat tgt 245
Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys Asn Cys
40 45 50
aat agt cgg cac gct gga ttt gta ggg cca gca aaa ttg cgg cag 290
Asn Ser Arg His Ala Gly Phe Val Gly Pro Ala Lys Leu Arg Gln
55 60 65
tgaaactagt ttcacttcta aagcccttca tttcccacaa ggtaaagctc tcgaaacccc 350
atttgatcct tggttcctat ttcgatcctc ctttggaaac tgaaaatcgg tctccatggt 410
gtatgcaaa 419

<210> 61
<211> 682
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 485..616

<221> polyA_site
<222> 669..682

<400> 61
ctcctttctc attccttctc ttgcgtgttt ttaccttttt ttcataacta agttttttgag 60
gaagtttagtg ttctttttcaa agaaccgggt cgaaatgtac ttttctttgc tactttttgt 120
tattttattg atcacatctt taatcttttg ttctctatac gtggcctgtt ttgattttatt 180
ttactattct tgcttttctaa ggtaagtatt ttgtttgtga gtgctttatt tttttcatct 240
ttctttctga ataataatga cattttttagg ttataaattt tcctctggta ctcagtttgc 300
ctcattaatt ttggcagtaa gcattctcct tttattgctt tctatgtagt ctttaatttt 360
gcttttaact tcttctttga tctaaggatt acctacttgt taatttccaa atattatctt 420
atctatctat ctatctatct atctatctat ctatctatct acctatgtga gacgaagtct 480
ggct atg tcg ccg agg ctg gag tgc agt ggt gca atc ttg gct cac tgc 529
Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys
1 5 10 15
aac ccc cgc ctc cca ggt tca agt tat tct cct gcc tca gct act tgg 577
Asn Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp
20 25 30
gtg aga gga tcc ctt gag ccg ggg agg ttg agg ctg cag tgagccataa 626
Val Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
35 40
ccactactct ccagcctgga taacaaaagt gagactctga ccaaaaaaaaa aaaaaa 682

<210> 62
 <211> 1191
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..995

<221> sig_peptide
 <222> 54..227
 <223> Von Heijne matrix
 score 4.1
 seq LVVHCPTWQWATG/EE

<221> polyA_signal
 <222> 1130..1135

<221> polyA_site
 <222> 1181..1191

<400> 62
 cacggctgca ctttccatcc cgtcgcgggg cgggcgcta ctccggcccc agg atg 56
 Met
 cag aat gtg att aat act gtg aag gga aag gca ctg gaa gtg gct gag 104
 Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala Glu
 -55 -50 -45
 tac ctg acc ccg gtc ctc aag gaa tca aag ttt agg gaa aca ggt gta 152
 Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly Val
 -40 -35 -30
 att acc cca gaa gag ttt gtg gca gct gga gat cac cta gtc cac cac 200
 Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His His
 -25 -20 -15 -10
 tgt cca aca tgg caa tgg gct aca ggg gaa gaa ttg aaa gtg aag gca 248
 Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Leu Lys Val Lys Ala
 -5 1 5
 tac cta cca aca ggc aaa caa ttt ttg gta acc aaa aat gtg ccg tgc 296
 Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro Cys
 10 15 20
 tat aag cgg tgc aaa cag atg gaa tat tca gat gaa ttg gaa gct atc 344
 Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala Ile
 25 30 35
 att gaa gaa gat gat ggt gat ggc gga tgg gta gat aca tat cac aac 392
 Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His Asn
 40 45 50 55
 aca ggt att aca gga ata acg gaa gcc gtt aaa gag atc aca ctg gaa 440
 Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu Glu
 60 65 70
 aat aag gac aat ata agg ctt caa gat tgc tca gca cta tgt gaa gag 488
 Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu Glu
 75 80 85
 gaa gaa gat gaa gat gaa gga gaa gct gca gat atg gaa gaa tat gaa 536
 Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr Glu
 90 95 100
 gag agt gga ttg ttg gaa aca gat gag gct acc cta gat aca agg aaa 584
 Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg Lys
 105 110 115
 ata gta gaa gct tgt aaa gcc aaa act gat gct ggc ggt gaa gat gct 632
 Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp Ala
 120 125 130 135
 att ttg caa acc aga act tat gac ctt tac atc act tat gat aaa tat 680

Ile	Leu	Gln	Thr	Arg	Thr	Tyr	Asp	Leu	Tyr	Ile	Thr	Tyr	Asp	Lys	Tyr		
				140					145					150			
tac	cag	act	cca	cga	tta	tgg	ttg	ttt	ggc	tat	gat	gag	caa	cgg	cag	728	
Tyr	Gln	Thr	Pro	Arg	Leu	Trp	Leu	Phe	Gly	Tyr	Asp	Glu	Gln	Arg	Gln		
			155					160					165				
cct	tta	aca	gtt	gag	cac	atg	tat	gaa	gac	atc	agt	cag	gat	cat	gtg	776	
Pro	Leu	Thr	Val	Glu	His	Met	Tyr	Glu	Asp	Ile	Ser	Gln	Asp	His	Val		
			170				175					180					
aag	aaa	aca	gtg	acc	att	gaa	aat	cat	cct	cat	ctg	cca	cca	cct	ccc	824	
Lys	Lys	Thr	Val	Thr	Ile	Glu	Asn	His	Pro	His	Leu	Pro	Pro	Pro	Pro		
			185				190				195						
atg	tgt	tca	gtt	cac	cca	tgc	agg	cat	gct	gag	gtg	atg	aag	aaa	atc	872	
Met	Cys	Ser	Val	His	Pro	Cys	Arg	His	Ala	Glu	Val	Met	Lys	Lys	Ile		
200					205				210					215			
att	gag	act	gtt	gca	gaa	gga	ggg	gga	gaa	ctt	gga	gtt	cat	atg	tat	920	
Ile	Glu	Thr	Val	Ala	Glu	Gly	Gly	Gly	Glu	Leu	Gly	Val	His	Met	Tyr		
				220				225					230				
ctt	ctt	att	ttc	ttg	aaa	ttt	gta	caa	gct	gtc	att	cca	aca	ata	gaa	968	
Leu	Leu	Ile	Phe	Leu	Lys	Phe	Val	Gln	Ala	Val	Ile	Pro	Thr	Ile	Glu		
			235					240				245					
tat	gac	tac	aca	aga	cac	ttc	aca	atg	taatgaagag	agcataaaat						1015	
Tyr	Asp	Tyr	Thr	Arg	His	Phe	Thr	Met									
			250				255										
ctatccta	at	tattgg	ttct	gatttt	taaa	gaatta	accc	atagat	gtga	ccattg	acca					1075	
tattcat	caa	tatata	cagt	ttctcta	ata	agggact	tat	atgttt	atgc	attaa	ataaa					1135	
aatatg	ttcc	actacc	agcc	ttactt	gttt	aataaaa	atc	agtgc	aaaaa	aaaaa						1191	

<210> 63
 <211> 1008
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 657..923

<221> sig_peptide
 <222> 657..896
 <223> Von Heijne matrix
 score 3.5
 seq RGLLSACAPWGDG/ST

<221> polyA_signal
 <222> 957..962

<221> polyA_site
 <222> 974..1008

<400> 63																	
ntcg	natgtg	gcac	aaaacc	cctct	gctgg	ctcat	gtgtg	caact	gagac	tg	tcag	agca				60	
tgg	ctagctc	tggg	gtccag	ctct	gctggg	tggg	ggctag	agag	gaagca	ggg	agtatct					120	
gcac	acagga	tg	cctgcgt	cagg	tggtg	caga	agtcag	tg	cccaggcc	cccc	acaca					180	
gt	ccccaaag	gt	ccggcctc	ccc	agcgcg	gg	ctcctcgt	ttg	aggggag	gtg	acttccc					240	
tcc	agcagg	ct	cttggaca	cag	taagctt	cccc	agccct	gc	ctgagcag	c	tttcctcc					300	
ttg	ccctgtt	cccc	acctcc	cgg	ctccagt	cc	agggagct	ccc	aggggaag	tg	gtcg	accc				360	
ct	ccagtggc	tggg	ccactc	tg	ctagagtc	cat	ccgccaa	g	ctgggggca	tc	ggcaaggc					420	
ca	agctgcgc	ag	catgaagg	ag	cgaaagct	gg	agaagaag	a	agcagaagg	ag	caggagca					480	
ag	tgagagcc	ac	gagccaag	gt	gggcactt	gat	gtcggat	ct	cttcaaca	ag	ctgggtcat					540	
ga	ggcgcaag	gg	catctctg	gg	aaagaacc	tggg	gctggt	ga	gggggcccg	ga	ggagcctt					600	
tg	cccgctg	tc	agactcca	tcc	ctcctct	gcc	gccaccg	cag	cagccac	ag	gtag	atg				659	

Met
-80

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agg aca agg acg act ggg aat cct agg ggg ctc cat gac acc ttc ccc      707
Arg Thr Arg Thr      Gly Asn Pro Arg Gly Leu His Asp Thr Phe Pro
      -75      -70      -65
cgc aga ccc aga ctt ggc cgt tgc tct gac atg gac aca gcc agg aca      755
Arg Arg Pro Arg Leu Gly Arg Cys Ser Asp Met Asp Thr Ala Arg Thr
      -60      -55      -50
agc tgc tca gac ctg ctt ccc tgg gag ggg gtg acg gaa cca gca ctg      803
Ser Cys Ser Asp Leu Leu Pro Trp Glu Gly Val Thr Glu Pro Ala Leu
      -45      -40      -35
tgt gga gac cag ctt caa gga acg gaa ggc tgg ctt gag gcc aca cag      851
Cys Gly Asp Gln Leu Gln Gly Thr Glu Gly Trp Leu Glu Ala Thr Gln
      -30      -25      -20
ctg ggg cgg gga ctt ctg tct gcc tgt gct cca tgg ggg gac ggc tcc      899
Leu Gly Arg Gly Leu Leu Ser Ala Cys Ala Pro Trp Gly Asp Gly Ser
      -15      -10      -5      1
acc cag cct gtg cca ctg tgt tct taagaggctt ccagagaaaa cggcacacca      953
Thr Gln Pro Val Pro Leu Cys Ser
      5
atcaataaag aactgagcag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaan      1008

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<210> 64
 <211> 568
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..311
 <221> sig_peptide
 <222> 18..62
 <223> Von Heijne matrix
 score 8.4
 seq AMWLLCVALAVLA/WG

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<400> 64
agtgtgtgctt acccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      50
      Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
      -15      -10      -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      98
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
      1      5      10
atg aag agt cgg gag cag gga gga cgg ctg gga gcc gaa agc cgg acc      146
Met Lys Ser Arg Glu Gln Gly Gly Arg Leu Gly Ala Glu Ser Arg Thr
      15      20      25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc      194
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
      30      35      40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      242
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
      45      50      55      60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa ggt ctt      290
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu
      65      70      75
acc tct gaa ccc ctc aca gcc tagggacagg agcggccggc ttacctggtg      341
Thr Ser Glu Pro Leu Thr Ala
      80
ggttggggga cgtcggcagc tcgcgtacta cgccagcagg attgaggagc agagaaacag      401

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ttgcagttgg ttgtattcag tacctgcatt tccgttgga actccacctg tacttggtat 461
tctgtggaac tttttttatt tgtagaagga gcaagaatat tgaccttact atatagcaca 521
cgaaacaatc tatgctgtat cgtgcctgct caatccttaa agttaac 568

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<210> 65
 <211> 538
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 151..426

<221> sig_peptide
 <222> 151..258
 <223> Von Heijne matrix
 score 5.2
 seq KVALAGLLGFGLG/KV

<221> polyA_signal
 <222> 505..510

<221> polyA_site
 <222> 527..538

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<400> 65
cactgggtca aggagtaagc agaggataaa caactggaag gagagcaagc acaaagtcac 60
catggcttca gcgtctgctc gtggaaacca agataaagat gccattttc caccaccaag 120
caagcagctc tgcctttttc tcttgtaagc atg ctt gtc acc cag gga cta gtc 174
                                Met Leu Val Thr Gln Gly Leu Val
                                -35                                -30
tac caa ggt tat ttg gca gct aat tct aga ttt gga tca ttg ccc aaa 222
Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys
                                -25                                -20                                -15
gtt gca ctt gct ggt ctc ttg gga ttt ggc ctt gga aag gta tca tac 270
Val Ala Leu Ala Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr
                                -10                                -5                                1
ata gga gta tgc cag agt aaa ttc cat ttt ttt gaa gat cag ctc cgt 318
Ile Gly Val Cys Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg
5                                10                                15                                20
ggg gct ggt ttt ggt cca cag cat aac agg cac tgc ctc ctt acc tgt 366
Gly Ala Gly Phe Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys
                                25                                30                                35
gag gaa tgc aaa ata aag cat gga tta agt gag aag gga gac tct cag 414
Glu Glu Cys Lys Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln
                                40                                45                                50
cct tca gct tcc taaattctgt gtctgtgact ttcgaagttt tttaaactc 466
Pro Ser Ala Ser
55
tgaatttgta cacatttaaa atttcaagtg tacttttaaaa taaaatactt ctaatggaac 526
aaaaaaaaaa aa 538

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<210> 66
 <211> 1747
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 10..1062

<221> sig_peptide

<222> 10..57

<223> Von Heijne matrix

score 4.9

seq FIYLLQAHTLCSG/WS

<221> polyA_signal

<222> 1710..1715

<221> polyA_site

<222> 1735..1747

<400> 66

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gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt      51
      Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys
            -15                -10                -5
tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg      99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
            1                5                10
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta      147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
15                20                25                30
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc      195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
            35                40                45
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc      243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
            50                55                60
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg      291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
65                70                75
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc      339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
80                85                90
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa      387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
95                100                105                110
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac      435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
            115                120                125
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg      483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
            130                135                140
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg      531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
145                150                155
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt      579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
160                165                170
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc      627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
175                180                185                190
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc      675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
            195                200                205
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg      723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
210                215                220
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac      771

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Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
      225                      230                      235
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg      819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
      240                      245                      250
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca      867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
      255                      260                      265                      270
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc      915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
      275                      280                      285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc      963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
      290                      295                      300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc ccn      1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
      305                      310                      315
ttt tgt cac ctt gga cat gga aga ctg tgg cta caa cat tcc aca gac      1059
Phe Cys His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp
      320                      325                      330
aga tgagtcaacc ctcatgacca tagcctatgt catggctgcc atctgcgccc      1112
Arg
335
tcttcatgct gccactctgc ctcatggtgt gtcagtggcg ctgcctcgcg tgcctgcgcc      1172
agcagcatga tgactttgct gatgacatct ccctgctgaa gtgaggaggc ccatgggcag      1232
aagataggga ttcccctgga ccacacctcc gtgggttcaact ttggtcacaa gtaggagaca      1292
cagatggcac ctgtggccag agcacctcag gacctcctcc acccaccaaa tgcctctgcc      1352
ttgatggaga aggaaaaggc tggcaagggtg gggtccagggt actgtacctg taggagacag      1412
aaaagagaag aaagaagcac tctgctggcg ggaatactct tggtcacctc aaatttaagt      1472
cgggaaaattc tgctgcttga aacttcagcc ctgaaccttt gtcaccattc ctttaaattc      1532
tccaacccaa agtattcttc ttttcttagt ttcagaagta ctggcatcac acgcaggtta      1592
ccttggcgtg tgctcctgtg gtaccctggc agagaagaga ccaagcttgt ttccctgctg      1652
gccaaagtca gtaggagagg atgcacagtt tgctatttgc tttagagaca gggactgtat      1712
aaacaagcct aacattggtg caaaaaaaaaa aaaaaa      1747

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<210> 67

<211> 1686

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 78..491

<221> sig_peptide

<222> 78..218

<223> Von Heijne matrix

score 5.8

seq LMCFGALIGLCAC/IC

<221> polyA_signal

<222> 1652..1657

<221> polyA_site

<222> 1673..1686

<400> 67

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ggtatagccc accagaaagg acagagtcac ttgatgtggt cacaaaatgt gtgagtttca      60
cactaactga gcagtttc atg gag aaa ttt gtt gat ccc gga aac cac aat      110
Met Glu Lys Phe Val Asp Pro Gly Asn His Asn

```

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<221> sig_peptide
<222> 69..287
<223> Von Heijne matrix
      score 4
      seq AVGFLEFWVIVLTS/WI
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<221> polyA_signal
<222> 510..515

<221> polyA_site
<222> 530..542

<400> 68
tggtacttag ggtcaaggct tgggtcttgc cccgcaaacc cttgggacga cccggcccca 60
gcgagct atg aac ctg gag cga gtg tcc aat gag gag aaa ttg aac ctg 110
Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu
-70 -65 -60
tgc cgg aag tac tac ctg ggg ggg ttt gct ttc ttg cct ttt ctc tgg 158
Cys Arg Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp
-55 -50 -45
ttg gtc aac atc ttc tgg ttc tac cga gag gcc ttc ctt gtc cca gcc 206
Leu Val Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala
-40 -35 -30
tac aca gaa cag agc caa atc aaa ggc tat gtc tgg cgc tca gct gtg 254
Tyr Thr Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val
-25 -20 -15
ggc ttc ctc ttc tgg gtg ata gtg ctc acc tcc tgg atc acc atc ttc 302
Gly Phe Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe
-10 -5 1 5
cag atc tac cgg ccc cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc 350
Gln Ile Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe
10 15 20
acc ata ccc ctg ggc acc ccc tgacaacttc tgcacatact ggggcctgc 401
Thr Ile Pro Leu Gly Thr Pro
25
ttattctccc aggacaggct ccttaaagca gaggagcctg tcctgggagc cccttctcaa 461
actcctaaga cttgttctca tgtccacgt tctctgctga catcccccaa taaaggaccc 521
taactttcaa aaaaaaaaaa a 542

<210> 69
<211> 1174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..757

<221> sig_peptide
<222> 2..205
<223> Von Heijne matrix
score 7.3
seq LRLILSPLPGAQP/QQ

<221> polyA_site
<222> 1160..1174

<400> 69
g atg cct gag ggc ccc gag ctg cac ctg gcc agc cag ttt gtg aat gag 49
Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
-65 -60 -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc 97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
-50 -45 -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca 145

Ser	Arg	Asn	Pro	Glu	Val	Pro	Phe	Glu	Ser	Ser	Ala	Tyr	Arg	Ile	Ser	
-35						-30					-25					
gct	tca	gcc	cgc	ggc	aag	gag	ctg	cgc	ctg	ata	ctg	agc	cct	ctg	cct	193
Ala	Ser	Ala	Arg	Gly	Lys	Glu	Leu	Arg	Leu	Ile	Leu	Ser	Pro	Leu	Pro	
-20					-15					-10					-5	
ggg	gcc	cag	cct	caa	cag	gag	cca	ctg	gcc	ctg	gtc	ttc	cgc	ttc	ggc	241
Gly	Ala	Gln	Pro	Gln	Gln	Glu	Pro	Leu	Ala	Leu	Val	Phe	Arg	Phe	Gly	
				1				5					10			
atg	tcc	ggc	tct	ttt	cag	ctg	gtg	ccc	cgc	gag	gag	ctg	cca	cgc	cat	289
Met	Ser	Gly	Ser	Phe	Gln	Leu	Val	Pro	Arg	Glu	Glu	Leu	Pro	Arg	His	
	15						20					25				
gcc	cac	ctg	cgc	ttt	tac	acg	gcc	ccg	cct	ggc	ccc	cgg	ctc	gcc	cta	337
Ala	His	Leu	Arg	Phe	Tyr	Thr	Ala	Pro	Pro	Gly	Pro	Arg	Leu	Ala	Leu	
	30					35					40					
tgt	ttc	gtg	gac	atc	cgc	cgg	ttc	ggc	cgc	tgg	gac	ctt	ggg	gga	aag	385
Cys	Phe	Val	Asp	Ile	Arg	Arg	Phe	Gly	Arg	Trp	Asp	Leu	Gly	Gly	Lys	
45					50				55					60		
tgg	cag	ccg	ggc	cgc	ggg	ccc	tgt	gtc	ttg	cag	gag	tac	cag	cag	ttc	433
Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Glu	Tyr	Gln	Gln	Phe	
				65				70					75			
agg	gag	aat	gtg	cta	cga	aac	cta	gcg	gat	aag	gcc	ttt	gac	cgg	ccc	481
Arg	Glu	Asn	Val	Leu	Arg	Asn	Leu	Ala	Asp	Lys	Ala	Phe	Asp	Arg	Pro	
		80						85				90				
atc	tgc	gag	gcc	ctc	ctg	gac	cag	agg	ttc	ttc	aat	ggc	att	ggc	aac	529
Ile	Cys	Glu	Ala	Leu	Leu	Asp	Gln	Arg	Phe	Phe	Asn	Gly	Ile	Gly	Asn	
		95					100					105				
tat	ctg	cgg	gca	gag	atc	ctg	tac	cgg	ctg	aag	atc	ccc	ttt	gag		577
Tyr	Leu	Arg	Ala	Glu	Ile	Leu	Tyr	Arg	Leu	Lys	Ile	Pro	Pro	Phe	Glu	
	110				115						120					
aag	gcc	cgc	tcg	gtc	ctg	gag	gcc	ctg	cag	cag	cac	agg	ccg	agc	ccg	625
Lys	Ala	Arg	Ser	Val	Leu	Glu	Ala	Leu	Gln	Gln	His	Arg	Pro	Ser	Pro	
	125				130				135				140			
gag	ctg	acc	ctg	agc	cag	aag	ata	agg	acc	aag	ctg	cag	aat	tca	gac	673
Glu	Leu	Thr	Leu	Ser	Gln	Lys	Ile	Arg	Thr	Lys	Leu	Gln	Asn	Ser	Asp	
				145				150					155			
ctg	ctg	gag	cta	tgt	cac	tca	gtg	ccc	aag	gaa	gtg	gtc	cag	ttg	ggt	721
Leu	Leu	Glu	Leu	Cys	His	Ser	Val	Pro	Lys	Glu	Val	Val	Gln	Leu	Gly	
		160						165				170				
gag	gcc	aaa	gat	ggc	agc	aac	ctc	tgc	ttc	agc	aaa	tgattgtgta				767
Glu	Ala	Lys	Asp	Gly	Ser	Asn	Leu	Cys	Phe	Ser	Lys					
	175						180									
accctggggc	acttgctccc	ctctggacct	gattcaccga	tttggaagtt	tgtagcccta											827
gctgatactc	aatggactag	gcctcctcac	ttgtcaatag	tgtttccagg	ctgggcgcag											887
tggctcatgc	ctgtggtccc	ggcacttcgg	gaggccgagt	ggggtggctc	acctgaggtc											947
aggagttcga	gaccatcctg	gccaacatgg	tgaaacccca	tctccactaa	aatgcaaaaa											1007
attagccagg	tgtggtggcg	ggcacctgta	gtctcagcta	ctcggggagga	tgaggcagga											1067
aaatcgcttg	aaccagaggag	gtggagggttg	cagttgagct	gagatcgtgc	cattgcactc											1127
cagcctgggc	aacgagagca	aaactccatc	tcaaaaaaaa	aaaaaaa												1174

<210> 70

<211> 1285

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..1051

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix
score 7.3
seq LRLILSPLPGAQP/QQ

<221> polyA_signal
<222> 1248..1253

<221> polyA_site
<222> 1272..1285

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Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
-65 -60 -55
gcc tgc agg ggc ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc 97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
-50 -45 -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca 145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
-35 -30 -25
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct 193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
-20 -15 -10 -5
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc 241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
1 5 10
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat 289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
15 20 25
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta 337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
30 35 40
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag 385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
45 50 55 60
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc 433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
65 70 75
agg ctg aag atc ccc ccc ttt gag aag gcc cgc tcg gtc ctg gag gcc 481
Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala
80 85 90
ctg cag cag cac agg ccg agc ccg gag ctg acc ctg agc cag aag ata 529
Leu Gln Gln His Arg Pro Ser Pro Glu Leu Thr Leu Ser Gln Lys Ile
95 100 105
agg acc aag ctg cag aat cca gac ctg ctg gag cta tgt cac tca gtg 577
Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu Glu Leu Cys His Ser Val
110 115 120
ccc aag gaa gtg gac cag ttg ggg ggc agg ggc tac ggg tca gag agc 625
Pro Lys Glu Val Asp Gln Leu Gly Gly Arg Gly Tyr Gly Ser Glu Ser
125 130 135 140
ggg gag gag gac ttt gct gcc ttt cga gcc tgg ctg cgc tgc tat ggc 673
Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala Trp Leu Arg Cys Tyr Gly
145 150 155
atg cca ggc atg agc tcc ctg cag gac cgg cat ggc cgt acc atc tgg 721
Met Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp
160 165 170
ttc cag ggg gat cct gga ccg ttg gca ccc aaa ggg cgc aag tcc cgc 769
Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg
175 180 185
aaa aag aaa tcc aag gcc aca cag ctg agt cct gag gac aga gtg gag 817
Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
190 195 200

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gac gct ttg cct cca agc aag gcc cct tcc aag aca cga agg gca aag      865
Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys
205                      210                      215                      220
aga gac ctt cct aag agg act gca acc cag cgg cct gag ggg acc agc      913
Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
                225                      230                      235
ctc cag cag gac cca gaa gct ccc aca gtg ccc aag aag ggg agg agg      961
Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
                240                      245                      250
aag ggg cga cag gca gcc tct ggc cac tgc aga ccc cgg aag gtc aag      1009
Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
                255                      260                      265
gct gac atc cca tcc ttg gaa cca gag ggg acc tca gcc tct      1051
Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
                270                      275                      280
tagcaggagg ctctccttgc ttgcactcac cctttcttat tgtcttgccc tgcattctggg      1111
ggtctgaatt tttgggagca ggcaatatct gaagggtgcaa acaggcccta cggctgttcc      1171
ctgcacaact ctcatggttt taattgtacc ccatcttcca catctttaa gctcatgtga      1231
aaaatgctgc atttttaata aactgatata tttgaactcc aaaaaaaaaa aaaa      1285

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<210> 71

<211> 1398

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..1171

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix

score 7.3

seq LRLILSPLPGAQP/QQ

<221> polyA_signal

<222> 1368..1373

<221> polyA_site

<222> 1386..1398

<400> 71

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Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
                -65                      -60                      -55
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc      97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
                -50                      -45                      -40
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca      145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
                -35                      -30                      -25
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct      193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
                -20                      -15                      -10                      -5
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc      241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
                1                      5                      10
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat      289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
                15                      20                      25

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gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta 337
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
 30 35 40
 tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag 385
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
 45 50 55 60
 tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc 433
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
 65 70 75
 agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc 481
 Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
 80 85 90
 atc tgc gag gcc ctc ctg gac cag agg ttc ttc aat ggc att ggc aac 529
 Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
 95 100 105
 tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag 577
 Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
 110 115 120
 aag gcc cgc tcg gtc ctg gag gcc ctg cag cag cac agg ccg agc ccg 625
 Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
 125 130 135 140
 gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat cca gac 673
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp
 145 150 155
 ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggg 721
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
 ggc aga ggc tac ggg tca gag agc ggg gag gag gac ttt gct gcc ttt 769
 Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe
 175 180 185
 cga gcc tgg ctg cgc tgc tat ggc atg cca ggc atg agc tcc ctg cag 817
 Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln
 190 195 200
 gac cgg cat ggc cgt acc atc tgg ttc cag ggg gat cct gga ccg ttg 865
 Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu
 205 210 215 220
 gca ccc aaa ggg cgc aag tcc cgc aaa aag aaa tcc aag gcc aca cag 913
 Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln
 225 230 235
 ctg agt cct gag gac aga gtg gag gac gct ttg cct ccg agc aag gcc 961
 Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
 240 245 250
 cct tcc agg aca cga agg gca aag aga gac ctt cct aag agg act gca 1009
 Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
 255 260 265
 acc cag cgg cct gag ggg acc agc ctc cag cag gac cca gaa gct ccc 1057
 Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
 270 275 280
 aca gtg ccc aag aag ggg agg agg aag ggg cga cag gca gcc tct ggc 1105
 Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
 285 290 295 300
 cac tgc aga ccc cgg aag gtc aag gct gac atc cca tcc ttg gaa cca 1153
 His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
 305 310 315
 gag ggg acc tca gcc tct tagcaggagg ctctccttgc ttgcactcac 1201
 Glu Gly Thr Ser Ala Ser
 320
 cctttcttat tgtcttgccc tgcattctggg ggtctgaatt tttgggagca ggcaatatct 1261
 gaagggtgcaa acaggcccta cggctgttcc ctgcacaact ctcatgggtt taattgtacc 1321
 ccatcttcca catctttaaa gctcatgtga aaaatgctgc atttttaata aactgatata 1381
 tttgaaaaaa aaaaaaa 1398

<210> 72
 <211> 821
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..611

<221> sig_peptide
 <222> 42..287
 <223> Von Heijne matrix
 score 4.4
 seq NLPHLQVVGLTWG/HI

<221> polyA_signal
 <222> 787..792

<221> polyA_site
 <222> 808..821

<400> 72
 ccgttgccag ttctgcgcgt gtcctgcgtc tccagtatgg a atg tat gtt tgg ccc 56
 Met Tyr Val Trp Pro
 -80
 tgt gct gtg gtc ctg gcc cag tac ctt tgg ttt cac aga aga tct ctg 104
 Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe His Arg Arg Ser Leu
 -75 -70 -65
 cca ggc aag gcc atc tta gag att gga gca gga gtg agc ctt cca gga 152
 Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly Val Ser Leu Pro Gly
 -60 -55 -50
 att ttg act gcc aaa tgt ggt gca gaa gta ata ctg tca gac agc tca 200
 Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile Leu Ser Asp Ser Ser
 -45 -40 -35 -30
 gaa ctg cct cac tgt ctg gaa gtc tgt cgg caa agc tgc caa atg aat 248
 Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln Ser Cys Gln Met Asn
 -25 -20 -15
 aac ctg cca cat ctg cag gtg gta gga cta aca tgg ggt cat ata tct 296
 Asn Leu Pro His Leu Gln Val Val Gly Leu Thr Trp Gly His Ile Ser
 -10 -5 1
 tgg gat ctt ctg gct cta cca cca caa gat att atc ctt gca tct gat 344
 Trp Asp Leu Leu Ala Leu Pro Gln Asp Ile Ile Leu Ala Ser Asp
 5 10 15
 gtg ttc ttt gaa cca gaa gat ttt gaa gac att ttg gct aca ata tat 392
 Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile Leu Ala Thr Ile Tyr
 20 25 30 35
 ttt ttg atg cac aag aat ccc aag gtc caa ttg tgg tct act tat caa 440
 Phe Leu Met His Lys Asn Pro Lys Val Gln Leu Trp Ser Thr Tyr Gln
 40 45 50
 gtt agg agt gct gac tgg tca ctt gaa gct tta ctc tac aaa tgg gat 488
 Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu Leu Tyr Lys Trp Asp
 55 60 65
 atg aaa tgt gtc cac att cct ctt gag tct ttt gat gca gac aaa gaa 536
 Met Lys Cys Val His Ile Pro Leu Glu Ser Phe Asp Ala Asp Lys Glu
 70 75 80
 gat ata gca gaa tct acc ctt cca gga aga cat aca gtt gaa atg ctg 584
 Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His Thr Val Glu Met Leu
 85 90 95
 gtc att tcc ttt gca aag gac agt ctc tgaattatac ctacaacctg 631
 Val Ile Ser Phe Ala Lys Asp Ser Leu

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100                               105
ttctgggaca gtatcaatac tgatgagcaa cctggcacac aaactatgag cagaccactt 691
cagcttgaga atgcagtggg tctgaagatg gtcaagtctg tctgccttag attttgatgt 751
cacctagaca acacttaaac tcatatgaaa caaaaattaa aatacgtatt acaagtaaaa 811
aaaaaaaaaa                                     821

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<210> 73
<211> 916
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 62..916

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<221> sig_peptide
<222> 62..757
<223> Von Heijne matrix
      score 4.2
      seq LVTPAALRPLVLG/GN

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<221> polyA_site
<222> 904..916

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g atg gga tgt gtt ttc cag agc aca gaa gac aaa cgt ata ttc aag ata 109
  Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
      -230                               -225                               -220
gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta 157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
      -215                               -210                               -205
tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc 205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
      -200                               -195                               -190                               -185
gta cac ttg atg ggg gac aac tta tgc aat gat ggc tct ctc ctg ctc 253
Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
      -180                               -175                               -170
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc 301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
      -165                               -160                               -155
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg 349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
      -150                               -145                               -140
ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att 397
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
      -135                               -130                               -125
cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag 445
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
      -120                               -115                               -110                               -105
gta gaa tgg ata ttt tca gga cgg cgc gca aag gag gag att gta ttt 493
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
      -100                               -95                               -90
cgt tac tac cac aaa ctc agg atg tct gcg gag tac tcc cag agc tgg 541
Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
      -85                               -80                               -75
ggc cac ttc cag aat cgt gtg aac ctg gtg ggg gac att ttc cgc aat 589
Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn
      -70                               -65                               -60
gac ggt tcc atc atg ctt caa gga gtg agg gag tca gat gga gga aac 637

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Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
-55 -50 -45
tac acc tgc agt atc cac cta ggg aac ctg gtg ttc aag aaa acc att 685
Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
-40 -35 -30 -25
gtg ctg cat gtc agc ccg gaa gag cct cga aca ctg gtg acc ccg gca 733
Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
-20 -15 -10
gcc ctg agg cct ctg gtc ttg ggt ggt aat cag ttg gtg atc att gtg 781
Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
-5 1 5
gga att gtc tgt gcc aca atc ctg ctg ctc cct gtc ctg ata ttg atc 829
Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
10 15 20
gtg aag aag acc tgt gga aat aag agt tca gtg aat tct aca gtc ttg 877
Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
25 30 35 40
gtg aag aac acg aag aag act aat cca aaa aaa aaa aaa 916
Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys Lys
45 50

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<210> 74
 <211> 1153
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..520

<221> polyA_signal
 <222> 1124..1129

<221> polyA_site
 <222> 1141..1153

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<400> 74
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g atg gga tgt gtt ttc cag agc aca gta gac aaa tgt ata ttc aag ata 109
Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
1 5 10 15
gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta 157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
20 25 30
tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc 205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
35 40 45
gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc 253
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
50 55 60
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc 301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65 70 75 80
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg 349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
85 90 95
ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att 397
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
100 105 110
cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag 445

```

Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys	
115 120 125	
gta gaa tgg ata ttt tca gga cgg cgc gca aag gta aca agg agg. aaa	493
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys	
130 135 140	
cat cac tgt gtt aga gaa ggc tct ggc tgaatggatc aggacaaagg	540
His His Cys Val Arg Glu Gly Ser Gly	
145 150	
tagaatcagg cacatgagga ggtgttgcaa gagcctgggc tttgggtgctt atcagaactg	600
gaccttctcc tagcaatttc agctttctgg tgggaaaagg aactccaatg aagaacaaga	660
acaagaagat gatgatgatg ctttaactttt tggatgccga tatgagattg tacatgtaaa	720
gcattttgta taagacttgg cccctgcatt ttagtttctt tctttctccc ttttccttcg	780
tatagagtcc atgggagaat gagggagatg atttttgtgg ccagccaag aaagcaatgg	840
gctagacatt aaaatgatta cacttttatt cttactgggg ttagttctgt gagttttcat	900
ctgtgcccca ttgccccatt tatgtgatgg agggaatttt catgggtact tcacgtgttg	960
ggattgattg atcctggggg ccaggggtgaa gggatatttta cgggacctct ataaagcagg	1020
aagaagcaag tttattcttt agaccagtag ctctcaacca tgatgtgggtc atatatattat	1080
gggtcaacat gtgttgtggg gatatcccaa gtaacttggt attaataaaa gttaagttgc	1140
aaaaaaaaaaa aaa	1153

<210> 75

<211> 1517

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..167

<400> 75

ctctgaaatg cttgtctttt atg ctg gna ggt gac cat agg gct ctg ctt tta	53
Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu	
1 5 10	
aag ata tgg ctg ctt caa agg cca gag tca cag gaa gga ctt ctt cca	101
Lys Ile Trp Leu Leu Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro	
15 20 25	
ggg aga tta gtg gtg atg gag agg aga gtt aaa atg acc tca tgt cct	149
Gly Arg Leu Val Val Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro	
30 35 40	
tct tgt cca cgg ttt tgt tgagttttca ctcttctaata gcaagggtct	197
Ser Cys Pro Arg Phe Cys	
45	
cacactgtga accacttagg atgtgatcac tttcagggtgg ccaggaatgt tgaatgtctt	257
tggctcagtt cattttaaaaa agatatctat ttgaaagttc tcagagttgt acatatgttt	317
cacagtacag gatctgtaca taaaagtttc tttcctaaac cattcaccaa gagccaatat	377
ctaggcattt tcttggtagc acaaattttc ttattgctta gaaaattgtc ctccttggtta	437
tttctgtttg taagacttaa gtgagttagg tctttaagga aagcaacgct cctctgaaat	497
gcttgtcttt tatgctggga ggtgaccata gggctctgct ttaaaagata tggctgcttc	557
aaaggccaga gtcacaggaa ggacttcttc cagggagatt agtgggtgat gagaggagag	617
ttaaaatgac ctcagtgcct tcttgtccac ggttttgttg agttttcact cttctaatagc	677
aagggtctca cactgtgaac cacttaggat gtgatcactt tcaggtggcc aggaatgttg	737
aatgtctttg gctcagttca tttaaaaaag atatctattt gaaagtcttc agagttgtac	797
atatgtttca cagtacagga tctgtacata aaagtttctt tcttaaacca ttcaccaaga	857
gccaatatct aggcattttc ttggtagcac aaattttctt attgcttaga aaattgtcct	917
ccttgttatt tctgtttgta agacttaagt gagttaggtc ttaaggaaa gcaacgctcc	977
tctgaaatgc ttgtctttna tgctgggagg tgaccatagg gctctgcttt taaagatatg	1037
gctgcttcaa aggccagagt cacaggaagg acttcttcca gggagattag tgggtgatgga	1097
gaggagagtt aaaatgacct catgtccttc ttgtccacgg tttgtttgag ttttcactct	1157
tctaatagcaa ggggtctcaca ctgtgaacca cttaggatgt gatcactttc aggtggccag	1217
gaatgttgaa tgtctttggc tcagttcatt taaaaaagat atctatttga aagttctcag	1277

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agttgtacat atgtttcaca gtacaggatc tgtacataaa agttttcttcc ctaaaccatt 1337
caccaagagc caatatctag gcatttttctt ggtagcacaa atttttcttat tgcttagaaa 1397
attgtcctcc ttgttatttc tgtttgtaag acttaagtga gttagggtctt taaggaaagc 1457
aacgctcctc tgaaatgctt gtcttttatg ctggggaggtg accatagggc tctgctttta 1517

```

<210> 76
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..318

<221> sig_peptide
 <222> 22..93
 <223> Von Heijne matrix
 score 4.6
 seq FFIFCSLNTLLLG/GV

<221> polyA_signal
 <222> 497..502

<221> polyA_site
 <222> 516..526

```

<400> 76
ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga ttt ctt cta      51
                               Met Lys Ser Ala Lys Leu Gly Phe Leu Leu
                               -20                               -15
aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg ggt ggt gtt      99
Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu Gly Gly Val
                               -10                               -5                               1
aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat ccc tgc aaa      147
Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys
                               5                               10                               15
ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt aga tat ttc      195
Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe Arg Tyr Phe
                               20                               25                               30
tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc tcc ggc tgt      243
Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe Ser Gly Cys
                               35                               40                               45                               50
aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt gaa gta gcc      291
Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg Glu Val Ala
                               55                               60                               65
tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg tgaactcatg      338
Cys Val Ala Lys Tyr Lys Pro Pro Arg
                               70                               75
aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcagactg attttgaaat      398
ctttgtaata tttccataat gctttaagct tccatatgtt tgctattttc ctgaccctag      458
ttttgtcttt cctggaaatt aactgtatga tcattagaat gaaagagtct ttctgtcaaa      518
aaaaaaaaa                                                                526

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<210> 77
 <211> 352
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 8..292

<221> sig_peptide

<222> 8..118

<223> Von Heijne matrix

score 5.6

seq WLLLDALLRLGDT/KK

<221> polyA_signal

<222> 317..322

<221> polyA_site

<222> 339..352

<400> 77

ctgagat atg gca agt ccc gct gta aac agg tgg aaa agg cca agg ttg	49
Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu	
-35 -30 -25	
aag ccg gtg tgg cca cgg cgc ttg gaa tcc tgg ttg ttg ctg gat gct	97
Lys Pro Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala	
-20 -15 -10	
ctt ttg cga tta gga gat acc aaa aaa aag cga cag cct gaa gca gcc	145
Leu Leu Arg Leu Gly Asp Thr Lys Lys Arg Gln Pro Glu Ala Ala	
-5 1 5	
aca aaa tcc tgt gtt aga agc agc tgt ggg ggt ccc agt gga gat ggg	193
Thr Lys Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly	
10 15 20 25	
cct ccc cca tgc ctc cag cag cct gac cct cgt gcc ctg tct cag gcg	241
Pro Pro Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala	
30 35 40	
ttc tct aga tcc ttt cct ctg ttt ccc tct ctc gct ggc aaa agt atg	289
Phe Ser Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met	
45 50 55	
atc taattgaaac aagactgaag gatcaataaa cagccatctg ccccttcaaa	342
Ile	
aaaaaaaaaa	352

<210> 78

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 16..378

<221> sig_peptide

<222> 16..84

<223> Von Heijne matrix

score 9.8

seq FLLFFFLFLLTRG/SL

<221> polyA_signal

<222> 502..507

<221> polyA_site

<222> 522..542

<400> 78

```

cacgacctgt gggcc atg atg cta ccc caa tgg ctg ctg ctg ctg ttc ctt      51
          Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu
                    -20                                -15
ctc ttc ttc ttt ctc ttc ctc ctc acc agg ggc tca ctt tct cca aca      99
Leu Phe Phe Phe Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr
      -10                                -5                                1                                5
aaa tat aac ctt ttg gag ctc aag gag tct tgc atc cgg aac cag gac      147
Lys Tyr Asn Leu Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp
                    10                                15                                20
tgc gag act ggc tgc tgc caa cgt gct cca gac aat tgc gag tgc cac      195
Cys Glu Thr Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
                    25                                30                                35
tgc gcg gag aag ggg tcc gag ggc agt ctg tgt caa acg cag gtg ttc      243
Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe
                    40                                45                                50
ttt ggc caa tat aga gcg tgt ccc tgc ctg cgg aac ctg act tgt ata      291
Phe Gly Gln Tyr Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile
                    55                                60                                65
tat tca aag aat gag aaa tgg ctt agc atc gcc tat ggc cgt tgt cag      339
Tyr Ser Lys Asn Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln
                    70                                75                                80                                85
aaa att gga agg cag aag ttg gct aag aaa atg ttc ttc tagtgctccc      388
Lys Ile Gly Arg Gln Lys Leu Ala Lys Lys Met Phe Phe
                    90                                95
tcctttcttgc tgctctctcc tcctccacct gctctcctcc ctaccagag ctctgtgttc      448
accctgttcc ccagagcctc caccatgagt ggaggggaagt ggggagtgat tgaaataaag      508
agcttttttca atgaaaaaaaa aaaaaaaaaa aaaa      542

```

<210> 79

<211> 233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..233

<400> 79

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gcaaaaccaa aaccagcacc gatcccgaca tagatcagtg acgtcttttt cttcag atg      59
          Met
          1
atc cta tgt ttc ctt ctt cct cat cat cgt ctt cag gaa gcc aga cag      107
Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg Gln
                    5                                10                                15
att caa gta ttg aag atg ctg cca agg gaa aaa tta aga aga aga gaa      155
Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg Glu
                    20                                25                                30
gag aga aaa caa ata aat ggg aaa aaa gaa agg aca aaa tat gaa aca      203
Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu Thr
                    35                                40                                45
cca aga aaa aga gaa gga aaa aaa aaa aaa      233
Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
                    50                                55

```

<210> 80

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 83..340

<221> sig_peptide

<222> 83..124

<223> Von Heijne matrix

score 7.5

seq VALNLLILVPCCAA/WC

<221> polyA_signal

<222> 573..578

<221> polyA_site

<222> 607..660

<400> 80

```

gaatttgtaa aacttctgct cgtttacact gcacattgaa tacaggtaac taattggaag      60
gagaggggag atcactcttt tg atg gtg gcc ctg aac ctc att ctg gtt ccc      112
                               Met Val Ala Leu Asn Leu Ile Leu Val Pro
                               -10                               -5

tgc tgc gct gct tgg tgt gac cca cgg agg atc cac tcc cag gat gac      160
Cys Cys Ala Ala Trp Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp

                               1                               5                               10

gtg ccc cgt agc tct gct gct gat act ggg tct gcg atg cag cgg cgt      208
Val Pro Arg Ser Ser Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg

                               15                               20                               25

gag gcc tgg gct ggt tgg aga agg tca caa ccc ttc tct gtt ggt ctg      256
Glu Ala Trp Ala Gly Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu

                               30                               35                               40

cct tct gct gaa aga ctc gag aac caa cca ggg aag ctg tcc tgg agg      304
Pro Ser Ala Glu Arg Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg

                               45                               50                               55                               60

tcc ctg gtc gga gag gga tat aga atc tgt gac ctc tgacaactgt      350
Ser Leu Val Gly Glu Gly Tyr Arg Ile Cys Asp Leu

                               65                               70

gaagccaccc tgggctacag aaaccacagt cttcccagca attattacaa ttcttgaatt      410
ccttggggat tttttactgc cttttcaaag cacttaagtg ttagatctaa cgtgttccag      470
tgtctgtctg aggtgactta aaaaatcaga acaaaacttc tattatccag agtcatggga      530
gagtacaccc tttccaggaa taatgttttg ggaaacactg aaatgaaatc ttcccagtat      590
tataaattgt gtatttaaaa aaagaaactt ttctgaatgc ctacctggcg gtgtatacca      650
ggcagtgtgc                                     660

```

<210> 81

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 47..541

<221> sig_peptide

<222> 47..220

<223> Von Heijne matrix

score 5.4

seq QLLDSVLWLGLG/LT

<221> polyA_site

<222> 597..605

<400> 81

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aaagtgggag gagcactagg tcttcccgtc acctccacct ctctcc atg acc cgg      55
                                     Met Thr Arg
ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg atc cca gtt cct      103
Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile Pro Val Pro
-55                               -50                               -45                               -40
cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt cca gtg cgt cca      151
Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro Val Arg Pro
                               -35                               -30                               -25
cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc ctg gac agt gtc      199
Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu Asp Ser Val
                               -20                               -15                               -10
cta tgg ctg ggg gca cta gga ctg aca atc cag gca gtc ttt tcc acc      247
Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val Phe Ser Thr
                               -5                               1                               5
act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc ctc acc ttt gac      295
Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe Leu Thr Phe Asp
10                               15                               20                               25
ctg ctc cat agg ccc gca ggt cac act ctg cca cag cgc aaa ctt ctc      343
Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg Lys Leu Leu
                               30                               35                               40
acc agg ggc cag agt cag ggg gcc ggt gaa ggt cct gga cag cag gag      391
Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly Gln Gln Glu
                               45                               50                               55
gct cta ctc ctg caa atg ggt aca gtc tca gga caa ctt agc ctc cag      439
Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu Ser Leu Gln
                               60                               65                               70
gac gca ctg ctg ctg ctg ctc atg ggg ctg ggc ccg ctc ctg aga gcc      487
Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu Leu Arg Ala
75                               80                               85
tgt ggc atg ccc ttg acc ctg ctt ggc ctg gct ttc tgc ctc cat cct      535
Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys Leu His Pro
90                               95                               100                               105
tgg gcc tgagagcccc tccccacaac tcagtgtcct tcaaataaac aatgaccacc      591
Trp Ala
cttcttcaaa aaaa      605

```

<210> 82

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..285

<221> sig_peptide

<222> 46..150

<223> Von Heijne matrix

score 3.6

seq LEPLSSSAACNG/KE

<221> polyA_signal

<222> 364..369

<221> polyA_site

<222> 385..396

[illegible]

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<210> 83
<211> 432
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 22..240
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```
<221> sig_peptide
<222> 22..84
<223> Von Heijne matrix
      score 12
      seq VLVLCVLLLOAOG/GY
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```
<221> polyA_signal
<222> 397..402
```

```
<221> polyA_site
<222> 421..432
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<400> 83															
gctcacgctc tggtcagagt t atg gca ccc cag act ctg ctg cct gtc ctg															51
Met Ala Pro Gln Thr Leu Leu Pro Val Leu															
-20 -15															
gtt ctc tgt gtg ctg ctg ctg cag gcc cag gga gga tac cgt gac aag															99
Val Leu Cys Val Leu Leu Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys															
-10 -5 1 5															
atg agg atg cag aga atc aag gtc tgt gag aag cga ccc agc ata gat															147
Met Arg Met Gln Arg Ile Lys Val Cys Glu Lys Arg Pro Ser Ile Asp															
10 15 20															
cta tgc atc cac cac tgt tca tgt ttc caa aag tgt gaa aca aat aag															195
Leu Cys Ile His His Cys Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys															
25 30 35															
ata tgc tgt tca gcc ttc tgt ggg aac att tgt atg agc atc cta															240
Ile Cys Cys Ser Ala Phe Cys Gly Asn Ile Cys Met Ser Ile Leu															
40 45 50															

```

tgagtgggag agtgggctgg gatgtgcac ctgtccctg aacccttcca tccgagactg 300
tgccacacac cgaagcacao ggacatcaaa tcatcagcac aagaacatca acaggaatgc 360
caccctcccc agtgtctgaa ctccctgtcc ctgtcaaag aaccagaaca aatgccccatg 420
aaaaaaaaaa aa 432

```

<210> 84
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..382

<221> polyA_site
 <222> 408..420

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<400> 84
gcttgccctga ccccatgct gcctctgtag gtagaagaag tatgtcttcc tggacccct 60
ggctggtgct gtaacaaaga cccatgtg atg ctg ggg gca gag aca gag gag 112
                               Met Leu Gly Ala Glu Thr Glu Glu
                               1                               5
aag ctg ttt gat gcc ccc ttg tcc atc agc aag aga gag cag ctg gaa 160
Lys Leu Phe Asp Ala Pro Leu Ser Ile Ser Lys Arg Glu Gln Leu Glu
   10                               15                               20
cag cag gtc cca gag aac tac ttc tat gtg cca gac ctg ggc cag gtg 208
Gln Gln Val Pro Glu Asn Tyr Phe Tyr Val Pro Asp Leu Gly Gln Val
   25                               30                               35                               40
cct gag att gat gtt cca tcc tac ctg cct gac ctg ccc ggc att gcc 256
Pro Glu Ile Asp Val Pro Ser Tyr Leu Pro Asp Leu Pro Gly Ile Ala
                               45                               50                               55
aac gac ctc atg tac att gcc gac ctg ggc ccc ggc att gcc ccc tct 304
Asn Asp Leu Met Tyr Ile Ala Asp Leu Gly Pro Gly Ile Ala Pro Ser
                               60                               65                               70
gcc cct ggc acc att cca gaa ctg ccc acc ttc cac act gag gta gcc 352
Ala Pro Gly Thr Ile Pro Glu Leu Pro Thr Phe His Thr Glu Val Ala
   75                               80                               85
gag cct ctc aag acc tac aag atg ggg tac taacagcacc accaccgccc 402
Glu Pro Leu Lys Thr Tyr Lys Met Gly Tyr
   90                               95
ccaccaaaaa aaaaaaaa 420

```

<210> 85
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..415

<221> sig_peptide
 <222> 80..142
 <223> Von Heijne matrix
 score 5.4
 seq TFCLIFGLGAVWG/LG

<221> polyA_signal

<222> 471..476

<221> polyA_site

<222> 488..501

<400> 85

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cccgcttgat tccaagaacc tcttcgatat ttatttttat ttttaaagag ggagacgatg      60
gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt      112
                Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys
                -20                      -15

ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc      160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser
-10                -5                1                5
cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc      208
Leu Gln Ile Asp Val Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr
                10                15                20

gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc      256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu
                25                30                35

ttt caa gat act ccc aga agc ata aaa gca tcc act gct aca gct gaa      304
Phe Gln Asp Thr Pro Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu
                40                45                50

cag ttt ttt cag aag ctg aga aat aaa cat gaa ttt act att ttg gtg      352
Gln Phe Phe Gln Lys Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val
55                60                65                70

acc cta aaa cag acc cac tta aat tca gga gtt att ctc tca att cac      400
Thr Leu Lys Gln Thr His Leu Asn Ser Gly Val Ile Leu Ser Ile His
                75                80                85

cac ttg gat cac agg taaatgtggt tgctggagtt tcctgtgttt tcattatatg      455
His Leu Asp His Arg
                90

tgggttaaattg aatatattaa agagaagtaa acaaaaaaaaa aaaaaa      501

```

<210> 86

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 152..361

<221> sig_peptide

<222> 152..283

<223> Von Heijne matrix

score 4.7

seq FL LSLSLITYCFW/DP

<400> 86

```

gacattttac ttttttctgt taacgcttac cctagaaatt agaaatgaca ccacgtattc      60
ttagcgaagt ccagttttca gcattttgtc cttattggac aatagcaagg atattagaac      120
gtgttggttc cgcgtgcttc cgtcttgagt t atg tgc tgc tat tgt cgg ata      172
                Met Cys Cys Tyr Cys Arg Ile
                -40

ttt tgt ctt aga tgt acg tac ttt cct gtt cat tgt ggt atg tgt aat      220
Phe Cys Leu Arg Cys Thr Tyr Phe Pro Val His Cys Gly Met Cys Asn
-35                -30                -25

ttg cgt tac ttt gaa ttt tcc acg ttt tta ctt tct ttg tct ctc atc      268
Leu Arg Tyr Phe Glu Phe Ser Thr Phe Leu Leu Ser Leu Ser Leu Ile
-20                -15                -10

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act tac tgc ttt tgg gac ccc ccc cat cgg ggt tca cat tcc ctc tcc      316
Thr Tyr Cys Phe Trp Asp Pro Pro His Arg Gly Ser His Ser Leu Ser
-5          1          5          10
cta gag cac act ccc ttg gat ttc ctc gag tgg ggt ctg ctg cgg      361
Leu Glu His Thr Pro Leu Asp Phe Leu Glu Trp Gly Leu Leu Arg
          15          20          25
tgaagctttc ccattttatg tgcagattat tttcagaggg tatatagaat tcaggcagct      421
gtttcgttgt agcacattaa aaatatatttc ccc      454

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<210> 87
<211> 1272
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 32..307

<221> sig_peptide
<222> 32..70
<223> Von Heijne matrix
      score 4.2
      seq MLFSLSLLSNLNQ/IG

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<221> polyA_signal
<222> 1240..1245

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<221> polyA_site
<222> 1261..1272

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<400> 87
gtcaggttgc accgcccttt gggtcccgag c atg ctg ttt tct ctc agc ctt      52
                               Met Leu Phe Ser Leu Ser Leu
                               -10
ctc tcc aac ctt aac caa atc ggc agc agc cac ctc gac cgc cca cac      100
Leu Ser Asn Leu Asn Gln Ile Gly Ser Ser His Leu Asp Arg Pro His
-5          1          5          10
att cct ggc caa tca gct cag ctg ttt att tac caa atg tct tca caa      148
Ile Pro Gly Gln Ser Ala Gln Leu Phe Ile Tyr Gln Met Ser Ser Gln
          15          20          25
caa cta cag cag cag cct tcg gct aac aaa aaa gca gga aaa atc cac      196
Gln Leu Gln Gln Gln Pro Ser Ala Asn Lys Lys Ala Gly Lys Ile His
          30          35          40
aac acc ccc ttc gcc aac caa cta aat cca acg caa cat ctg gca aaa      244
Asn Thr Pro Phe Ala Asn Gln Leu Asn Pro Thr Gln His Leu Ala Lys
          45          50          55
cct ttt cag caa att ctt cct ggc cgt cag tcc ggc agc ctc acc tca      292
Pro Phe Gln Gln Ile Leu Pro Gly Arg Gln Ser Gly Ser Leu Thr Ser
          60          65          70
cca ttt cta gct tgc tgaaacccaa aactaatctc caagaaggag aagcttctct      347
Pro Phe Leu Ala Cys
75
cgcagccgga gcaggtccct ttctagagat aggagaagag agagatcgct gtctcgggag      407
agaaatcaca agccgtcccg atccttctct aggtctcgta gtcgatttag gtcaaatagaa      467
aggaaataga agacagtttg caagagaagt ggtgtacagg aaattacttc atttgacagg      527
agtatgtaca gaaaattcaa gttttgtttg agacttcata agcttggtgc atttttaaga      587
tgtttttagct gttcaaattct gtttgtctct tgaaacagtg acacaaaagt gtaattctct      647
atggtttgaa atggatcata cgaggcatgt aataccaaga attgttactt tacaatgttc      707
ccttaagcaa aattgaattt gctttgaact tttagttatg cacagactga taataaacct      767
ctaaacctgc ccagcggaag tgtgtttttt tttaaattta aatacagaaa caactggcaa      827

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aaattgaact aagatttact tttttttcca tagctgggat ataggctgca gctatagttg 887
aacaagcagt ctttaaaaaac tgctgtgaaa cacaggccat cagggaaaac gaaatgctgc 947
actattaaat tagagggttt tgaaaaatcc aactctcatc ctgggcagag gttgcctagt 1007
tggtatagaa tgtaagttt caagaaagtt tacctttgct ttaggtcgta agttccttat 1067
ttgattgccg tatatggata catggctgtt cgtgacatc tttatgtgca aatttgtgat 1127
ttcaaaaatg tcctgccagt ttaagggtagc attgtagagc cgaactttga gttactgtgc 1187
aagatttttt ttcattgctgt catttgtaat atgttttgtg agaatccttg ggattaaagt 1247
tttggttaca gattaaaaaa aaaaa 1272

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<210> 88
<211> 804
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 114..734

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<221> sig_peptide
<222> 114..239
<223> Von Heijne matrix
      score 5.2
      seq LLFDLVCHEFCQS/DD

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<221> polyA_signal
<222> 768..773

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<221> polyA_site
<222> 793..804

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<400> 88
ccaacaccag gaagagtctg aagagcagcc agtgtttcgg cttgtgccct gtatacttga 60
agctgccaaa caagtacggg agttctgaaa atccagaatg gcttgatgtt tac atg 116
                                     Met
cac att tta caa ctg ctt act aca gtg gat gat gga att caa gca att 164
His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile
      -40                               -35                               -30
gta cat tgt cct gac act gga aaa gac att tgg aat tta ctt ttt gac 212
Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp
-25                               -20                               -15                               -10
ctg gtc tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt 260
Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu
      -5                               1                               5
caa gaa cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc 308
Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala
      10                               15                               20
atc tat gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta 356
Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val
      25                               30                               35
gat ctt cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa 404
Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu
40                               45                               50                               55
cag tgt cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa 452
Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu
      60                               65                               70
act aaa agg act gat tta acc caa gat gat ctc cac ttg aaa atc tta 500
Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile Leu
      75                               80                               85
aag gat att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca 548
Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr

```

90	95	100	
aag gag acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag			596
Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln			
105	110	115	
aag tgt tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg			644
Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val			
120	125	130	135
gtg gaa gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct			692
Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala			
140	145	150	
gat gac ttg gaa aaa aac ttc cca agt ttg aag gtt cag act			734
Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr			
155	160	165	
taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa			794
aaaaaaaaaa			804

<210> 89
 <211> 802
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..801

<221> polyA_signal
 <222> 780..785

<221> polyA_site
 <222> 791..802

<400> 89	
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gaagaggaat tcggtgtggt tggaaatcgc tctcgctttg ccaagggaga ctatttacga	120
tgctgcaaga tctgttatec gctctgtggt tttgtcatcc ttgctgctg tgttggtggc	180
tgtgttggtgct tgggtgtgg atg cag gtt gct ctc aag gag gat ctg gat gcc	231
Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala	
1 5 10	
ctc aag gaa aaa ttt cga aca atg gaa tct aat cag aaa agc tca ttc	279
Leu Lys Glu Lys Phe Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe	
15 20 25	
caa gaa atc ccc aaa ctt aat gaa gaa cta ctc agc aag caa aaa caa	327
Gln Glu Ile Pro Lys Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln	
30 35 40	
ctt gag aag att gaa tct gga gag atg ggt ttg aac aaa gtc tgg ata	375
Leu Glu Lys Ile Glu Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile	
45 50 55	
aac atc aca gaa atg aat aag cag att tct ctg ttg act tct gca gtg	423
Asn Ile Thr Glu Met Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val	
60 65 70 75	
aac cac ctc aaa gcc aat gtt aag tca gct gca gac ttg att agc ctg	471
Asn His Leu Lys Ala Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu	
80 85 90	
cct acc act gta gag gga ctt cag aag agt gta gct tcc att ggc aat	519
Pro Thr Thr Val Glu Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn	
95 100 105	
act tta aac agc gtc cat ctt gct gtg gaa gca cta cag aaa act gtg	567
Thr Leu Asn Ser Val His Leu Ala Val Glu Ala Leu Gln Lys Thr Val	
110 115 120	
gat gaa cac aag aaa acg atg gaa tta ctg cag agt gat atg aat cag	615

<400> 90																	
tcatcatcca gagcagccag tgtccgggag gcagaag atg ccc cac tcc agc ctg																	55
Met Pro His Ser Ser Leu																	
-35																	
cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc cag aag gca gcc																	103
His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys Ala Ala																	
-30 -25 -20																	
ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg ggg cta gga gag																	151
Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu Gly Glu																	
-15 -10 -5 1																	
cca cca gag cac act ctc cgg tac ctg gtc ctc cac cta gcc tcc ctg																	199
Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala Ser Leu																	
5 10 15																	
cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg gct gag gag ctg																	247
Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu Glu Leu																	
20 25 30																	
cgc cac atc cac tcc agg tac cgg ggc agc tac tgg agg act gtg cgg																	295
Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr Val Arg																	
35 40 45																	
gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg ttg ctg ctg tcc																	343
Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu Leu Ser																	
50 55 60 65																	
atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc ccg ccc ttc act																	391
Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly Pro Pro Phe Thr																	

70										75					80					
tgg	atg	ctt	gcc	ctc	ctg	ggc	ctc	tgc	cag	gca	ctg	aac	atc	ctc	ctg	439				
Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	Gln	Ala	Leu	Asn	Ile	Leu	Leu					
85																90	95			
ggc	ctc	aag	ggc	ctg	gcc	cca	gct	gag	atc	tct	gca	gtg	tgt	gaa	aaa	487				
Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	Ile	Ser	Ala	Val	Cys	Glu	Lys					
100																105	110			
ggg	aat	ttc	aac	gtg	gcc	cat	ggg	ctg	gca	tgg	tca	tat	tac	atc	gga	535				
Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	Ala	Trp	Ser	Tyr	Tyr	Ile	Gly					
115																120	125			
tat	ctg	cgg	ctg	atc	ctg	cca	gag	ctc	cag	gcc	cgg	att	cga	act	tac	583				
Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln	Ala	Arg	Ile	Arg	Thr	Tyr					
130																135	140			
aat	cag	cat	tac	aac	aac	ctg	cta	cgg	ggt	gca	gtg	agc	cag	cgg	ctg	631				
Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly	Ala	Val	Ser	Gln	Arg	Leu					
150																155	160			
tat	att	ctc	ctc	cca	ttg	gac	tgt	ggg	gtg	cct	gat	aac	ctg	agt	atg	679				
Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val	Pro	Asp	Asn	Leu	Ser	Met					
165																170	175			
gct	gac	ccc	aac	att	cgc	ttc	ctg	gat	aaa	ctg	ccc	cag	cag	acc	ggt	727				
Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys	Leu	Pro	Gln	Gln	Thr	Gly					
180																185	190			
gac	cgt	gct	ggc	atc	aag	gat	cgg	gtt	tac	agc	aac	agc	atc	tat	gag	775				
Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr	Ser	Asn	Ser	Ile	Tyr	Glu					
195																200	205			
ctt	ctg	gag	aac	ggg	cag	cgg	gcg	ggc	acc	tgt	gtc	ctg	gag	tac	gcc	823				
Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr	Cys	Val	Leu	Glu	Tyr	Ala					
210																215	220			
acc	ccc	ttg	cag	act	ttg	ttt	gcc	atg	tca	caa	tac	agt	caa	gct	ggc	871				
Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser	Gln	Tyr	Ser	Gln	Ala	Gly					
230																235	240			
ttt	agc	cgg	gag	gat	agg	ctt	gag	cag	gcc	aaa	ctc	ttc	tgc	cgg	aca	919				
Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala	Lys	Leu	Phe	Cys	Arg	Thr					
245																250	255			
ctt	gag	gac	atc	ctg	gca	gat	gcc	cct	gag	tct	cag	aac	aac	tgc	cgc	967				
Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu	Ser	Gln	Asn	Asn	Cys	Arg					
260																265	270			
ctc	att	gcc	tac	cag	gaa	cct	gca	gat	gac	agc	agc	ttc	tgc	ctg	tcc	1015				
Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp	Ser	Ser	Phe	Ser	Leu	Ser					
275																280	285			
cag	gag	gtt	ctc	cgg	cac	ctg	cgg	cag	gag	gaa	aag	gaa	gag	gtt	acc	1063				
Gln	Glu	Val	Leu	Arg	His	Leu	Arg	Gln	Glu	Glu	Lys	Glu	Glu	Val	Thr					
290																295	300			
gtg	ggc	agc	ttg	aag	acc	tca	gcg	gtg	ccc	agt	acc	tcc	acg	atg	tcc	1111				
Val	Gly	Ser	Leu	Lys	Thr	Ser	Ala	Val	Pro	Ser	Thr	Ser	Thr	Met	Ser					
310																315	320			
caa	gag	cct	gag	ctc	ctc	ctc	agt	gga	atg	gga	aag	ccc	ctc	cct	ctc	1159				
Gln	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Gly	Met	Gly	Lys	Pro	Leu	Pro	Leu					
325																330	335			
cgc	acg	gat	ttc	tct	tgagacccag	ggtcaccagg	ccagagcctc	cagtgggtctc								1214				
Arg	Thr	Asp	Phe	Ser																
340																				
caagcctctg	gactgggggc	tctcttcagt	ggctgaatgt	ccagcagagc	tatttccttc											1274				
cacagggggc	cttgacggga	aggggtccagg	acttgacatc	ttaagatgog	tcttggtcccc											1334				
ttggggcagt	catttccct	ctctgagcct	cgggtgtcttc	aacctgtgaa	atgggatcat											1394				
aatcaactgcc	ttacctccct	cacgggtgtt	gtgaggactg	agtgtgtgga	agtttttcat											1454				
aaactttgga	tgctagtgtg	cttaaaaaaa	aaaaaa													1490				

<210> 91

<211> 361

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 26...361

<221> polyA_site

<222> 350...361

<400> 91

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tcgagaagct gcccttagc caacc atg ccg tct gag ggt cgc tgc tgg gag      52
                        Met Pro Ser Glu Gly Arg Cys Trp Glu
                        1          5

acc ttg aag gcc cta cgc agt tcc gac aaa ggt cgc ctt tgc tac tac      100
Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr Tyr
10          15          20          25

cgc gac tgg ctg ctg cgg cgc gag gat gtt tta gaa gaa tgt atg tct      148
Arg Asp Trp Leu Leu Arg Arg Glu Asp Val Leu Glu Glu Cys Met Ser
          30          35          40

ctt ccc aag cta tct tct tat tct gga tgg gtg gta gag cac gtc cta      196
Leu Pro Lys Leu Ser Ser Tyr Ser Gly Trp Val Val Glu His Val Leu
          45          50          55

ccc cat atg cag gag aac caa cct ctg tct gag act tcg cca tcc tct      244
Pro His Met Gln Glu Asn Gln Pro Leu Ser Glu Thr Ser Pro Ser Ser
          60          65          70

acg tca gct tca gcc cta gat caa ccc tca ttt gtt ccc aaa tct cct      292
Thr Ser Ala Ser Ala Leu Asp Gln Pro Ser Phe Val Pro Lys Ser Pro
          75          80          85

gac gca agc tct gcc ttt tcc cca gcc tcc cct gca aca cca aat gga      340
Asp Ala Ser Ser Ala Phe Ser Pro Ala Ser Pro Ala Thr Pro Asn Gly
90          95          100          105

acc aag ggc aaa aaa aaa aaa
Thr Lys Gly Lys Lys Lys Lys
          110

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<210> 92

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 3..131

<221> polyA_site

<222> 591..605

<400> 92

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ca tcc ctt ccc cag gct tta tgg ttc cag ttc ttc tac cac tct gga      47
  Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly
  1          5          10          15

agc tcc cta gaa tct cct gga atg ctt aat gga cct ttc cag cac cga      95
Ser Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg
          20          25          30

aat tca aga att atg act cat cgg tca gca gaa aag tgaggatacc      141
Asn Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
          35          40

ttttcctaacc ctacctgctt cccctgcagt ttcttcacaa tcttactctt tatattttag      201
catatgtagc ttctcaggat gttaattctg ttctctctgt gttgggtgtct gagcaccag      261

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aaggtagagc caggggcact tataaaccag gagcattatt tgacaggcac ttaagaaaga 321
cactggctac gtaatcccag cactttggga ggctgaggcg gatggatcac atgaggtcag 381
gagttcgaga ccagcctggc cagcatggtg aaaccctgtc tctactaaaa atacaaaaat 441
tagctgggtg tggttgcaca cgctgtaat ccagctacc tgggaggctg aggcaggaga 501
atcgcttgaa cttgggagggc ggaggttgca gtgagcctag attttgccat tgcactccag 561
cctgggtgac aagggcgaaa ctccatccca aaaaaaaaaa aaaa 605

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<210> 93
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..185

<221> sig_peptide
 <222> 33..80
 <223> Von Heijne matrix
 score 3.7
 seq IALTLIPSMLSRA/AG

<221> polyA_signal
 <222> 570..575

<221> polyA_site
 <222> 586..591

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<400> 93
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                                   Met Leu Arg Ile Ala Leu Thr
                                   -15                               -10
ctc atc cca tct atg ctg tca agg gct gct ggt tgg tgc tgg tac aag 101
Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys
                                   -5                               5
gag ccc act cag cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg 149
Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp
                                   10                               15                               20
aat aag aaa ggc aac gtt ttg cag ctt cca aat ttc tgaagaaact 195
Asn Lys Lys Gly Asn Val Leu Gln Leu Pro Asn Phe
                                   25                               30                               35
aatctcagat tggcagttaa agtcaaaatg ttgccaaata tttattcctt ttgcctaagt 255
ttggctaccc ggttcaattg ctttttattt ttaatgtcct gactcttcag agttcgtacc 315
tcaaaagaac aatgagaaca tttgctttgc tttctgctga atccctaata tcaacaatct 375
atacctggac tgtccagttc tcctcctgtg ctatcttctc ttctatccaa gtagaatgta 435
tggcaggagc tccttccctc tagcaatttc tactaaaatg tccaagtaga atgtttcctt 495
ttacaatcaa attactgtat ttattaattt gctagaatcc agtaaatacat tttggtagct 555
ctggtgtgct tatcaataaa aagatgaaag caaaaa 591

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<210> 94
 <211> 1150
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 184..915

<221> sig_peptide
 <222> 184..237
 <223> Von Heijne matrix
 score 3.5
 seq LLGLELSEAEAI/AD

<221> polyA_signal
 <222> 1119..1124

<221> polyA_site
 <222> 1139..1150

<400> 94
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 ttgaaacagg atagtaggta tccggagtcg attgagggcc agagcaggca ctgggggttcg 120
 gatcctgggc aaagtttccc acgttgaggg tctcgaggac gcctagatct ctttcccagg 180
 gcc atg gcg aac ccg aag ctg ctg gga ctg gag cta agc gag gcg gag 228
 Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
 -15 -10 -5
 gcg atc ggt gct gat tcg gcg cga ttt gag gag ctg ctg ctg cag gcc 276
 Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
 1 5 10
 tcg aag gag ctc cag caa gcc cag aca acc aga cca gaa tcg aca caa 324
 Ser Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln
 15 20 25
 atc cag cct cag cct ggt ttc tgc ata aag acc aac tcc tcg gaa ggg 372
 Ile Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly
 30 35 40 45
 aag gtt ttc atc aac atc tgc cac tcc ccc tct atc cct cct ccc gcc 420
 Lys Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala
 50 55 60
 gac gtg acc gag gag gag ctg ctt cag atg cta gag gag gac caa gct 468
 Asp Val Thr Glu Glu Glu Leu Leu Met Leu Glu Glu Asp Gln Ala
 65 70 75
 ggg ttt cgc atc ccc atg agt ctg gga gag cct cat gca gaa ctg gat 516
 Gly Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp
 80 85 90
 gca aaa ggc cag gga tgt acc gcc tac gac gta gct gtc aac agc gac 564
 Ala Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp
 95 100 105
 ttc tac cgg agg atg cag aac agc gat ttc ttg cgg gag ctc gtg atc 612
 Phe Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile
 110 115 120 125
 acc atc gcc agg gag ggc ctt gag gac ata tac aac ttg cag ctg aat 660
 Thr Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn
 130 135 140
 ccg gaa tgg cgc atg atg aag aac cgg cca ttc atg ggc tcc atc tcg 708
 Pro Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser
 145 150 155
 cag cag aac atc cgc tcg gag cag cgt cct cgg atc cag gag ctg ggg 756
 Gln Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly
 160 165 170
 gac ctg tac acg ccc gcc ccc ggg aga gct gag tca ggg cct gaa aag 804
 Asp Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys
 175 180 185
 cct cac ctg aac ctg tgg ctg gaa gcc ccc gac ctc ctc ttg gcc gaa 852
 Pro His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu
 190 195 200 205
 gtt gac ctc ccc aaa ctg gat gga gcc ctg ggg ctg tcg ctg gag atc 900
 Val Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile
 210 215 220
 ggg aga acc gcc tgg tgatgggggg cccccagcag ctgtatcatc tagacgctta 955

Gly Arg Thr Ala Trp

225

tatcccgccg	cagatcaact	ctcatgagag	caaggcagcc	ttccaccgga	agagaaagca	1015
attaatggtg	gccatgccgc	ttctgccggt	gccttcttga	tcagggtgtc	tccttgtgct	1075
tctgagatgt	ggagaagagg	ctgctggctt	ccctaaaagt	tgaaataaaa	gatttttgcc	1135
tttaaaaaaa	aaaaa					1150

<210> 95

<211> 1513

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..1116

<221> sig_peptide

<222> 58..159

<223> Von Heijne matrix

score 4

seq IAVLYLHLYDVFG/DP

<221> polyA_signal

<222> 1486..1491

<221> polyA_site

<222> 1504..1513

<400> 95

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atg gag aga ggc	ctg aaa tca gca gac	cct cgg gat ggc	acc ggt tac			105
Met Glu Arg Gly	Leu Lys Ser Ala Asp	Pro Arg Asp Gly	Thr Gly Tyr			
	-30	-25	-20			
act ggc tgg gca	ggt att gct gtg	ctt tac tta	cat ctt tat	gat gta		153
Thr Gly Trp Ala	Gly Ile Ala Val	Leu Tyr Leu	His Leu Tyr	Asp Val		
	-15	-10	-5			
ttt ggg gac cct	gcc tac cta	cag tta gca	cat ggc	tat gta	aag caa	201
Phe Gly Asp Pro	Ala Tyr Leu	Gln Leu Ala	His Gly	Tyr Val	Lys Gln	
	1	5	10			
agt ctg aac tgc	tta acc aag	cgc tcc atc	acc ttc	ctt tgt	ggg gat	249
Ser Leu Asn Cys	Leu Thr Lys Arg	Ser Ile Thr	Phe Leu	Cys Gly	Asp	
	15	20	25	30		
gca ggc ccc ctg	gca gtg gcc	gct gtg cta	tat cat	aag atg	aac aat	297
Ala Gly Pro Leu	Ala Val Ala	Ala Val Leu	Tyr His	Lys Met	Asn Asn	
	35	40	45			
gag aag cag gca	gaa gat tgc	atc aca	cgg cta	att cac	cta aat	345
Glu Lys Gln Ala	Glu Asp Cys	Ile Thr Arg	Leu Ile	His Leu	Asn Lys	
	50	55	60			
att gat cct cat	gct cca aat	gaa atg	ctc tat	ggg cga	ata ggc	393
Ile Asp Pro His	Ala Pro Asn	Glu Met	Leu Tyr	Gly Arg	Ile Gly	
	65	70	75			
atc tat gct ctt	ctt ttt gtc	aat aag	aac ttt	gga gtg	gaa aag	441
Ile Tyr Ala Leu	Leu Phe Val	Asn Lys	Asn Phe	Gly Val	Glu Lys	
	80	85	90			
cct caa agc cat	att cag	cag att	tgt gaa	aca att	tta acc	489
Pro Gln Ser His	Ile Gln	Gln Ile	Cys Glu	Thr Ile	Leu Thr	
	95	100	105	110		
gaa aac cta gct	agg aag	aga aac	ttc acg	gca aag	tct cca	537
Glu Asn Leu Ala	Arg Lys Arg	Asn Phe	Thr Ala	Lys Ser	Pro Leu	
	115	120	125			

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tat gaa tgg tac cag gaa tat tat gta ggg gct gct cat ggc ctg gct      585
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala
      130      135      140
gga att tat tac tac ctg atg cag ccc agc ctt caa gtg agc caa ggg      633
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly
      145      150      155
aag tta cat agt ttg gtc aag ccc agt gta gac tac gtc tgc cag ctg      681
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu
      160      165      170
aaa ttc cct tct ggc aat tac cct cca tgt ata ggt gat aat cga gat      729
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp
      175      180      185      190
ctg ctt gtc cat tgg tgc cat ggc gcc cct ggg gta atc tac atg ctc      777
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu
      195      200      205
atc cag gcc tat aag gta ttc aga gag gaa aag tat ctc tgt gat gcc      825
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala
      210      215      220
tat cag tgt gct gat gtg atc tgg caa tat ggg ttg ctg aag aag gga      873
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly
      225      230      235
tat ggg ctg tgc cac ggt tct gca ggg aat gcc tat gcc ttc ctg aca      921
Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
      240      245      250
ctc tac aac ctc aca cag gac atg aag tac ctg tat agg gcc tgt aag      969
Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
      255      260      265      270
ttt gct gaa tgg tgc tta gag tat gga gaa cat gga tgc aga aca cca      1017
Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
      275      280      285
gac acc cct ttc tct ctc ttt gaa gga atg gct ggg aca ata tat ttc      1065
Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
      290      295      300
ctg gct gac ctg cta gtc ccc aca aaa gcc agg ttc cct gca ttt gaa      1113
Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
      305      310      315
ctc tgaaaggata gcatgccacc tgcaactcac tgcattgaccc tttctgtata      1166
Leu
ttcaaaccga agctaagtgc ttccgttgct ttccaaggaa acaaagagtc aaactgtgga      1226
cttgattttg ttagcttttt tcagaattta tctttcattc agttcccttc cattatcatt      1286
tacttttact tagaagtatc caaggaagtc ttttaacttt aatttccatt tcttctctaaa      1346
gggagagtgga gtgatatgta cagtgttttg agattgtata catatattcc agaacttgga      1406
ggaaatctta ttttaagtta tgaatataac catctgttac tgttctaaaa atgttttaaaa      1466
gaaactcaat acagataaag ataaatatgt gactattaaa aaaaaaaa      1513

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<210> 96
 <211> 417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 327..416

<221> polyA_site
 <222> 404..417

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<400> 96
tggttttgagg tggtggcatt cttecgctgat ttggctgttc ccaatgttta cattatttta      60
tcttgcaaaa atggttctgt gcaacttgat gtgaaatgct gtccagtttt atttttttta      120

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tggtgttatc cttggatgta caaaaaattc agaaaatgat ctctgtagat attctgtttt 180
atatttggtca tctttagaag ttatcaggaa tgtgttttaa acaagaagag aactttttcta 240
aggaatgata catagaaaag attttatttt aaaatgagtt gtaaagcttg tgtttctttg 300
ttgctgcaag ctatctgccc aagtta atg caa atg gac aca ttt ttt atg tca 353
                               Met Gln Met Asp Thr Phe Phe Met Ser
                               1           5
gaa aaa cac aca cac aca cac aca cat ata cac aca cac aca cga aaa 401
Glu Lys His Thr His Thr His Thr His Ile His Thr His Thr Arg Lys
10           15           20           25
aca aaa aaa aaa aaa a 417
Thr Lys Lys Lys Lys
30

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<210> 97
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..398

<221> sig_peptide
 <222> 63..206
 <223> Von Heijne matrix
 score 4.9
 seq PSLAAGLLFGSLA/GL

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<400> 97
ggggccttcg tgagaccggt gcaggcctgg ggtagtctcc tgtctggaca gagaagagaa 60
aa atg cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt 107
   Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe
       -45           -40           -35
ggc tac gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa 155
Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys
       -30           -25           -20
gca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta 203
Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
       -15           -10           -5
gcc ggc ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg 251
Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp
   1           5           10           15
gtt ttc cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg 299
Val Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg
       20           25           30
ttc tac cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc 347
Phe Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala
       35           40           45
agt ttg ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc 395
Ser Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro
       50           55           60
cat tagcagaagt catgttccag cttagactga tgaagaatta aaaatctgca 448
His
tcttccacta ttttcaatat attaagagaa ataagtgcag catttttgca tctgacattt 508
tacctaataaa aaaagacacc aaacttggca gagaggtgga aaatcagtca tgattacaaa 568
cctacagagg tggcgagtat gtaacacaag agctt 603

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<210> 98

<211> 522
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..163

<221> polyA_signal
 <222> 488..493

<221> polyA_site
 <222> 511..522

<400> 98
 c gag att gcg ggc tat ggc gcc gaa ggt ttt tcg tca gta ctg gga tat 49
 Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
 1 5 10 15
 ccc cga tgg cac cga ttg cca ccg caa agc cta cag cac cac cag tat 97
 Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
 20 25 30
 tgc cag cgt cgc tgg cct gac cgc cgc tgc cta cag agt cac act caa 145
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
 35 40 45
 tcc tcc ggg cac ctt cct nntgaaggag tggctaaggt tggacaatac 193
 Ser Ser Gly His Leu Pro
 50
 acgttcactg cagctgctgt cggggccgtg tttggcctca ccacctgcat cagcgcccat 253
 gtccgcgaga agcccgaaga ccccctgaac tacttccccg gtggctgcgc cnggaggcct 313
 gactctggga gcacgcacgc acaactacgg gattggcgcc gccgcctgcg tgtactttgg 373
 catagcggcc tccctgggtca agatgggccc gctggagggc tgggaggtgt ttgcaaaacc 433
 caaggtgtga gccctgtgcc tgccgggacc tccagcctgc agaatgcgtc cagaaataaa 493
 ttctgtgtct gtgtgtgaaa aaaaaaaaaa 522

<210> 99
 <211> 956
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 13..465

<221> sig_peptide
 <222> 13..75
 <223> Von Heijne matrix
 score 3.9
 seq PVAVTAAVAPVLS/IN

<400> 99
 ngagtcggga aa atg gct gcg agt acn tcn atg gnc ccg gtg gct gtg acg 51
 Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr
 -20 -15 -10
 gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg 99
 Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
 -5 1 5
 cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag 147
 Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
 10 15 20
 cgg ggc cta cta cac agt agc aaa tgg tcg gcg gag ttg gct ttc tct 195

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Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
25          30          35          40
ctc cct gca ttg cct cnt ggc cag ctg caa ccg cct ccg cct att aca      243
Leu Pro Ala Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr
          45          50          55
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac      291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
          60          65          70
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc      339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
          75          80          85
aat agc aag aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg      387
Asn Ser Lys Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
          90          95          100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
105          110          115          120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
          125          130
gaatgaatgt actttataca tagcaataat aaaaaaaaga tatcataaat aaagttaaaa      545
aggatggttag agaagaaaat attcttagga atgactaaca ggataagtaa caacctgatt      605
atattatttac tttagggttat ataagggttct tcatgcctgt gaattaatat tattgtgtaa      665
gaattaagtt aaaaagcctg ggctgacttt taaatttata aattcattta tcatgtttat      725
agtatattta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca      785
agnaaaccaa cttaatactg tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tacttttcta cttttttcta gttgttatct atataaattg attaaaaaaa      905
cattttatgt acntnncatt tcctagtaca gggttgagtat cccttatttg a          956

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<210> 100
 <211> 1041
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..703

 <221> sig_peptide
 <222> 20..94
 <223> Von Heijne matrix
 score 3.9
 seq ATVGLLLMLGVTLF/NS

<221> polyA_signal
 <222> 1000..1005

<221> polyA_site
 <222> 1023..1041

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<400> 100
cagggtcctg catcctacc atg tcg atg gct gtg gaa acc ttt ggc ttc ttc      52
          Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe
          -25          -20          -15
atg gca act gtg ggg ctg ctg atg ctg ggg gtg act ctg cca aac agc      100
Met Ala Thr Val Gly Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser
          -10          -5          1
tac tgg cga gtg tcc act gtg cac ggg aac gtc atc acc acc aac acc      148
Tyr Trp Arg Val Ser Thr Val His Gly Asn Val Ile Thr Thr Asn Thr
          5          10          15

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atc ttc gag aac ctc tgg ttt agc tgt gcc acc gac tcc ctg ggc gtc      196
Ile Phe Glu Asn Leu Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val
    20                      25                      30
tac aac tgc tgg gag ttc ccg tcc atg ctg gcc ctc tct ggg tat att      244
Tyr Asn Cys Trp Glu Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile
    35                      40                      45                      50
cag gcc tgc cgg gca ctc atg atc acc gcc atc ctc ctg ggc ttc ctc      292
Gln Ala Cys Arg Ala Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu
                      55                      60                      65
ggc ctc ttg cta ggc ata gcg ggc ctg cgc tgc acc aac att ggg ggc      340
Gly Leu Leu Leu Gly Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly
                      70                      75                      80
ctg gag ctc tcc agg aaa gcc aag ctg gcg gcc acc gca ggg gcc ccc      388
Leu Glu Leu Ser Arg Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro
    85                      90                      95
cac att ctg gcc ggt atc tgc ggg atg gtg gcc atc tcc tgg tac gcc      436
His Ile Leu Ala Gly Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala
    100                      105                      110
ttc aac atc acc cgg gac ttc ttc gac ccc ttg tac ccc gga acc aag      484
Phe Asn Ile Thr Arg Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys
    115                      120                      125                      130
tac gag ctg ggc ccc gcc ctc tac ctg ggg tgg agc gcc tca ctg atc      532
Tyr Glu Leu Gly Pro Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile
                      135                      140                      145
tcc atc ctg ggt ggc ctc tgc ctc tgc tcc gcc tgc tgc tgc ggc tct      580
Ser Ile Leu Gly Gly Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser
                      150                      155                      160
gac gag gac cca gcc gcc agc gcc cgg cgg ccc tac cag gct cca gtg      628
Asp Glu Asp Pro Ala Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val
    165                      170                      175
tcc gtg atg ccc gtc gcc acc tcg gac caa gaa ggc gac agc agc ttt      676
Ser Val Met Pro Val Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe
    180                      185                      190
ggc aaa tac ggc aga aac gcc tac gtg tagcagctct ggcccgtggg      723
Gly Lys Tyr Gly Arg Asn Ala Tyr Val
    195                      200
ccccgctgtc ttccactgc cccaaggaga ggggacctgg ccgggggcca ttcccctata      783
gtaacctcag gggccggcca cgccccgctc ccgtagcccc gccccggcca cggccccgtg      843
tcttgacttc tcatggcccc tccaggccaa gaactgctct tgggaagtcg catatctccc      903
ctctgaggct ggatccctca tcttctgacc ctgggttctg ggctgtgaag gggacggtgt      963
ccccgcacgt ttgtattgtg tataaatata ttcattaata aatgcatatt gtgaccgtta      1023
aaaaaaaaaa aaaaaaaaaa      1041

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<210> 101
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..294

<221> sig_peptide
 <222> 103..243
 <223> Von Heijne matrix
 score 5.9
 seq TWLGLLSFQNLHC/FP

<400> 101
 ttcccatggt ttagaagcat aacctgtaat gtaatgcaag tcccctaact ccctgggtgc 60

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taacattaac ttccttaagt aataatcaat gaaagaaatt ct atg cat ggt ttt      114
                                   Met His Gly Phe
                                   -45
gaa ata ata tcc ttg aaa gag gaa tca cca tta gga aag gtg agt cag      162
Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly Lys Val Ser Gln
-40 -35 -30
ggt cct ttg ttt aat gtg act agt ggc tca tca tca cca gtg acc tgg      210
Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser Pro Val Thr Trp
-25 -20 -15
ttg ggc cta ctc tcc ttc cag aac ctg cat tgc ttc cca gac ctc ccc      258
Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe Pro Asp Leu Pro
-10 -5 1 5
act gag atg cct cta aga gcc aaa gga gtc aac act tgagcctagg      304
Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
10 15
gtgggctaca acaaaagatt ctaatttacc ttgcttcac taggtccagg ccccaagtag      364
cttgctgaag gaacttaaaa agtagctgtt atttattgta ttgtataagc taaaaacatt      424
tatttttgtt gaatcgaaac aattccatgt agcaatcttt tttctgttca cgggtgttgt      484
gatagaacct taaattccgc aagcatcagt tttttgaaaa aatgggaatt gaccggatag      544
taacaggcaa agtt      558

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<210> 102
 <211> 730
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..518

<221> sig_peptide
 <222> 81..173
 <223> Von Heijne matrix
 score 3.9
 seq ILFHGVFYAGGFA/IV

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<400> 102
ctcgatcatgc tctttgtagc gtgggtgcttc tgttgctcac aggacaactt gcctttgatg      60
attttcaaga gagttgtgct atg atg tgg caa aag tat gca gga agc agg cgg      113
                                   Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg
                                   -30 -25
tca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc      161
Ser Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
-20 -15 -10 -5
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg      209
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
1 5 10
gct tta tat tac aag ttg gca gtg gag cag ctg cag agc cat ccc gag      257
Ala Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu
15 20 25
gca cag gaa gct ctg ggc cct ctc aac atc cat tat ctc aag ctc      305
Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
30 35 40
atc gac agg gaa aac ttc gtg gac att gtt gat gcc aag ttg aag att      353
Ile Asp Arg Glu Asn Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile
45 50 55 60
cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc      401
Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
65 70 75
aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag      449

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Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
 80 85 90
 ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac 497
 Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
 95 100 105
 ggt gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt 548
 Gly Asp Glu Val Lys Lys Glu
 110 115
 ctagtccatc ctccctcat ctctaccata tggccactgg ggtggtggcc catctcagtg 608
 acagacactc ctgcaaccca gttttccagc caccagtggg atgatgggtat gtgccagcac 668
 atggtaattt tgggtgtaatt ctaacttggg cacaacgaat gctatttgtc atttttaaac 728
 tg 730

<210> 103
 <211> 1098
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..326

<221> polyA_signal
 <222> 1066..1071

<221> polyA_site
 <222> 1087..1098

<400> 103
 ctccctttga atgagagaaa ctaacccgct tccgaagccc ctgaaagaca ctgctccttc 60
 ctctc atg gag ttg gct ccg aca gcc cgt ctg cca ggc cat ggt tcc 110
 Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser
 1 5 10 15
 ttg ccc cat ggt gtc ctg gga ccc aga gca aca gga tct gtc acc cac 158
 Leu Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His
 20 25 30
 ctc tct ctt ctc ccc cag atc aag caa cgt gcc tca gag gct ttg ccc 206
 Leu Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro
 35 40 45
 gaa ttg ctt cgt cct gtc acc ccc atc acc aat ttt gag ggc agc cag 254
 Glu Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln
 50 55 60
 tct cag gac cac agt gga atc ttt ggc ctg gta aca aac ctg gaa gag 302
 Ser Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu
 65 70 75
 ctg gag gtg gac gat tgg gag ttc tgagcctctg caaactgtgc gcattctcca 356
 Leu Glu Val Asp Asp Trp Glu Phe
 80 85
 gccagggatg cagaggccac ccagaggccc ttctgaggg ccggccacat tcccgccttc 416
 ctgggcagat tgggtagaaa ggacattctt ccaggaaagt tgactgctgg ctgattggga 476
 aagaaaatcc tggagagata cttcactgct ccaaggcttt tgagacacaa gggaatctca 536
 acaaccaggg atcaggaggg tccaaagccg acattcccag tcctgtgagc tcaggtgacc 596
 tcctccgcag aagagagatg ctgctctggc cctgggagct gaattccaag cccagggttt 656
 ggctccttaa acccgaggac cgccacctct tcccagtgtc tgcgaccagc ctcattctac 716
 ttaactttgc tctcagatgc ctcagatgct ataggtcagt gaaagggcga gtagtaagct 776
 gcctgcctcc ctccctcag acctctccct cataattcca gagaagggca tttctgtctt 836
 ttaagcaca gactaaggct ggaacagtcc atccttatcc ctcttctggc ttgggcccctg 896
 acacctaagt ctttcccacg gtttatgtgt gtgcctcatt cttttccac caagaatcca 956
 tcttagcgcc tctgcccagc tgccctgggtg ctttctccaa gggccatcag tgtcttgctt 1016
 agcttgaggg cttaagtctt tatgctgtgt tagtttcgtt gtcagaacaa attaaaattt 1076

tcagagacgc aaaaaaaaaa aa

1098

<210> 104
 <211> 346
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 170..289

<221> sig_peptide
 <222> 170..250
 <223> Von Heijne matrix
 score 3.6
 seq LTLILLITPSPSPL/LF

<400> 104
 ccatttgagc cccaccacgg aggttatgtg gtcccaaaag gaatgatggc caagcaatta 60
 atttttcctc ctagtcttta gcttgcttct gcattgattg gctttacaca actggcattt 120
 agtctgcatt acacaaatag acactaattt atttgggaaca agcagcaaa atg aga act 178
 Met Arg Thr
 -25
 tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act ctg ctt cta 226
 Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr Leu Leu Leu
 -20 -15 -10
 atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt ctg tcc ctc 274
 Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly Leu Ser Leu
 -5 1 5
 aga tca gca atg tct tagccctct cctctcttcc attccttctt gttgggtactc 329
 Arg Ser Ala Met Ser
 10
 atttcttcta acttttta 346

<210> 105
 <211> 685
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..497

<221> polyA_signal
 <222> 650..655

<221> polyA_site
 <222> 663..685

<400> 105
 aagttctgcg ctggtcggcg gagtagcaag tggcc atg ggg agc ctc agc ggt 53
 Met Gly Ser Leu Ser Gly
 1 5
 ctg cgc ctg gca gca gga agc tgt ttt agg tta tgt gaa aga gat gtt 101
 Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val
 10 15 20
 tcc tca tct cta agg ctt acc aga agc tct gat ttg aag aga ata aat 149
 Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn

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      25              30              35
gga ttt tgc aca aaa cca cag gaa agt ccc gga gct cca tcc cgc act 197
Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr
      40              45              50
tac aac aga gtg cct tta cac aaa cct acg gat tgg cag aaa aag atc 245
Tyr Asn Arg Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile
      55              60              65              70
ctc ata tgg tca ggt cgc ttc aaa aag gaa gat gaa atc cca gag act 293
Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu Asp Glu Ile Pro Glu Thr
      75              80              85
gtc tcg ttg gag atg ctt gat gct gca aag aac aag atg cga gtg aag 341
Val Ser Leu Glu Met Leu Asp Ala Ala Lys Asn Lys Met Arg Val Lys
      90              95              100
agc agc tat cta atg att gcc ctg acg gtg gta gga tgc atc ttc atg 389
Ser Ser Tyr Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met
      105              110              115
gtt att gag ggc aag aag gct gcc caa aga cac gag act tta aca agc 437
Val Ile Glu Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser
      120              125              130
ttg aac tta gaa aag aaa gct cgt ctg aaa gag gaa gca gct atg aag 485
Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys Glu Glu Ala Ala Met Lys
      135              140              145              150
gcc aaa aca gag tagcagaggt atccgtgttg gctggatttt gaaaatccag 537
Ala Lys Thr Glu
gaattatggt ataacgtgcc tgtattaaaa aggatgtggt atgaggatcc atttcataaaa 597
gtatgatttg cccaaacctg taccatttcc gtatttctgc cgtagaagta gaaataaatt 657
ttcttaaaaa aaaaaaaaaa aaaaaaaaaa 685

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<210> 106

<211> 554

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 18..320

<221> polyA_signal

<222> 539..544

<221> polyA_site

<222> 542..554

<400> 106

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aaccgtcgtg gggaagg atg gtg tgc gaa aaa tgt gaa aag aaa ctt ggt 50
Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly
      1              5              10
act gtt atc act cca gat aca tgg aaa gat ggt gct agg aat acc aca 98
Thr Val Ile Thr Pro Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr
      15              20              25
gaa agt ggt gga aga aag ctg aat aaa aat aaa gct ttg act tca aaa 146
Glu Ser Gly Gly Arg Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys
      30              35              40
aaa gca aga ttt gat cca tat gga aag aat aag ttc tcc act tgt aga 194
Lys Ala Arg Phe Asp Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg
      45              50              55
att tgt aaa agt tct gtg cac caa cca ggt tct cat tac tgc cag ggc 242
Ile Cys Lys Ser Ser Val His Gln Pro Gly Ser His Tyr Cys Gln Gly
      60              65              70              75
tgt gcc tac aaa aaa ggc atc tgt gcg atg tgt ggn aaa aaa gtt ttg 290

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Cys Ala Tyr Lys Lys Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu
 80 85 90
 gat acc aaa aac tac aag caa aca tct gtc tagatgtatt gatggaattt 340
 Asp Thr Lys Asn Tyr Lys Gln Thr Ser Val
 95 100
 ctggctttct aaatgatttt actttctgcc ttgaattttc aaggcataga tgtcaactta 400
 cagaataaca tgttttaaga taattaagtt taaaccagag aatttgattg ttactcattt 460
 tgctctcatg ttctaaacag caacagtgtg actagtcttt tgttgtaaata gggtattttc 520
 cttataagaa ttttaagaac taaaaaaaaa aaaa 554

<210> 107
 <211> 1678
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 71..1438

<221> sig_peptide
 <222> 71..136
 <223> Von Heijne matrix
 score 3.5
 seq AAPVAAGLGPVIS/RP

<221> polyA_signal
 <222> 1644..1649

<221> polyA_site
 <222> 1665..1678

<400> 107
 ccgacttcca gaggagcgct gtgcacgtgg agaagagcgg ggactcggcg accctgcctt 60
 cccgaccctc atg ttc gaa gag cct gag tgg gcc gag gcg gcc cca gta 109
 Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val
 -20 -15 -10
 gcc gcg ggc ctt ggg ccc gta atc tca cga cct ccg cct gcg gcc tcc 157
 Ala Ala Gly Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser
 -5 1 5
 tcg caa aac aag ggc tcc aag cgc cgc cag ctc ttg gcc aca tta cgg 205
 Ser Gln Asn Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg
 10 15 20
 gcc cta gag gca gca tct ctt tcc cag cat ccc ccc agc cta tgt ata 253
 Ala Leu Glu Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile
 25 30 35
 agt gac tct gag gag gag gag gag gaa agg aag aag aaa tgc ccc aaa 301
 Ser Asp Ser Glu Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys
 40 45 50 55
 aag gca tca ttt gcc agt gcc tct gct gaa gta ggg aag aaa ggg aag 349
 Lys Ala Ser Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys
 60 65 70
 aag aaa tgt caa aaa cag ggc cca cct tgc agt gac tct gag gaa gaa 397
 Lys Lys Cys Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Glu
 75 80 85
 gta gaa agg aag aag aaa tgc cac aaa cag gct ctt gtt ggc agt gac 445
 Val Glu Arg Lys Lys Lys Cys His Lys Gln Ala Leu Val Gly Ser Asp
 90 95 100
 tct gct gaa gat gag aaa aga aag agg aaa tgc cag aaa cat gcc cct 493
 Ser Ala Glu Asp Glu Lys Arg Lys Arg Lys Cys Gln Lys His Ala Pro
 105 110 115

ata aat tca gcc cag cac ctg gac aat gtt gac caa aca ggt ccc aaa	541
Ile Asn Ser Ala Gln His Leu Asp Asn Val Asp Gln Thr Gly Pro Lys	
120 125 130 135	
gcc tgg aag ggt agt act aca aat gat cca cca aag caa agc cct ggg	589
Ala Trp Lys Gly Ser Thr Thr Asn Asp Pro Pro Lys Gln Ser Pro Gly	
140 145 150	
tcc act tcc cct aaa ccc cct cat aca tta agc cgc aag cag tgg cgg	637
Ser Thr Ser Pro Lys Pro Pro His Thr Leu Ser Arg Lys Gln Trp Arg	
155 160 165	
aac cgg caa aag aat aag aga aga tgt aag aac aag ttt cag cca cct	685
Asn Arg Gln Lys Asn Lys Arg Arg Cys Lys Asn Lys Phe Gln Pro Pro	
170 175 180	
cag gtg cca gac cag gcc cca gct gag gcc ccc aca gag aag aca gag	733
Gln Val Pro Asp Gln Ala Pro Ala Glu Ala Pro Thr Glu Lys Thr Glu	
185 190 195	
gtg tct cct gtt ccc agg aca gac agc cat ggg gct cgg gca ggg gct	781
Val Ser Pro Val Pro Arg Thr Asp Ser His Gly Ala Arg Ala Gly Ala	
200 205 210 215	
ttg cga gcc cgc atg gca cag cgg ctg gat ggg gcc cga ttt cgc tac	829
Leu Arg Ala Arg Met Ala Gln Arg Leu Asp Gly Ala Arg Phe Arg Tyr	
220 225 230	
ctc aat gaa cag ttg tac tca ggg ccc agc agt gct gca cag cgt ctc	877
Leu Asn Glu Gln Leu Tyr Ser Gly Pro Ser Ser Ala Ala Gln Arg Leu	
235 240 245	
ttc cag gaa gac cct gag gct ttt ctt ctc tac cac cgc ggc ttc cag	925
Phe Gln Glu Asp Pro Glu Ala Phe Leu Leu Tyr His Arg Gly Phe Gln	
250 255 260	
agc caa gtg aag aag tgg cca ctg cag cca gtg gac cgc atc gcc agg	973
Ser Gln Val Lys Lys Trp Pro Leu Gln Pro Val Asp Arg Ile Ala Arg	
265 270 275	
gat ctt cgc cag cgg cct gca tcc cta gtg gtg gct gac ttc ggc tgt	1021
Asp Leu Arg Gln Arg Pro Ala Ser Leu Val Val Ala Asp Phe Gly Cys	
280 285 290 295	
ggg gat tgc cgc ttg gct tca agt atc cgg aac cct gtg cat tgc ttt	1069
Gly Asp Cys Arg Leu Ala Ser Ser Ile Arg Asn Pro Val His Cys Phe	
300 305 310	
gac ttg gct tct ctg gac cct agg gtc act gtg tgt gac atg gcc cag	1117
Asp Leu Ala Ser Leu Asp Pro Arg Val Thr Val Cys Asp Met Ala Gln	
315 320 325	
gtt cct ttg gag gat gag tct gtg gat gtg gct gtg ttt tgc ctt tca	1165
Val Pro Leu Glu Asp Glu Ser Val Asp Val Ala Val Phe Cys Leu Ser	
330 335 340	
ctg atg gga acc aac atc agg gac ttc cta gag gag gca aat aga gta	1213
Leu Met Gly Thr Asn Ile Arg Asp Phe Leu Glu Glu Ala Asn Arg Val	
345 350 355	
ctg aag cca ggg ggt ctc ctg aaa gtg gct gag gtc agc agc cgc ttt	1261
Leu Lys Pro Gly Gly Leu Leu Lys Val Ala Glu Val Ser Ser Arg Phe	
360 365 370 375	
gag gat gtt cga acc ttt ctg cgg gct gtg acc aag cta ggc ttc aag	1309
Glu Asp Val Arg Thr Phe Leu Arg Ala Val Thr Lys Leu Gly Phe Lys	
380 385 390	
att gtc tcc aag gac ctg acc aac agc cat ttc ttc ttg ttt gat ttc	1357
Ile Val Ser Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe	
395 400 405	
caa aag act ggg ccc cct ctg gta ggg ccc aag gct cag ctt tca ggc	1405
Gln Lys Thr Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly	
410 415 420	
ctg cag ctt cag cca tgt ctc tac aag cgc agg tgacctctgg atcttccttg	1458
Leu Gln Leu Gln Pro Cys Leu Tyr Lys Arg Arg	
425 430	
agagggggagg cagatctcaa actccaggct cagaactgtg aagactgttt ccggcctggc	1518
tgtgagccaa gacctgggttc ctggtggacc ctgaggacaa agtgtgataa aacctctggc	1578

tcagacttgc tctactgaag gcttcttggg tataagatgc ataaagtcac tggggctagc 1638
 taaacaataa agaggtttatt gtgaggaaaa aaaaaaaaaa 1678

<210> 108
 <211> 494
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..318

<221> sig_peptide
 <222> 25..75
 <223> Von Heijne matrix
 score 7.4
 seq FFLLLQFFLRIDG/VL

<221> polyA_signal
 <222> 452..457

<221> polyA_site
 <222> 482..494

<400> 108
 aggctgagtg tgaagattag agta atg cct tct agc ttt ttc ctg ctg ttg 51
 Met Pro Ser Ser Phe Phe Leu Leu Leu
 -15 -10
 cag ttt ttc ttg aga att gat ggg gtg ctt atc aga atg aat gac acg 99
 Gln Phe Phe Leu Arg Ile Asp Gly Val Leu Ile Arg Met Asn Asp Thr
 -5 1 5
 aga ctt tac cat gag gct gac aag acc tac atg tta cga gaa tat acg 147
 Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr Met Leu Arg Glu Tyr Thr
 10 15 20
 tca cga gaa agc aaa att tct agt ttg atg cat gtt cca cct tcc ctc 195
 Ser Arg Glu Ser Lys Ile Ser Ser Leu Met His Val Pro Pro Ser Leu
 25 30 35 40
 ttc acg gaa cct aat gaa ata tcc cag tat tta cca ata aag gaa gca 243
 Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr Leu Pro Ile Lys Glu Ala
 45 50 55
 gtt tgt gag aag cta ata ttt cca gaa aga att gat cct aac cca gca 291
 Val Cys Glu Lys Leu Ile Phe Pro Glu Arg Ile Asp Pro Asn Pro Ala
 60 65 70
 gac tca caa aaa agt aca caa gtg gaa taaaatgtga tacaacatat 338
 Asp Ser Gln Lys Ser Thr Gln Val Glu
 75 80
 actcactatg gaatctgact ggacaccttg gctatttgta aggggttatt tttattatga 398
 gaattaattg ccttggttat gtacagattt tctgtagcct taaaggaaaa aaaaataaag 458
 atcgttacag gcaggtttca ctcaaaaaaa aaaaac 494

<210> 109
 <211> 714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..332


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cctcttttcag cccgggatcg ccccagcagg g atg ggc gac aag atc tgg ctg      52
                               Met Gly Asp Lys Ile Trp Leu
                               -20
ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg cct      100
Pro Phe Pro Val Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro
-15 -10 -5
ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt acc      148
Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr
1 5 10 15
ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg aag      196
Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys
20 25 30
gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta gat      244
Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp
35 40 45
att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt gaa      292
Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu
50 55 60
caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt gat      340
Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp
65 70 75 80
tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag gtg      388
Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val
85 90 95
att ttc ttt gaa tta atc ctg gat aat atg gga gaa cag gca caa gaa      436
Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu
100 105 110
caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat atg      484
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp Met
115 120 125
aaa ctg gaa gac atc ctg gaa tcc atc agc agc atc aag tcc aga cta      532
Lys Leu Glu Asp Ile Leu Glu Ser Ile Ser Ser Ile Lys Ser Arg Leu
130 135 140
agc aaa agt ggg cac ata caa att ctg ctt aga gca ttt gaa gct cgt      580
Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe Glu Ala Arg
145 150 155 160
gat cga aac ata caa gaa agc aac ttt gat aga gtc aat ttc tgg tct      628
Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val Asn Phe Trp Ser
165 170 175
atg gtt aat tta gtg gtc atg gtg gtg gtg tca gcc att caa gtt tat      676
Met Val Asn Leu Val Val Met Val Val Val Ser Ala Ile Gln Val Tyr
180 185 190
atg ctg aag agt ctg ttt gaa gat aag agg aaa agt aga act      718
Met Leu Lys Ser Leu Phe Glu Asp Lys Arg Lys Ser Arg Thr
195 200 205
taaaactcca aactagagta cgtaacattg aaaaatgagg cataaaaaatg caataaactg      778
ttacagtcaa gaccaaaaaa aaaaaaa      805

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<210> 111

<211> 787

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 26..481

<221> sig_peptide

<222> 26..88

<223> Von Heijne matrix

score 4.4
seq AVASSFFCASLFS/AV

<221> polyA_signal
<222> 755..760

<221> polyA_site
<222> 775..787

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<400> 111
gacagcctgg ataaaggctc actttg atg gct cag ttg gga gca gtt gtg gct      52
                               Met Ala Gln Leu Gly Ala Val Val Ala
                               -20                               -15

gtg gct tcc agt ttc ttt tgt gca tct ctc ttc tca gct gtg cac aag      100
Val Ala Ser Ser Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys
      -10                               -5                               1

ata gaa gag gga cat att ggg gta tat tac aga ggc ggt gcc ctg ctg      148
Ile Glu Glu Gly His Ile Gly Val Tyr Tyr Arg Gly Gly Ala Leu Leu
      5                               10                               15                               20

act tcg acc agc ggc cct ggt ttc cat ctc atg ctc cct ttc atc aca      196
Thr Ser Thr Ser Gly Pro Gly Phe His Leu Met Leu Pro Phe Ile Thr
      25                               30                               35

tca tat aag tct gtg cag acc aca ctc cag aca gat gag gtg aag aat      244
Ser Tyr Lys Ser Val Gln Thr Thr Leu Gln Thr Asp Glu Val Lys Asn
      40                               45                               50

gta cct tgt ggg act agt ggt ggt gtg atg atc tac ttt gac aga att      292
Val Pro Cys Gly Thr Ser Gly Gly Val Met Ile Tyr Phe Asp Arg Ile
      55                               60                               65

gaa gtg gtg aac ttc ctg gtc ccg aac gca gtg cat gat ata gtg aag      340
Glu Val Val Asn Phe Leu Val Pro Asn Ala Val His Asp Ile Val Lys
      70                               75                               80

aac tat act gct gac tat gac aag gcc ctc atc ttc aac aag atc cac      388
Asn Tyr Thr Ala Asp Tyr Asp Lys Ala Leu Ile Phe Asn Lys Ile His
      85                               90                               95                               100

cac gaa ctg aac cag ttc tgc agt gtg cac acg ctt caa gag gtc tac      436
His Glu Leu Asn Gln Phe Cys Ser Val His Thr Leu Gln Glu Val Tyr
      105                               110                               115

att gag ctg ttt gga ctg gaa aat gat ttt tcc cag gaa tct tca      481
Ile Glu Leu Phe Gly Leu Glu Asn Asp Phe Ser Gln Glu Ser Ser
      120                               125                               130

taaaagggac cctgagcaag aacatttttc atagcagaca ggaggactca tccacatcgc      541
cagcaatcat aattaagcaa accgcctttt gcaccattta agatttagga aatcatccaa      601
attactttta atgtttctgc agtagaaaat gaatctaaat tcattttata gggtttgtag      661
tcttttatct gttttggatt cactgtgctt ttaagaaaaa gttggtaaatt ttgccgttga      721
tttttctttt taacctcaaa ctaatagaat tttataaaat attaattttc tccaaaaaaa      781
aaaaaa
      787

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<210> 112
<211> 569
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..562

<221> sig_peptide
<222> 26..187
<223> Von Heijne matrix
score 4.1

seq AVVAAAARTGSEA/RV

<400> 112

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agaaacaggt ctgggctaca aaagt atg gcc gct tct gag gcg gcg gtg gtg      52
                               Met Ala Ala Ser Glu Ala Ala Val Val
                               -50
tct tcg ccg tct ttg aaa aca gac aca tcc cct gtc ctt gaa act gca      100
Ser Ser Pro Ser Leu Lys Thr Asp Thr Ser Pro Val Leu Glu Thr Ala
-45                               -40                               -35                               -30
gga acg gtc gca gca atg gct gcg acc ccg tca gca agg gct gca gcc      148
Gly Thr Val Ala Ala Met Ala Ala Thr Pro Ser Ala Arg Ala Ala Ala
                               -25                               -20                               -15
gcg gtg gtt gcg gcc gcg gcc agg acc gga tcc gaa gcc agg gtc tcc      196
Ala Val Val Ala Ala Ala Ala Arg Thr Gly Ser Glu Ala Arg Val Ser
                               -10                               -5                               1
aag gcc gct ttg gct acc aag ctg ctg tcc ttg agc ggc gtg ttc gcc      244
Lys Ala Ala Leu Ala Thr Lys Leu Leu Ser Leu Ser Gly Val Phe Ala
5                               10                               15
gtg cac aag ccc aaa ggg ccc act tca gcc gag ctg ctg aat cgg ttg      292
Val His Lys Pro Lys Gly Pro Thr Ser Ala Glu Leu Leu Asn Arg Leu
20                               25                               30                               35
aag gag aag ctg ctg gca gaa gct gga atg cct tct cca gaa tgg acc      340
Lys Glu Lys Leu Leu Ala Glu Ala Gly Met Pro Ser Pro Glu Trp Thr
                               40                               45                               50
aag agg aaa aag cag act ttg aaa att ggg cat gga ggg act cta gac      388
Lys Arg Lys Lys Gln Thr Leu Lys Ile Gly His Gly Gly Thr Leu Asp
                               55                               60                               65
agc gca gcc cga gga gtt ctg gtt gtt gga att gga agc gga aca aaa      436
Ser Ala Ala Arg Gly Val Leu Val Val Gly Ile Gly Ser Gly Thr Lys
70                               75                               80
atg ttg acc agt atg ttg tca ggg tcc aag agg tat act gcc att gga      484
Met Leu Thr Ser Met Leu Ser Gly Ser Lys Arg Tyr Thr Ala Ile Gly
85                               90                               95
gaa ctg ggg aaa gct act gat aca cta gat tct acg ggg aag gta aca      532
Glu Leu Gly Lys Ala Thr Asp Thr Leu Asp Ser Thr Gly Lys Val Thr
100                               105                               110                               115
gaa gaa aaa cct tac ggt atg aac ctc atc taagtag      569
Glu Glu Lys Pro Tyr Gly Met Asn Leu Ile
                               120                               125

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<210> 113

<211> 893

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..810

<221> sig_peptide

<222> 4..279

<223> Von Heijne matrix

score 6.8

seq AVMLYTWRSCSRA/IP

<221> polyA_signal

<222> 858..863

<221> polyA_site

<222> 881..893

<400> 113
 gcc atg atc acg cac gtc acc ctg gaa gat gcc ctg tcc aac gtg gac 48
 Met Ile Thr His Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp
 -90 -85 -80
 ctg ctt gaa gag ctt ccc ctc ccc gac cag cag cca tgc atc gag cct 96
 Leu Leu Glu Leu Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro
 -75 -70 -65
 cca cct tcc tcc atc atg tac cag gct aac ttt gac aca aac ttt gag 144
 Pro Pro Ser Ser Ile Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu
 -60 -55 -50
 gac agg aat gca ttt gtc acg ggc att gca agg tac att gag cag gct 192
 Asp Arg Asn Ala Phe Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala
 -45 -40 -35 -30
 aca gtc cac tcc agc atg aat gag atg ctg gag gaa gga cat gag tat 240
 Thr Val His Ser Ser Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr
 -25 -20 -15
 gcg gtc atg ctg tac acc tgg cgc agc tgt tcc cgg gcc att ccc cag 288
 Ala Val Met Leu Tyr Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln
 -10 -5 1
 gtg aaa tgc aac gag cag ccc aac cga gta gag atc tat gag aag aca 336
 Val Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr
 5 10 15
 gta gag gtg ctg gag ccg gag gtc acc aag ctc atg aag ttc atg tat 384
 Val Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr
 20 25 30 35
 ttt cag cgc aag gcc atc gag cgg ttc tgc agc gag gtg aag cgg ctg 432
 Phe Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu
 40 45 50
 tgc cat gcc gag cgc agg aag gac ttt gtc tct gag gcc tac ctc ctg 480
 Cys His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu
 55 60 65
 acc ctt ggc aag ttc atc aac atg ttt gct gtc ctg gat gag cta aag 528
 Thr Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys
 70 75 80
 aac atg aag tgc agc gtc aag aat gac cac tcc gcc tac aag agg gca 576
 Asn Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala
 85 90 95
 gca cag ttc ctg cgg aag atg gca gat ccc cag tct atc cag gag tcg 624
 Ala Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser
 100 105 110 115
 cag aac ctt tcc atg ttc ctg gcc aac cac aac agg atc acc cag tgt 672
 Gln Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys
 120 125 130
 ctc cac cag caa ctt gaa gtg atc cca ggc tat gag gag ctg ctg gct 720
 Leu His Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala
 135 140 145
 gac att gtc aac atc tgt gtg gat tac tac gag aac aag atg tac ctg 768
 Asp Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu
 150 155 160
 act ccc agt gag aaa cat atg ctc ctc aag gta aaa ctc ccc 810
 Thr Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro
 165 170 175
 tgaggccgca cccatggagc ctgggcttac cctctcacct tcttcttatt aaaaatccgt 870
 ttttaaaaaac aaaaaaaaaa aaa 893

<210> 114

<211> 1475

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 55..459

<221> sig_peptide

<222> 55..120

<223> Von Heijne matrix

score 7.2

seq GLWLALVDGLVRS/SP

<221> polyA_signal

<222> 1444..1449

<221> polyA_site

<222> 1462..1475

<400> 114

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cagttccgca gctacgtgtg ggacccgctg ctgacccctgt cgcagatcgt cctc atg      57
                                     Met
cag acc gtg tat tac ggc tcg ctg ggc ctg tgg ctg gcg ctg gtg gac      105
Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val Asp
      -20                      -15                      -10
ggg cta gtg cga agc agc ccc tcg ctg gac cag atg ttc gac gcc gag      153
Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala Glu
      -5                      1                      5                      10
atc ctg ggc ttt tcc acc cct cca ggc cgg ctc tcc atg atg tcc ttc      201
Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser Phe
      15                      20                      25
atc ttc aac gcc ctc acc tgt gcc ctg ggc ttg ctg tac ttc atc cgg      249
Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile Arg
      30                      35                      40
cga gga aag cag tgt ctg gat ttc act gtc act gtc cat ttc ttt cac      297
Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe His
      45                      50                      55
ctc ctg ggc tgc tgg ttc tac agc tcc cgt ttc ccc tcg gcg ctg acc      345
Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu Thr
      60                      65                      70                      75
tgg tgg ctg gtc caa gcc gtg tgc att gca ctc atg gct gtc atc ggg      393
Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile Gly
      80                      85                      90
gag tac ctg tgc atg cgg acg gag ctc aag gag ata ccc ctc aac tca      441
Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn Ser
      95                      100                      105
gcc cct aaa tcc aat gtc tagaatcagg ccctttggac atcccgtga      489
Ala Pro Lys Ser Asn Val
      110
cacttggggc ccttaacacc ttgggctgct cagaccctcc agatgagggtc cagcccagat      549
ctgagaggaa ccctggaaat gtgaagtctc tgttggtgtg ggagagatag tgagggcctg      609
tcaaagaagg caggtagcag tcagcatgac agctgcaaga atgacctctg tctgttgaag      669
ccttggtatc tgagaggtca ggaaggggac ctctttgagg gtaataacat aattggaacc      729
atgccactct tgagccacaa tacctgtcac cagcctgttg ttttaagaga gaaaaaaaaat      789
caaggatata tgattggagc aaaccacttc tttagtcata tgtcttacct ccctgggaca      849
gctgttacct ttgcagtgtt gccgaatcac agcagttacc tttgcaatgt tgccgaatca      909
cagcagttct gttggagaaa cgcttggttt ccggatccag agccacagaa agaaatgtag      969
gtgtgaagta ttaggctgct gtcaggagga gtagggcaga tggaggcatc aagcacaagg      1029
aaaatgcaca acctgtgccc tgttatacac acgttcattgt gcgcccaaga acctatgact      1089
ttcttccagt tccttctacc aggtcccat cctgctgcca gctctcaaca tagcaggcca      1149
taggacccag agaagaatcc cagtgttgct caaagtctga ccatcataaa gacactgcct      1209
gtcttctagg aatgaccagg caccagctc ccactggact ccaatttttt ttctgcctt      1269
atttagaatt ctttgccggg aagggtatga tgggttccca gagacaagaa gcccaacctt      1329
ctggcctggg ctgtgctgat agtgctgagg gagataggaa tttgctgcta agatttttct      1389

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ttgggggtgga gtttcctctg tgaggggctt gcagctatcc ttcctgtgta tacaaataca 1449
gtattttcca tgaaaaaaaa aaaaaa 1475

<210> 115
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 48..248

<221> sig_peptide
<222> 48..161
<223> Von Heijne matrix
score 6.3
seq LVFALVTAVCCCLA/DG

<221> polyA_signal
<222> 283..288

<221> polyA_site
<222> 308..321

<400> 115
gctgagaaga gttgagggaa agtgctgctg ctgggtctgc agacgcg atg aat aac 56
Met Asn Asn
gtg cag cgc aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc 104
Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly
-35 -30 -25 -20
cac gtg aag atg ctg cgg ctg gtg ttt gca ctt gtg aca gca gta tgc 152
His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr Ala Val Cys
-15 -10 -5
tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc 200
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro
1 5 10
aac ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg 248
Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
15 20 25
tgattttata ttacttttta gtttgatact aagtattaaa catatttctg tatttctcca 308
aaaaaaaaaa aaa 321

<210> 116
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..399

<221> sig_peptide
<222> 25..186
<223> Von Heijne matrix
score 3.5
seq SILAQVLDQSARA/RL

<400> 116

ctgctccagc gctgacgccg agcc atg gcg gac gag gag ctt gag gcg ctg 51
Met Ala Asp Glu Glu Leu Glu Ala Leu
-50
agg aga cag agg ctg gcc gag ctg cag gcc aaa cac ggg gat cct ggt 99
Arg Arg Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly
-45 -40 -35 -30
gat gcg gcc caa cag gaa gca aag cac agg gaa gca gaa atg aga aac 147
Asp Ala Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn
-25 -20 -15
agt atc tta gcc caa gtt ctg gat cag tcg gcc cgg gcc agg tta agt 195
Ser Ile Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser
-10 -5 1
aac tta gca ctt gta aag cct gaa aaa act aaa gca gta gag aat tac 243
Asn Leu Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr
5 10 15
ctt ata cag atg gca aga tat gga caa cta agt gag aag gta tca gaa 291
Leu Ile Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu
20 25 30 35
caa ggt tta ata gaa atc ctt aaa aaa gta agc caa caa aca gaa aag 339
Gln Gly Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys
40 45 50
aca aca aca gtg aaa ttc aac aga aga aaa gta atg gac tct gat gaa 387
Thr Thr Thr Val Lys Phe Asn Arg Arg Lys Val Met Asp Ser Asp Glu
55 60 65
gat gac gat tat tgaactacaa gtgtcacag actagaactt aacggaacaa 439
Asp Asp Asp Tyr
70
gtctaggaca g 450

<210> 117
<211> 1173
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..1137
<221> sig_peptide
<222> 10..72
<223> Von Heijne matrix
score 6.5
seq LLTLLLPPLLYT/RH

<221> polyA_signal
<222> 1144..1149

<221> polyA_site
<222> 1162..1173

<400> 117
gagctgctt atg gga cac cgc ttc ctg cgc ggc ctc tta acg ctg ctg ctg 51
Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu
-20 -15 -10
ccg ccg cca ccc ctg tat acc cgg cac cgc atg ctc ggt cca gag tcc 99
Pro Pro Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser
-5 1 5
gtc ccg ccc cca aaa cga tcc cgc agc aaa ctc atg gca ccg ccc cga 147
Val Pro Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg
10 15 20 25

atc ggg acg cac aat ggc acc ttc cac tgc gac gag gca ctg gca tgc	195
Ile Gly Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys	
30 35 40	
gca ctg ctt cgc ctc ctg ccg gag tac cgg gat gca gag att gtg cgg	243
Ala Leu Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg	
45 50 55	
acc cgg gat ccc gaa aaa ctc gct tcc tgt gac atc gtg gtg gac gtg	291
Thr Arg Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val	
60 65 70	
ggg ggc gag tac gac cct cgg aga cac cga tat gac cat cac cag agg	339
Gly Gly Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg	
75 80 85	
tct ttc aca gag acc atg agc tcc ctg tcc cct ggg agg ccg tgg cag	387
Ser Phe Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln	
90 95 100 105	
acc aag ctg agc agt gcg gga ctc atc tat ctg cac ttc ggg cac aag	435
Thr Lys Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys	
110 115 120	
ctg ctg gcc cag ttg ctg ggc act agt gaa gag gac agc atg gtg ggc	483
Leu Leu Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly	
125 130 135	
acc ctc tat gac aag atg tat gag aac ttt gtg gag gag gtg gat gct	531
Thr Leu Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala	
140 145 150	
gtg gac aat ggg atc tcc cag tgg gca gag ggg gag cct cga tat gca	579
Val Asp Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala	
155 160 165	
ctg acc act acc ctg agt gca cga gtt gct cga ctt aat cct acc tgg	627
Leu Thr Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp	
170 175 180 185	
aac cac ccc gac caa gac act gag gca ggg ttc aag cgt gca atg gat	675
Asn His Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp	
190 195 200	
ctg gtt caa gag gag ttt ctg cag aga tta gat ttc tac caa cac agc	723
Leu Val Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser	
205 210 215	
tgg ctg cca gcc cgg gcc ttg gtg gaa gag gcc ctt gcc cag cga ttc	771
Trp Leu Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe	
220 225 230	
cag gtg gac cca agt gga gag att gtg gaa ctg gcg aaa ggt gca tgt	819
Gln Val Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys	
235 240 245	
ccc tgg aag gag cat ctc tac cac ctg gaa tct ggg ctg tcc cct cca	867
Pro Trp Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro	
250 255 260 265	
gtg gcc atc ttc ttt gtt atc tac act gac cag gct gga cag tgg cga	915
Val Ala Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg	
270 275 280	
ata cag tgt gtg ccc aag gag ccc cac tca ttc caa agc cgg ctg ccc	963
Ile Gln Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro	
285 290 295	
ctg cca gag cca tgg cgg ggt ctt cgg gac gag gcc ctg gac cag gtc	1011
Leu Pro Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val	
300 305 310	
agt ggg atc cct ggc tgc atc ttc gtc cat gca agc ggc ttc att ggc	1059
Ser Gly Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly	
315 320 325	
ggt cac cgc acc cga gag ggt gcc ttg agc atg gcc cgt gcc acc ttg	1107
Gly His Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu	
330 335 340 345	
gcc cag cgc tca tac ctc cca caa atc tcc tagtctaata aaaccttcca	1157
Ala Gln Arg Ser Tyr Leu Pro Gln Ile Ser	

350
tctcaaaaaa aaaaaa

355

1173

<210> 118
<211> 785
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..704

<221> sig_peptide
<222> 72..161
<223> Von Heijne matrix
score 13.2
seq LLLLSTLVIPSAA/AP

<221> polyA_signal
<222> 772..777

<400> 118
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aggggcgggg t atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat 110
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His
-30 -25 -20
ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct 158
Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala
-15 -10 -5
gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc 206
Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu
1 5 10 15
aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa 254
Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys
20 25 30
ggg aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac 302
Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp
35 40 45
ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag cac 350
Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His
50 55 60
cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag gta 398
Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val
65 70 75
ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg 446
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
80 85 90 95
gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att 494
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
100 105 110
aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac 542
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
115 120 125
tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc 590
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
130 135 140
cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc 638
Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser
145 150 155
tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc 686

Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
 160 165 170 175
 agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 734
 Arg Pro Ser Arg Gln Leu
 180
 tagcccccac cagaccctgc cccaagcacc atatggaaat aaagttcttt c 785

<210> 119
 <211> 559
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..505

<221> sig_peptide
 <222> 44..223
 <223> Von Heijne matrix
 score 4
 seq LVRRTLLVAALRA/WM

<400> 119
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 Met Gly Ser Lys
 -60
 tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag agg cgg 103
 Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln Arg Arg
 -55 -50 -45
 cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg aag gca 151
 Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val Lys Ala
 -40 -35 -30 -25
 gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc agg acc 199
 Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg Arg Thr
 -20 -15 -10
 ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg tgg agg 247
 Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp Trp Arg
 -5 1 5
 acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg ttg agg 295
 Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu Leu Arg
 10 15 20
 gtc tac gtc atc cag gag cag gcg acg gtc aag ctc cag tcc tgc atc 343
 Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu Gln Ser Cys Ile
 25 30 35 40
 cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat gct ctc 391
 Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn Ala Leu
 45 50 55
 tgc ttg ttc cag gtc cca gag agc agc ctt gcc ttc cag act gat ggc 439
 Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe Gln Thr Asp Gly
 60 65 70
 ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag ttc cac 487
 Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu Phe His
 75 80 85
 att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg 535
 Ile Glu Ile Leu Ser Ile
 90
 cactacccta ataaatgtct gacc 559

<210> 120
 <211> 770
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..393

<221> sig_peptide
 <222> 25..150
 <223> Von Heijne matrix
 score 4.6
 seq LDPVLSAPAFSA

<221> polyA_signal
 <222> 734..739

<221> polyA_site
 <222> 757..770

<400> 120
 cgagagaaagg agagacacac atac atg aaa gga gga gct ttc tcc aat ctt 51
 Met Lys Gly Ala Phe Ser Asn Leu
 -40 -35
 aat gat tcc cag ctc tca gcc tcg ttt ctg caa ccc agc ctg caa gca 99
 Asn Asp Ser Gln Leu Ser Ala Ser Phe Leu Gln Pro Ser Leu Gln Ala
 -30 -25 -20
 aac tgt cct gct ttg gac cct gct gtg tca ctc tcc gca cca gcc ttt 147
 Asn Cys Pro Ala Leu Asp Pro Ala Val Ser Leu Ser Ala Pro Ala Phe
 -15 -10 -5
 gcc tct gct ctt cgc tct atg aag tcc tcc cag gct gca cgg aag gac 195
 Ala Ser Ala Leu Arg Ser Met Lys Ser Ser Gln Ala Ala Arg Lys Asp
 1 5 10 15
 gac ttt ctc agg tct ctt agt gat gga gac tca ggg aca tca gaa cac 243
 Asp Phe Leu Arg Ser Leu Ser Asp Gly Asp Ser Gly Thr Ser Glu His
 20 25 30
 atc tca gcg gtg gtg act agc cct cgg att tcc tgc cat ggt gct gcc 291
 Ile Ser Ala Val Val Thr Ser Pro Arg Ile Ser Cys His Gly Ala Ala
 35 40 45
 att ccc acc gcc cgt gcc ctc tgc cta ggc tgt tcc tgc tgc acc gaa 339
 Ile Pro Thr Ala Arg Ala Leu Cys Leu Gly Cys Ser Cys Cys Thr Glu
 50 55 60
 cgc ctc ctc ctg cca ccg ccc tcc ctc ctt tct tta gaa gcc cct gcc 387
 Arg Leu Leu Leu Pro Pro Ser Leu Leu Ser Leu Glu Ala Pro Ala
 65 70 75
 agc acc tgagctctct gctgattgct gttcctccca gtctgtggaa gctttgccca 443
 Ser Thr
 80
 tatgctttcc ttaaaagggt tctgggcagg gcaggcgccc ccattttctca gggatcccct 503
 ccaggacaac gccttttccct tgtgtcttca gctctcctta ccagatatct atatatttgt 563
 atatattcag tttcaccaac aatgcatcaa gtactttttt ttttaagtaa agaaccgcag 623
 tcatcgaaact ggagcccat tgattccctc cccctcgcc ccccaaatct ggcacctgcc 683
 caaggtatcc tcagaaccat ttgggggtgtc ctttggcatt ggataataga aataaaattt 743
 tacctctttc tacaataaaaa aaaaaaac 770

<210> 121
 <211> 1213
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 58..1095

<221> sig_peptide

<222> 58..114

<223> Von Heijne matrix

score 5.4

seq LSHLLPSLRQVIQ/EP

<221> polyA_site

<222> 1202..1213

<400> 121

cctggctttg cctttgccct gctgtgtgat cttagctccc tgcccaggcc cacagcc	57
atg gcc atg gcc cag aaa ctc agc cac ctc ctg ccg agt ctg cgg cag	105
Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln	
-15 -10 -5	
gtc atc cag gag cct cag cta tct ctg cag cca gag cct gtc ttc acg	153
Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr	
1 5 10	
gtg gat cga gct gag gtg ccg ccg ctc ttc tgg aag ccg tac atc tat	201
Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr	
15 20 25	
gcg ggc tac cgg ccg ctg cat cag acc tgg cgc ttc tat ttc cgc acg	249
Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr	
30 35 40 45	
ctg ttc cag cag cac aac gag gcc gtg aat gtc tgg acc cac ctg ctg	297
Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu	
50 55 60	
gcg gcc ctg gta ctg ctg ctg ccg ctg gcc ctc ttt gtg gag acc gtg	345
Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val	
65 70 75	
gac ttc tgg gga gac cca cac gcc ctg ccc ctc ttc atc att gtc ctt	393
Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu	
80 85 90	
gcc tct ttc acc tac ctc tcc ctc agt gcc ttg gct cac ctc ctg cag	441
Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln	
95 100 105	
gcc aag tct gag ttc tgg cat tac agc ttc ttc ttc ctg gac tat gtg	489
Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val	
110 115 120 125	
ggg gtg gcc gtg tac cag ttt ggc agt gcc ttg gca cac ttc tac tat	537
Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr	
130 135 140	
gct atc gag ccc gcc tgg cat gcc cag gtg cag gct gtt ttt ctg ccc	585
Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro	
145 150 155	
atg gct gcc ttt ctc gcc tgg ctt tcc tgc att ggc tcc tgc tat aac	633
Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn	
160 165 170	
aag tac atc cag aaa cca ggc ctg ctg ggc cgc aca tgc cag gag gtg	681
Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val	
175 180 185	
ccc tcc gtc ctg gcc tac gca ctg gac att agt cct gtg gtg cat cgt	729
Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg	
190 195 200 205	
atc ttc gtg tcc tcc gac ccc acc acg gat gat cca gct ctt ctc tac	777
Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr	
210 215 220	
cac aag tgc cag gtg gtc ttc ttt ctg ctg gct gct gcc ttc ttc tct	825

```

His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
      225                      230                      235
acc ttc atg ccc gag cgc tgg ttc cct ggc agc tgc cat gtc ttc ggg      873
Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
      240                      245                      250
cag ggc cac caa ctt ttc cat atc ttc ttg gtg ctg tgc acg ctg gct      921
Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
      255                      260                      265
cag ctg gag gct gtg gca ctg gac tat gag gcc cga cgg ccc atc tat      969
Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
      270                      275                      280                      285
gag cct ctg cac acg cac tgg cct cac aac ttt tct ggc ctc ttc ctg      1017
Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
      290                      295                      300
ctc acg gtg ggc agc agc atc ctc act gca ttc ctc ctg agc cag ctg      1065
Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
      305                      310                      315
gta cag cgc aaa ctt gat cag aag acc aag tgaaggggga tggcatctgg      1115
Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
      320                      325
tagggaggga ggtatagttg ggggacaggg gtctggggttt ggctccaagt gggaacaagg      1175
cctggtaaaag ttgtttgtgt ctggccaaaa aaaaaaaaaa      1213

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<210> 122
 <211> 1318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..660

<221> sig_peptide
 <222> 31..90
 <223> Von Heijne matrix
 score 5.4
 seq AFVIACVLSLIST/IY

<221> polyA_signal
 <222> 1288..1293

<221> polyA_site
 <222> 1307..1318

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<400> 122
ggaggatggg cgagcagtct gaatgccaga atg gat aac cgt ttt gct aca gca      54
                                Met Asp Asn Arg Phe Ala Thr Ala
                                -20                      -15

ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
      -10                      -5                      1

gct tcc att ggc aca gac ttc tgg tat gag tat cga agt cca gtt caa      150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
      5                      10                      15                      20

gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt      198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
      25                      30                      35

gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat      246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn
      40                      45                      50

```



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ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg      294
Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met
      55                      60                      65
cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca      342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr
      70                      75                      80
aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt      390
Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val
      85                      90                      95                      100
gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt      438
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu
      105                      110                      115
tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc      486
Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys
      120                      125                      130
ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat      534
Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr
      135                      140                      145
ccc acc att gcc acg ggc att ctc cat ctc ctt gca gtg aca aag gag      582
Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Val Thr Lys Glu
      150                      155                      160
agc atg ctt cca gct gga gct gag tcc aag cac aca gcc act cct gca      630
Ser Met Leu Pro Ala Gly Ala Glu Ser Lys His Thr Ala Thr Pro Ala
      165                      170                      175                      180
cac gca tgc gtg caa aca ggg aag ccc aag taggagaaga ggaaagaggt      680
His Ala Cys Val Gln Thr Gly Lys Pro Lys
      185                      190
tgtagggatt tgggaagaac cttgattatt ccctggagga aaagacaaat ctacttccct      740
gaaatcaccc tcgaatctac ttccaccctc agaacttaaa atgaactgca tccttttttt      800
catcttcttt tcttctccag tgaatatgat ctccaaaccc ttattttttc tttgaactgt      860
aaaatttcca ctcatggacg atgcaaccaa cagatgcaat ctctgagaag atgaaaattg      920
ggacctctta ttataaaatt gacctagctg gactcaggaa accaggggaa aagtcaatgc      980
aggcatttaa aatgtaaagt tttttctggt taaatctatt tatttttctt gtaggttgag      1040
tatttcttcc cagtttttct gctctggtgt ataacaaaca ggtcaaaaatt tcccatcttt      1100
cctcctgata gtagttgaat cctaccttgc atacttaatg catagtgaag tggcatctag      1160
cagaaatata cacccccata acacaccacc atttcattag gtgcccataa aattctgtat      1220
ttagcttatt tatttattgt tatttttgct ttttcttaac ccactatata ttgactgcaa      1280
acgaattaat aaattatccc ttctggaaaa aaaaaaaaaa      1318

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<210> 123

<211> 853

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..582

<221> sig_peptide

<222> 31..90

<223> Von Heijne matrix

score 5.4

seq AFVIACVLSLIST/IY

<221> polyA_signal

<222> 816..821

<221> polyA_site

<222> 840..853

<400> 123																		
ggaggatggg	cgagcagtct	gaatgccaga	atg	gat	aac	cgt	ttt	gct	aca	gca							54	
									Met	Asp	Asn	Arg	Phe	Ala	Thr	Ala		
								-20									-15	
ttt	gta	att	gct	tgt	gtg	ctt	agc	ctc	att	tcc	acc	atc	tac	atg	gca		102	
Phe	Val	Ile	Ala	Cys	Val	Leu	Ser	Leu	Ile	Ser	Thr	Ile	Tyr	Met	Ala			
				-10													1	
gcc	tcc	att	ggc	aca	gac	ttc	tgg	tat	gaa	tat	cga	agt	cca	gtt	caa		150	
Ala	Ser	Ile	Gly	Thr	Asp	Phe	Trp	Tyr	Glu	Tyr	Arg	Ser	Pro	Val	Gln			
5					10									15	20			
gaa	aat	tcc	agt	gat	ttg	aat	aaa	agc	atc	tgg	gat	gaa	ttc	att	agt		198	
Glu	Asn	Ser	Ser	Asp	Leu	Asn	Lys	Ser	Ile	Trp	Asp	Glu	Phe	Ile	Ser			
				25									30	35				
gat	gaa	gca	gat	gaa	aag	act	tat	aat	gat	gca	cct	ttt	cga	tac	aat		246	
Asp	Glu	Ala	Asp	Glu	Lys	Thr	Tyr	Asn	Asp	Ala	Pro	Phe	Arg	Tyr	Asn			
				40									45	50				
ggc	aca	gtg	gga	ttg	tgg	aga	cgg	tgt	atc	acc	ata	ccc	aaa	aac	atg		294	
Gly	Thr	Val	Gly	Leu	Trp	Arg	Arg	Cys	Ile	Thr	Ile	Pro	Lys	Asn	Met			
				55									60	65				
cat	tgg	tat	agc	cca	cca	gaa	agg	aca	gag	tca	ttt	gat	gtg	gtc	aca		342	
His	Trp	Tyr	Ser	Pro	Pro	Glu	Arg	Thr	Glu	Ser	Phe	Asp	Val	Val	Thr			
				70									75	80				
aaa	tgt	gtg	agt	ttc	aca	cta	act	gag	cag	ttc	atg	gag	aaa	ttt	gtt		390	
Lys	Cys	Val	Ser	Phe	Thr	Leu	Thr	Glu	Gln	Phe	Met	Glu	Lys	Phe	Val			
85					90									95	100			
gat	ccc	gga	aac	cac	aat	agc	ggg	att	gat	ctc	ctt	agg	acc	tat	ctt		438	
Asp	Pro	Gly	Asn	His	Asn	Ser	Gly	Ile	Asp	Leu	Leu	Arg	Thr	Tyr	Leu			
				105									110	115				
tgg	cgt	tgc	cag	ttc	ctt	tta	cct	ttt	gtg	agt	tta	ggt	ttg	atg	tgc		486	
Trp	Arg	Cys	Gln	Phe	Leu	Leu	Pro	Phe	Val	Ser	Leu	Gly	Leu	Met	Cys			
				120									125	130				
ttt	ggg	gct	ttg	atc	gga	ctt	tgt	gct	tgc	att	tgc	cga	agc	tta	tat		534	
Phe	Gly	Ala	Leu	Ile	Gly	Leu	Cys	Ala	Cys	Ile	Cys	Arg	Ser	Leu	Tyr			
				135									140	145				
ccc	acc	att	gcc	acg	ggc	att	ctc	cat	ctc	ctt	gca	gat	acc	atg	ctg		582	
Pro	Thr	Ile	Ala	Thr	Gly	Ile	Leu	His	Leu	Leu	Ala	Asp	Thr	Met	Leu			
				150									155	160				
tgaagtccag	gccacatgga	ggtgtcctgt	gtagatgctc	cagctgaaat	cccaagctaa												642	
gctcccaact	gacagccaac	atcatttcca	gccatgtgtg	ggagccatcc	tggatgtcca												702	
gccttaaac	gccttcagag	gactttcagcc	acagctatta	tcttactaca	tccttgtgag												762	
actctaataa	agaaccaact	agctgagccc	aatcaacct	tgggaactgat	agaaataaaa												822	
tqaattqtgt	ttttgcgaaa	aaaaaaaaaa	a													853		

<210> 124

<211> 826

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..695

<221> sig peptide

<222> 15..80

<223> Von Heijne matrix

score 8.5

seq AALLGLMMVVTG/DE

<221> polyA signal

<222> 795..800

<221> polyA_site

<222> 814..826

<400> 124

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aaccagaggt gcc atg ggt tgg aca atg agg ctg gtc aca gca gca ctg      50
                Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu
                -20                                -15
tta ctg ggt ctc atg atg gtg gtc act gga gac gag gat gag aac agc      98
Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
-10                                -5                                1                                5
ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag      146
Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
                10                                15                                20
ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt      194
Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
                25                                30                                35
gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag      242
Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
                40                                45                                50
ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg      290
Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
55                                60                                65                                70
gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga      338
Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
                75                                80                                85
ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag      386
Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
                90                                95                                100
aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc      434
Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
                105                                110                                115
cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt      482
Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
                120                                125                                130
cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga      530
Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
135                                140                                145                                150
ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa      578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
                155                                160                                165
cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca      626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
                170                                175                                180
acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac      674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
                185                                190                                195
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt      725
Gln Ala Glu Ile Ala Ala Cys
                200                                205
ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccct      785
tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a                        826

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<210> 125

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 74..295

<221> sig_peptide

<222> 74..196

<223> Von Heijne matrix

score 5.4

seq RLLYIGFLGYCSG/LI

<221> polyA_signal

<222> 545..550

<221> polyA_site

<222> 561..571

<400> 125

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cgggtagtggtg tcgtcgtggt tttccttgta gttcgtggtc tgagaccagg cctcaagtgg      60
aaacggcgctc acc atg atc gca cgg cgg aac cca gta ccc tta cgg ttt      109
               Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe
               -40                               -35               -30
ctg ccg gat gag gcc cgg agc ctg ccc ccg ccc aag ctg acc gac ccg      157
Leu Pro Asp Glu Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro
               -25                               -20               -15
cgg ctc ctc tac atc ggc ttc ttg ggc tac tgc tcc ggc ctg att gat      205
Arg Leu Leu Tyr Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp
               -10                               -5               1
aac ctg atc cgg cgg agg ccg atc gcg acg gct ggt ttg cat cgc cag      253
Asn Leu Ile Arg Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln
               5                               10               15
ctt cta tat att acg gcc ttt ttt ttg ctg gat att atc ttg      295
Leu Leu Tyr Ile Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
20                               25                               30
taaaacgtga agactacctg tatgctgtga gggaccgtga aatgttttga tatatgaaat      355
tacatccaga ggattttcct gaagaagata agaaaacata tggtgaaatt tttgaaaaat      415
tccatccaat acgttgaagt cttcaaaatg cttgctccag tttcactgat acctgctgtt      475
cctgaatttg atggaacatg tttcttatga cagttgaagc ttatgctaata ctgtatgttg      535
acaccttgta attaaaatac gtaccaaaaa aaaaaa      571

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<210> 126

<211> 659

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 440..658

<221> polyA_signal

<222> 601..606

<400> 126

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cgccttacga gctgggaggt ggtgcctctc acccagctaa ttgctctcta gcccttggcc      60
ttcacagggtg ttggtgcctg ccgtgaacgc attctgacct gggccgtatc tgtctcccaa      120
gactttgtgc ctatggttgg ggacagagtg aggtcgttgc cttgacgacg acagcatgcg      180
gcccggtggtc ctcctaagtg tgagcttgcg gcggaccgag gccacacctg ctccttgcct      240
gcttcgcccc ggactcgtga ctgcgtccgc agaagaaatc acaacagcgc tgggaattgct      300
agtttgctag gcagcatctt ttggacctgc gaaccatatg catttcacct caaatctgtt      360
tccaagttga aaaccttttg gtctttctat gcgaacggat tgaagaaacg caaaaagtgt      420
ctacggactt taaattaaa atg gaa aaa tat gaa aac ctg ggt ttg gtt gga      472
               Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly
               1                               5               10

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gaa ggg agt tat gga atg gtg atg aag tgt agg aat aaa gat act gga      520
Glu Gly Ser Tyr Gly Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly
      15                      20                      25
aga att gtg gcc ata aag aag ttc tta gaa agt gac gat gac aaa atg      568
Arg Ile Val Ala Ile Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met
      30                      35                      40
gtt aaa aag att gca atg cga gaa gtc aag tta cta aag caa ctt agg      616
Val Lys Lys Ile Ala Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg
      45                      50                      55
cat gaa aac ttg gtg aat ctc ttg gaa gtg tgt aaa aaa aaa a      659
His Glu Asn Leu Val Asn Leu Leu Glu Val Cys Lys Lys Lys
      60                      65                      70

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<210> 127
<211> 301
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 38..283

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<221> sig_peptide
<222> 38..85
<223> Von Heijne matrix
      score 4.1
      seq LLPATSLAGPVLS/TL

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<221> polyA_signal
<222> 257..262

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<400> 127
cacctgaatc ccaggaaccc tcaatgaggt cttcaag atg aag aga ctg ctg cca      55
                        Met Lys Arg Leu Leu Pro
                        -15
gct acc agc ctg gct ggc cct gtc ctg tcc acc ctc att gcc cca act      103
Ala Thr Ser Leu Ala Gly Pro Val Leu Ser Thr Leu Ile Ala Pro Thr
-10                      -5                      1                      5
ccc atg ttg ttt tgt gaa gat aaa agc tgg gat ctt ttt ctt ttt ttt      151
Pro Met Leu Phe Cys Glu Asp Lys Ser Trp Asp Leu Phe Leu Phe Phe
      10                      15                      20
aag tct cac aag aca tgg ggc atc tcc aca aat tta agt tcc tgt cca      199
Lys Ser His Lys Thr Trp Gly Ile Ser Thr Asn Leu Ser Ser Cys Pro
      25                      30                      35
ttt gga aat ttg ttt cta tgt gta cag ttt gtc aga gaa aaa caa agt      247
Phe Gly Asn Leu Phe Leu Cys Val Gln Phe Val Arg Glu Lys Gln Ser
      40                      45                      50
ttt tgt atg aat aca gaa tgt gat tta cgc aag aat tgacaaaaaa      293
Phe Cys Met Asn Thr Glu Cys Asp Leu Arg Lys Asn
55                      60                      65
aaaaaaaaa      301

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<210> 128
<211> 477
<212> DNA
<213> Homo sapiens

<220>

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<221> CDS
<222> 121..477

<221> sig_peptide
<222> 121..288
<223> Von Heijne matrix
score 3.5
seq SSCADSFVSSSSS/QP

<400> 128
cctcggagca ggcggagtaa agggacttga gcgagccagt tgccggatta ttctatttcc 60
cctccctctc tcccgccccg tatctctttt cacccttctc ccaccctcgc tcgcgtagcc 120
atg gcg gag ccg tcg gcg gcc act cag tcc cat tcc atc tcc tcg tcg 168
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
tcc ttc gga gcc gag ccg tcc gcg ccc ggc ggc ggc ggg agc cca gga 216
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
gcc tgc ccc gcc ctg ggg acg aag agc tgc agc tcc tcc tgt gcg gat 264
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
tcc ttt gtt tct tcc tct tcc tct cag cct gta tct cta ttt tcg acc 312
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
tca caa gag gga ttg agc tct ctt tgc tct gat gag cca tct tca gaa 360
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
att atg act tct tcc ttt ctt tca tct tct gaa ata cat aac act ggc 408
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
ctt aca ata cta cat gga gaa aaa agc cat gtg tta ggg agc cag cct 456
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
att tta gcc aaa aaa aaa aaa 477
Ile Leu Ala Lys Lys Lys Lys
60

<210> 129
<211> 323
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..163

<221> polyA_signal
<222> 292..297

<221> polyA_site
<222> 310..323

<400> 129
a gct ttc gtg tgg gag cca gct atg gtg cgg atc aat gcg ctg aca gca 49
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
gcc tct gag gct gcg tgc ctg atc gtg tct gta gat gaa acc atc aag 97
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
aac ccc cgc tcg act gtg gat gct ccc aca gca gca ggc cgg ggc cgt 145

Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
 35 40 45
 ggt cgt ggc cgc ccc cac tgagaggcac cccacccatc acatggctgg 193
 Gly Arg Gly Arg Pro His
 50
 ctggctgctg ggtgcactta cctccttgg cttgggtact tcattttaca aggaaggggt 253
 agtaattggc ccactctctt cttactggag gctattttaa taaaatgtaa gacttcaaaa 313
 aaaaaaaaaa 323

<210> 130
 <211> 1392
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..675

<221> sig_peptide
 <222> 46..87
 <223> Von Heijne matrix
 score 5.3
 seq LTLGLSFILAGL/IV

<221> polyA_signal
 <222> 1364..1369

<221> polyA_site
 <222> 1383..1392

<400> 130
 ctccgagttg ccacccagga aaaagagggc tcctctggga gatgt atg ctt act ctc 57
 Met Leu Thr Leu
 tta ggc ctt tca ttc atc ttg gca gga ctt att gtt ggt gga gcc tgc 105
 Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys
 -10 -5 1 5
 att tac aag tac ttc atg ccc aag agc acc att tac cgt gga gag atg 153
 Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met
 10 15 20
 tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag 201
 Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
 25 30 35
 cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac 249
 Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp
 40 45 50
 aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac 297
 Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp
 55 60 65 70
 cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg 345
 Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu
 75 80 85
 gac ttg ttg ctg ggg atc tgc tat ctg atg ccc ctc aat act tct att 393
 Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu Asn Thr Ser Ile
 90 95 100
 gtt atg cct cca aaa aat ctg gta gag ctc ttt ggc aaa ctg gcg agt 441
 Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly Lys Leu Ala Ser
 105 110 115
 ggc aga tat ctg cct caa act tat gtg gtt cga gaa gac cta gtt gct 489
 Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu Asp Leu Val Ala
 120 125 130

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gtg gag gaa att cgt gat gtt agt aac ctt ggc atc ttt att tac caa      537
Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile Phe Ile Tyr Gln
135                               140                               145                               150
ctt tgc aat aac aga aag tcc ttc cgc ctt cgt cgc aga gac ctc ttg      585
Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg Arg Asp Leu Leu
155                               160                               165
ctg ggt ttc aac aaa cgt gcc att gat aaa tgc tgg aag att aga cac      633
Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp Lys Ile Arg His
170                               175                               180
ttc ccc aac gaa ttt att gtt gag acc aag atc tgt caa gag              675
Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys Gln Glu
185                               190                               195
taagaggcaa cagatagagt gtccttggtg ataagaagtc agagatttac aatatgactt      735
taacattaag gtttatggga tactcaagat atttactcat gcatttactc tattgcttat      795
gctttaaaaa aaggaaaaaa aaaaaactac taaccactgc aagctcttgt caaatTTtag      855
tttaattggc attgcttggt ttttgaaact gaaattacat gagtttcatt ttttctttgc      915
atztataggg tttagatttc tgaaagcagc atgaatatat cacctaakat cctgacaata      975
aattccatcc gttgtttttt ttgtttgttt gttttttctt ttcctttaag taagctcttt    1035
attcatctta tgggtggagca attttaaaat ttgaaatatt ttaaattggt tttgaacttt    1095
ttgtgtaaaa tatatcagat ctcaacattg ttggtttctt ttgtttttca ttttgtacaa    1155
ctttcttgaa tttagaaatt acatctttgc agttctgtta ggtgctctgt aattaacctg    1215
acttatatgt gaacaatttt catgagacag tcatTTTTaa ctaatgcagt gattctttct    1275
cactactatc tgtattgtgg aatgcacaaa attgtgtagg tgctgaatgc tgtaaggagt    1335
ttaggttgta tgaattctac aaccctataa taaattttac tctatacaaa aaaaaaa      1392

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<210> 131

<211> 999

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 62..385

<221> polyA_signal

<222> 974..979

<221> polyA_site

<222> 987..999

<400> 131

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cctgaatgac ttgaatgttt cccgcctga gctaacagtc catgtgggtg attcagctct      60
g atg gga tgt gtt ttc cag agc aca gaa gac aaa tgt ata ttc aag ata      109
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
1      5      10      15
gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta      157
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
20      25      30
tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc      205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
35      40      45
gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc      253
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
50      55      60
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc      301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65      70      75      80
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg      349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
85      90      95

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ctt cca gag gag ccc aaa ggt acg caa atg ctt act taaagagggg 395
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
      100                      105
ccaaggggca agagctttca tgtgcaagag gcaaggaaac tgattatctt gagtaaattgc 455
cagccttttg gctaagtact taccacagag tgaatcttca aaaaatgatac ataattatctt 515
cagtcataata aaatagagtt attttattaa ataaaatatt gataattatt gtattattac 575
tttaaacaca cttccccctc acaaaaagccc tgtgaaggat gttttgttca catatatgtc 635
caaatatgtt ttggacacat attttattaaa tgggaataaat agtacttgaa ccctggcacc 695
tctgacaaca aagtccatgt tcttttttact atgcctaat acctttcatc agttatccac 755
attgatgcta catctgtatt ttataggtac cctatgttag gtgttctggg ggatagaaaa 815
gaaataagca ggccaggctc agtggctcat gcctgtaatc ctagcatttt gggaggctga 875
ggcagcagaa ctgcctgagc cccagggttc aagactgcag tgagctatga tggcaccact 935
gcattctagc ctgggtgaca gagcaagact ctgtctaaaa taaaaaaga gaaaaaaaaa 995
aaaa

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<210> 132
<211> 725
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 422..550

<221> sig_peptide
<222> 422..475
<223> Von Heijne matrix
score 4.5
seq LRWLMPVIPALWG/AE

<221> polyA_site
<222> 714..725

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<400> 132
tctgcgaggg tgggagagaa aattaggggg agaaaggaca gagagagcaa ctaccatcca 60
tagccagata ggtgagtaaa tatatttgca gtaacctatt tgctattcct tgctgcaact 120
gtgtttaatg ttccttcag aatcagagag agtattgcca tccaagaaat cgtttttaga 180
tatgacattt gagctatcat cttgagacca atacctaaaa caatttcagt ttaagaaatg 240
tctagggtatg gtgaaaacac agttttaaacc cagcaaaaaca gaatttattg ccctcagcga 300
atacccacaa tgtacatata ccttgtatct ctgaaagcaa agcaagcatg ccaagtagtt 360
tttattttacc tgtacctata atacagcaag gtgaaacagg atatattttt gaagtttaaa 420
a atg tct tca ggc cgg ctg cgg tgg ctc atg cct gta atc cca gca ctt 469
Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
      -15                      -10                      -5
tgg gga gcc gag aag ggt gaa tca cct gag gtc agc agt ttt gag acc 517
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
      1                      5                      10
agg ctg gcc aac atg gcg aaa ccc tgt ctc tac tgaaaataca aaaattagct 570
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
      15                      20                      25
gggtgtggtg gcgggcgcct gtagtcccag ctacttggga gactgaggca ggagaattgc 630
ttgaacacgg aaggcggaag ttgcagtaag ctgagatcgt gccaccgcac accagcttgg 690
gcaacagagt gagactccct ctcaaaaaaa aaaaaa 725

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<210> 133
<211> 400
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 124..231

<221> polyA_site
 <222> 387..400

<400> 133
 ctcgcctctc ctggcttctg gtatgcacca gcaattcctg gcgttccttg gctcctagaa 60
 gcatcactcc tatcacatgg tcattcttcac cctgtgtggtc ttcacactac cctttctctg 120
 tgc atg tct gcc cga atc cct ttt tat aag gac acc agt cag att aga 168
 Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg
 1 5 10 15
 tta ggg tct acc ata ata cct cat ttt aac tta atc acc ttt gta aag 216
 Leu Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys
 20 25 30
 acc ttt ttc caa ata tagtcactct ctgaggtact gatggtagg atctcaacat 271
 Thr Phe Phe Gln Ile
 35
 accttttttg ggaggacaca attgaacca taacagggtg tttgcaagga agagttaaaa 331
 tttgaaagaa aggtggtatt tgcttagata gatagggcac agctttctag gtgacaaaaa 391
 aaaaaaaaaa 400

<210> 134
 <211> 1053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 131..1051

<221> sig_peptide
 <222> 131..169
 <223> Von Heijne matrix
 score 4.2
 seq MLAVSLTVPLLGA/MM

<221> polyA_signal
 <222> 1019..1024

<400> 134
 gagcgaggcg gacgggctgc gacagcgccg gccctgcgg ccgcaggctg tcacagacga 60
 tgatggccag gccccggagg ctaaggacgg cagctccttt agcggcagag ttttccgagt 120
 gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc 169
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
 -10 -5
 atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa 217
 Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
 1 5 10 15
 gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga 265
 Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg
 20 25 30
 cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata 313
 Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile
 35 40 45
 gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc 361
 Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val
 50 55 60

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gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg      409
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser
65                               70                               75                               80
ggc cct tgc aaa acc cga gat gat gag cct gtg tgt ggg aga ccc ctg      457
Gly Pro Cys Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu
85                               90                               95
ggg atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tgc      505
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys
100                              105                              110
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg      553
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu
115                              120                              125
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat      601
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn
130                              135                              140
gat ctt aca gtc tct cag gat ggg agg aag att tat ttc acc gat tct      649
Asp Leu Thr Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser
145                              150                              155                              160
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc      697
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly
165                              170                              175
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta      745
Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val
180                              185                              190
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct      793
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser
195                              200                              205
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata      841
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile
210                              215                              220
cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt      889
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe
225                              230                              235                              240
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct      937
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser
245                              250                              255
ggg ggg tac tgg gtg ggc atg tcg acc atc cgc cct aac cct ggg ttt      985
Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe
260                              265                              270
tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att      1033
Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile
275                              280                              285
ttt aag gca aaa aaa aaa aa
Phe Lys Ala Lys Lys Lys
290

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<210> 135
 <211> 1128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..403

<221> sig_peptide
 <222> 86..181
 <223> Von Heijne matrix
 score 8.8
 seq VPMLLLIVGGSFG/LR

<221> polyA_signal
<222> 1097..1102

<221> polyA_site
<222> 1117..1128

<400> 135
cgtcttggtg agagcgtgag ctgctgagat ttgggagttt gcgctaggcc cgcttgaggat 60
tctgagccga tggaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct 112
Met Phe Ala Pro Ala Val Met Arg Ala
-30 -25
ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg 160
Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu
-20 -15 -10
att gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat 208
Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr
-5 1 5
gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa 256
Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys
10 15 20 25
gag aat aaa ata tct tta gag tgc gaa tat gag aaa atc aaa gac tcc 304
Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser
30 35 40
aag ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat 352
Lys Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp
45 50 55
cct gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca 400
Pro Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr
60 65 70
act tgactctgct gattcttttt tccnnntttt ttttttttta aataaaaaata 453
Thr
ctattaactg gacttcctaa tatatacttc tatcaagtgg aaaggaaatt ccaggcccat 513
ggaaacttgg atatgggtaa tttgatgaca aataatcttc actaaagggtc atgtacaggt 573
ttttatactt cccagctatt ccatctgtgg atgaaagtaa caatgttggc cacgtatatt 633
ttacacctcg aaataaaaaaa tgtgaatact gctccaaaaaa aaaaaaccag taccgtgtag 693
tctctctcgt ggcttggatt tacactgggc aacgtggttg gaatgtatct ggctcagaac 753
tatgatatac caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaag 813
aagaaacccc ctagtgcctg agactgcctc cagcactgcc ttcaggatat accgattcta 873
ctgctcttga gggcctcggt tactatctga accaaaagct tttgttttcg tctccagcct 933
cagcacttct cttcttttgc agaccctgtg ttttttgctt taaagcaagc aaaatggggc 993
cccaatttga gaactacccg acgtttccaa catactcacc tcttcccata atccctttcc 1053
aactgcatgg gaggttctaa gactggaatt atggtgctag attagtaaac atgactttta 1113
acgaaaaaaa aaaaa 1128

<210> 136
<211> 254
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 37..162

<221> sig_peptide
<222> 37..93
<223> Von Heijne matrix
score 9.5
seq LMCLSLCTAFALS/KP

<221> polyA_signal
<222> 224..229

<221> polyA_site
<222> 243..254

<400> 136
tgtgctgtgg gggctacgag gaaagatcta attatc atg gac ctg cga cag ttt 54
Met Asp Leu Arg Gln Phe
-15
ctt atg tgc ctg tcc ctg tgc aca gcc ttt gcc ttg agc aaa ccc aca 102
Leu Met Cys Leu Ser Leu Cys Thr Ala Phe Ala Leu Ser Lys Pro Thr
-10 -5 1
gaa aag aag gac cgt gta cat cat gag cct cag ctc agt gac aag gtt 150
Glu Lys Lys Asp Arg Val His His Glu Pro Gln Leu Ser Asp Lys Val
5 10 15
cac aat gat att tgatagaacc aattgttgta cataaaacag atctgcgcat 202
His Asn Asp Ile
20
atatatatat gtataaaaaa taataaaata atggaagatg aaaaaaaaaa aa 254

<210> 137
<211> 886
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..381

<221> sig_peptide
<222> 31..90
<223> Von Heijne matrix
score 5.4
seq AFVIACVLSLIST/IY

<221> polyA_site
<222> 875..886

<400> 137
ggaggatggg cgagcagtct gaatggcaga atg gat aac cgt ttt gct aca gca 54
Met Asp Asn Arg Phe Ala Thr Ala
-20 -15
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca 102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
-10 -5 1
gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa 150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
5 10 15 20
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt 198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
25 30 35
gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat 246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn
40 45 50
ggc aca gtg gga ttg tgg gga cgg tgt atc acc ata ccc aaa aac atg 294
Gly Thr Val Gly Leu Trp Gly Arg Cys Ile Thr Ile Pro Lys Asn Met
55 60 65
cat tgg tat agc cca cca gaa agg aca ggt att tct ctt att tta act 342
His Trp Tyr Ser Pro Pro Glu Arg Thr Gly Ile Ser Leu Ile Leu Thr

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      70              75              80
tct gtc ttc ttc acc tgg tta ata ata gac aaa acg acg taatgattgc      391
Ser Val Phe Phe Thr Trp Leu Ile Ile Asp Lys Thr Thr
85              90              95
ccaattacat gtaagcaggt ttgttggttc tctctctcct taaagaaata aatcgtgtat      451
cttctctttc tactgccttc tctccccaac ttctttgcat taccatggta ctcatacaata      511
ttggttggtat gaggaacttt tcttatcttg ggaaagcctt aatggctttt ttttttctta      571
tttactcact cattaataata cttttcatta ctctaacaca tgttataaag aaatagttgg      631
aaaagtgcac cgaaagactt ttaaaaaatat ttggttaacta gtaaaaaggac taccatcgaa      691
aatcaactca aaaaattgtc cttttatggg ttagctgtat tataatacat atctatcatt      751
tgcccctgtg tcttagagga tataatttga ccagctctac atttaaatctg tgtaattatg      811
agactgtttt acaacaatct tgatgcagag ttggtaggtt aagaaatttg tattacagaa      871
gttaaaaaaa aaaaaa
886

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<210> 138
 <211> 1244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..579

<221> sig_peptide
 <222> 46..156
 <223> Von Heijne matrix
 score 3.5
 seq LVFNLLILTILT/IW

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<400> 138
cccttatcca ggtntttatc tanggaatcc cnnnaagact gggga atg gag aga cag      57
                                     Met Glu Arg Gln
                                     -35
tca agg gtt atg tca gaa aag gat gag tat cag ttt caa cat can nna      105
Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe Gln His Xaa Xaa
                                     -30      -25      -20
gcg gng gan ctg ctt gtc ttc aat ttt ttg ctc atc ctt acc att ttg      153
Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile Leu Thr Ile Leu
                                     -15      -10      -5
aca atc tgg tta ttt aaa aat cat cga ttc cgc ttc ttg cat gaa act      201
Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe Leu His Glu Thr
1              5              10              15
gga gga gca atg gtg tat ggc ctt ata atg gga cta att tca cga tat      249
Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu Ile Ser Arg Tyr
20              25              30
gct aca gca cca act gat att gaa agt gga act gtc tgt gac tgt gta      297
Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val Cys Asp Cys Val
35              40              45
aaa cta act ttc agt cca cca act ctg ctg gtt aat gtc act gac caa      345
Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn Val Thr Asp Gln
50              55              60
gtt tat gaa tat aaa tac aaa aga gaa ata agt cag cac aac atc aat      393
Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln His Asn Ile Asn
65              70              75
cct cat caa gga aat gct ata ctt gaa aag atg aca ttt gat cca gaa      441
Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr Phe Asp Pro Glu
80              85              90              95
atc ttc ttc aat gtt tta ctg cca cca att ata ttt cat gca gga tat      489
Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe His Ala Gly Tyr
100              105              110

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agt cta aag aag aga cac ttt ttt caa aac tta gga tct att tta acg      537
Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly Ser Ile Leu Thr
      115                      120                      125
tat gcc ttc ttg gga act gcc atc tcc tgc atc gtc ata ggg      579
Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val Ile Gly
      130                      135                      140
taagtgcacat tcggagctca agttgcaggt ggctgtgggg tctgtgatct gtgtgaggg      639
tctaacactt ccaggattct tgctggctgg gaaaattgtc ttttttttag tatacacat      699
atttgatgt tttttctgac ttaattccac ggcttctgac aaatacaagg cttcaaata      759
aagcaacta gaggattgct ggactttctc tgtgagttct ggacttctga cttagggaa      819
gtggatcact tgccttgagt tatgtgaagc gcattgcatt cttcttttag tttgagtaa      879
gccgatatgg tcaactgcatt cttttttgtc ttgtattgag agaccttacc tgtatttgg      939
aggagtgcaa aagtaactat atgccaagag ttttctttct aaaggaaagt ttacaagaca      999
gcagtctgaa acagatatgn tccaaatatn naacagagtt gcttaataca gggatagctt    1059
ttcagttaat accctgtaga atgcagactc tttntttcat tgtattttct tgattatgct    1119
actgagccct aagtcacacg ttatatactc tggcttgacg ctcatacataa agtaaaatgt    1179
ggtaccaaat ggtgaaggca atccagcctn tgataatccc gtccaataca ttaaagntcc    1239
actgc                                          1244

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<210> 139
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..469

<221> sig_peptide
 <222> 92..172
 <223> Von Heijne matrix
 score 7.9
 seq VVVLALGFLGICYG/AK

<221> polyA_signal
 <222> 454..459

<221> polyA_site
 <222> 458..471

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<400> 139
gcaagtgcag aagtcgggtga cgggtgggcat ctgggtgtca atcgatgggg catcctttct      60
gaagatcttc gggccactgt cgtccagtcg c atg cag ttt gtc aac gtg ggc      112
                               Met Gln Phe Val Asn Val Gly
                               -25
tac ttc ctc atc gca gcc ggc gtt gtg gtc ctt gct ctt ggt ttc ctg      160
Tyr Phe Leu Ile Ala Ala Gly Val Val Val Leu Ala Leu Gly Phe Leu
-20                      -15                      -10                      -5
ggc tgc tat ggt gct aag act gag agc atg tgt gcc ctc gtg acg ttc      208
Gly Cys Tyr Gly Ala Lys Thr Glu Ser Met Cys Ala Leu Val Thr Phe
      1                      5                      10
ttc ttc atc ctc ctc ctc atc ttc att gct gag gtt gca gct gct gtg      256
Phe Phe Ile Leu Leu Leu Ile Phe Ile Ala Glu Val Ala Ala Ala Val
      15                      20                      25
gtc gcc ctg gtg tac acc aca atg gct gag cac ttc ctg acg ttg ctg      304
Val Ala Leu Val Tyr Thr Thr Met Ala Glu His Phe Leu Thr Leu Leu
      30                      35                      40
gta gtg cct gcc atc aag aaa gat tat ggt tcc cag gaa gac ttc act      352
Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp Phe Thr
      45                      50                      55                      60

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caa gtg tgg aac acc acc atg aaa ggg ctc aag tgc cgt ggc ttc acc      400
Gln Val Trp Asn Thr Thr Met Lys Gly Leu Lys Cys Arg Gly Phe Thr
                        65                        70                        75
aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg cat aaa cct      448
Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met His Lys Pro
                        80                        85                        90
gtt aca atg aaa aaa aaa aaa aa      471
Val Thr Met Lys Lys Lys Lys
                        95

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<210> 140
 <211> 849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..675

<221> sig_peptide
 <222> 154..498
 <223> Von Heijne matrix
 score 4.8
 seq PLRLLNLLILIEG/GV

<221> polyA_signal
 <222> 819..824

<221> polyA_site
 <222> 838..849

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<400> 140
cccctatctc cagacctcat tcgcaatgaa gtagaatgtc tgaaagcaga tttcaaccac      60
agaatcaagg aggttctctt caactccctc ttcagtgccct actatgttgc atttctcccc      120
ctgtgttttg tgaagagtac ccagtactat gac atg cgc tgg tca tgt gag cac      174
                        Met Arg Trp Ser Cys Glu His
                        -115                        -110
ctc gtt atg gtg tgg atc aat gct ttt gtc atg ctc acc acg caa ctg      222
Leu Val Met Val Trp Ile Asn Ala Phe Val Met Leu Thr Thr Gln Leu
                        -105                        -100                        -95
ttg cca tcc aaa tac tgt gat ttg cta cat aaa tca gct gct cac ctg      270
Leu Pro Ser Lys Tyr Cys Asp Leu Leu His Lys Ser Ala Ala His Leu
                        -90                        -85                        -80
ggc aag tgg cag aag ttg gaa cat ggg tcc tac agc aat gct cca cag      318
Gly Lys Trp Gln Lys Leu Glu His Gly Ser Tyr Ser Asn Ala Pro Gln
                        -75                        -70                        -65
cac att tgg tca gaa aat aca ata tgg cct caa ggg gtg ctg gtg cgg      366
His Ile Trp Ser Glu Asn Thr Ile Trp Pro Gln Gly Val Leu Val Arg
                        -60                        -55                        -50                        -45
cac agc aga tgt tta tat aga gcc atg ggg cct tac aac gtg gca gtg      414
His Ser Arg Cys Leu Tyr Arg Ala Met Gly Pro Tyr Asn Val Ala Val
                        -40                        -35                        -30
cct tca gat gta tct cat gcc cgc ttt tat ttc tta ttt cat cga cca      462
Pro Ser Asp Val Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro
                        -25                        -20                        -15
tta agg ctg tta aat ctg ctc atc ctt att gag ggc ggt gtc gtc ttc      510
Leu Arg Leu Leu Asn Leu Leu Ile Leu Ile Glu Gly Gly Val Val Phe
                        -10                        -5                        1
tat cag ctc tat tcc ttg ctg cgg tgc gag aag tgg aac cac aca ctt      558
Tyr Gln Leu Tyr Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu

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5          10          15          20
tcc atg gct ctc atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt      606
Ser Met Ala Leu Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu
          25          30          35
ctc cgg gac aga ata gta tta ggc agg gca tac tcc tac cca ctc aac      654
Leu Arg Asp Arg Ile Val Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn
          40          45          50
agt tat gaa ctc aag gca aac taagctgcct ctcaacaatg agggagaact      705
Ser Tyr Glu Leu Lys Ala Asn
          55
cagataaaaaa ttttttcata cgttctatatt ttttcttggtg atttttataa atattttaaga      765
tgtttttatat tttgtatact attatgtttt gaaagtcggg aagagtaagg gatattaaat      825
gtatccgtaa acaaaaaaaaaa aaaa      849

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<210> 141
 <211> 155
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

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<400> 141
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
   -30          -25          -20
Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
  -15          -10          -5          1
Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His Ala Val
          5          10          15
Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
          20          25          30
Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
          35          40          45
Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu
          50          55          60          65
Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
          70          75          80
Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
          85          90          95
Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu Phe Leu
          100          105          110
Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
          115          120

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<210> 142
 <211> 55
 <212> PRT
 <213> Homo sapiens

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<400> 142
Met Ala Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg
1          5          10          15
Met Tyr Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe
          20          25          30
Phe Met Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln
          35          40          45
Lys Gln Lys Lys Arg Ser Asn

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50

55

<210> 143
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 143
 Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
 -20 -15 -10 -5
 Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg
 1 5 10
 Leu Glu Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val
 15 20 25
 Gln Glu Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe
 30 35 40
 Gly Arg Lys
 45

<210> 144
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 144
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
 -20 -15 -10
 Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
 -5 1 5 10
 Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
 15 20 25
 Leu Asn Gly Val Tyr Arg Thr Thr Gly Trp Leu Thr Lys Ala Arg
 30 35 40
 Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
 45 50 55
 Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
 60 65 70 75
 Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu Gln Ala Glu Ala Thr
 80 85 90
 Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
 95 100 105
 Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser Ala Trp Leu Gly Pro
 110 115 120
 Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His Ala Asp Lys Gln Ser
 125 130 135
 His Ile Leu Trp Ala Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu
 140 145 150 155
 Met Val Ala Gln Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His
 160 165 170
 Thr Ala Ala Leu Pro Ala

175

<210> 145
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 145
 Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
 -25 -20 -15 -10
 Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5
 Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
 10 15 20
 Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Lys Xaa
 25 30 35
 Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn Leu Ser Phe
 40 45 50 55
 Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg Lys Asn Trp
 60 65 70
 Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu Gly Thr Tyr
 75 80 85
 Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln Ser Gln Ser
 90 95 100
 Lys Gln Lys Ser Ile Glu Glu
 105 110

<210> 146
 <211> 255
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -70...-1

<400> 146
 Met Gln Gln Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe
 -70 -65 -60 -55
 Pro Gln Ile Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val
 -50 -45 -40
 Ile Ala Asn Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn
 -35 -30 -25
 Val Val Ser Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu
 -20 -15 -10
 Ala Pro Phe Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val
 -5 1 5 10
 Gly Leu Gly Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val
 15 20 25
 Glu Asn Thr Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr
 30 35 40
 Ala Thr Ser Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp
 45 50 55
 Ile Thr Pro Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr

60		65		70
Lys Met Ile Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr				
75		80		90
Val Gly Arg Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val				
	95		100	105
Glu Thr Leu Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val				
	110		115	120
Ala Arg Asn Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp				
	125		130	135
Val Val Asn Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Glu Lys				
	140		145	150
Ser Glu Ser Ala Glu Leu Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu				
155		160		170
Asn Leu Asn Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly				
	175		180	185

<210> 147
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 147
Met Pro Gly Thr Glu Val Leu Glu Gly Ala Thr Asp Gly Leu Ala Ala
Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu Gly Gly Ser Val Ile Ser
Met Ile Val Leu Leu Ile Cys Val Val Cys Leu Tyr Ile Val Cys Arg
Cys Gly Ser His Leu Trp Arg Glu Ser His His
1 5 10

<210> 148
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 148
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln Leu
1 5 10 15
Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly Asp Gly
20 25 30
Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln Leu Ser Ala
35 40 45
Thr Lys Ser Asp Asp Thr Val Ala Ile Pro Tyr Gly Ser Arg His
50 55 60
Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu Tyr Leu Glu Thr Lys
65 70 75 80
Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser Leu Ser Ser Thr Gly Thr
85 90 95
Phe Leu Val Asp Asn Ser Ser Val Asp Phe Gln Lys Phe Pro Asp Lys
100 105 110
Glu Ile Leu Arg Met Ala Gly Pro Leu Thr Ala Asp Phe Ile Val Lys
115 120 125
Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr Val Gln Phe Ile Phe Tyr

130		135		140	
Gln Pro Ile Ile His Arg Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser					
145		150		155	160
Ala Thr Cys Gly Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp					
	165		170		175
Leu Arg Ser Asn					
180					

<210> 149
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 149	
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala	
	-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu	
	-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe	
10	15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val	
	30 35 40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu	
	45 50 55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr	
	60 65 70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe	
	75 80 85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Pro Asp Asn	
90	95 100 105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr	
	110 115 120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Val Ser Met	
	125 130 135
Val Phe	

<210> 150
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 150	
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala	
	-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu	
	-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe	
10	15 20 25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val	
	30 35 40

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 45 50 55
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 60 65 70
 Cys Ile Arg Ser Lys Asn Gly Pro Gly Thr Ala Val His Ala Tyr Asn
 75 80 85
 Pro Ser Thr Phe Arg Gly Gln Val
 90 95

<210> 151
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 151
 Met Val Glu Met Thr Gly Val
 1 5

<210> 152
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 152
 Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
 -40 -35 -30
 Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
 -25 -20 -15
 Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
 -10 -5 1 5
 Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
 10 15 20
 Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
 25 30 35
 Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
 40 45 50
 Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu
 55 60 65 70
 Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
 75 80 85
 Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
 90 95 100
 Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val
 105 110 115
 Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Val Leu Ala
 120 125 130
 Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 135 140 145 150
 Gly Leu Lys Arg Lys Ala Glu
 155

<210> 153

<211> 43
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Pro Phe Arg Met Ser Gly Tyr Ile Pro Phe Gly Thr Pro Ile Val
 1 5 10 15
 Ser Val Thr Phe Lys Gly Phe Pro Phe Leu Lys Asn Tyr Phe Lys Cys
 20 25 30
 Leu Thr Leu Cys Tyr Cys Ser Arg Val Phe Asp
 35 40

<210> 154
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 154
 Met Glu Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro
 -35 -30 -25
 Gly Trp Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe
 -20 -15 -10
 Ser Gly Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala
 -5 1 5 10
 Gln Glu

<210> 155
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 155
 Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
 1 5 10 15
 His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
 20 25 30
 Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
 35 40 45
 Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
 50 55 60
 Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
 65 70 75 80
 Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
 85 90 95
 Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
 100 105 110
 Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
 115 120 125
 Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
 130 135 140
 Gln Val Ser Gln Gln Glu Glu Leu Lys
 145 150

<210> 156
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 156
 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Lys Leu Met Met
 1 5 10 15
 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
 20 25 30
 Gly Lys Asp Ile Asp Leu Asn Lys Val Arg Thr Lys Thr Ala Ala Lys
 35 40 45
 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ala Ala Val
 50 55 60
 Pro Pro Glu
 65

<210> 157
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 157
 Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala Arg
 1 5 10 15
 Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val Phe
 20 25 30
 Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys Gly
 35 40 45
 Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln Ala
 50 55 60
 Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp Lys
 65 70 75 80
 Leu Ala Glu Glu His Ser Ser
 85

<210> 158
 <211> 250
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -85...-1

<400> 158
 Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
 -85 -80 -75 -70
 Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His
 -65 -60 -55
 Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp
 -50 -45 -40
 Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu Thr
 -35 -30 -25
 Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu Ala
 -20 -15 -10
 Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu Ala


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-5          1          5          10
Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val Tyr
15          20          25
Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu Glu
30          35          40
Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser Ala
45          50          55
Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val Leu
60          65          70          75
Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu Gln
80          85          90
Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu Lys
95          100          105
Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Ala Thr Ser Gln
110          115          120
Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly Thr
125          130          135
Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu Arg
140          145          150          155
Gly Ser Ala Lys Ile Trp Ser Lys Ser Asn
160          165

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<210> 159

<211> 24

<212> PRT

<213> Homo sapiens

<400> 159

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Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
1          5          10          15
His Ile Asn Ile Ser Phe His Arg
20

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<210> 160

<211> 228

<212> PRT

<213> Homo sapiens

<400> 160

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Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
1          5          10          15
His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp Pro Lys Arg Arg
20          25          30
Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe Val Pro Gly Lys
35          40          45
His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser Cys Phe Asp Leu
50          55          60
Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val Pro Thr Ile Phe
65          70          75          80
Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys Ser Arg Asn Leu
85          90          95
Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro Ser Ser Leu Lys
100          105          110
Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His Ser Tyr Ala Phe
115          120          125
Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys Leu Glu Lys Glu
130          135          140
Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu Gln Lys Glu Arg

```

145 150 155 160
 Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu Val Lys Asn Leu
 165 170 175
 Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu His Met Leu Pro
 180 185 190
 Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys Ile Leu Glu Gln
 195 200 205
 Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu Lys Gln Thr Lys
 210 215 220
 Ser Thr Phe Ile
 225

<210> 161
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 161
 Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
 -20 -15 -10 -5
 Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
 1 5 10
 Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
 15 20 25
 Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
 30 35 40
 Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
 45 50 55 60
 Pro Ala Lys Leu Arg Gln
 65

<210> 162
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Asn
 1 5 10 15
 Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp Val
 20 25 30
 Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
 35 40

<210> 163
 <211> 314
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58..-1

<400> 163
 Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
 -55 -50 -45
 Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly
 -40 -35 -30
 Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
 -25 -20 -15
 His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
 -10 -5 1 5
 Ala Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro
 10 15 20
 Cys Tyr Lys Arg Cys Lys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala
 25 30 35
 Ile Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His
 40 45 50
 Asn Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu
 55 60 65 70
 Glu Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu
 75 80 85
 Glu Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr
 90 95 100
 Glu Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg
 105 110 115
 Lys Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp
 120 125 130
 Ala Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys
 135 140 145 150
 Tyr Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg
 155 160 165
 Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His
 170 175 180
 Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro
 185 190 195
 Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys
 200 205 210
 Ile Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met
 215 220 225 230
 Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile
 235 240 245
 Glu Tyr Asp Tyr Thr Arg His Phe Thr Met
 250 255

<210> 164
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -80...-1

<400> 164
 Met Arg Thr Arg Thr Thr Gly Asn Pro Arg Gly Leu His Asp Thr Phe
 -80 -75 -70 -65
 Pro Arg Arg Pro Arg Leu Gly Arg Cys Ser Asp Met Asp Thr Ala Arg
 -60 -55 -50
 Thr Ser Cys Ser Asp Leu Leu Pro Trp Glu Gly Val Thr Glu Pro Ala
 -45 -40 -35
 Leu Cys Gly Asp Gln Leu Gln Gly Thr Glu Gly Trp Leu Glu Ala Thr

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 167

```

Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly
  -15                -10                -5
Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
1      5      10      15
Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
      20      25      30
Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
      35      40      45
Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
      50      55      60
Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro
65      70      75      80
Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
      85      90      95
Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
      100     105     110
Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
      115     120     125
Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
      130     135     140
Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
145     150     155     160
Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
      165     170     175
Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
      180     185     190
Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
      195     200     205
Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
      210     215     220
Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
225     230     235     240
Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
      245     250     255
Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
      260     265     270
Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
      275     280     285
Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
      290     295     300
His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Cys
305     310     315     320
His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp Arg
      325     330     335

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<210> 168

<211> 138

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 168

```

Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu
      -45                -40                -35
Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser
      -30                -25                -20
Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile
      -15                -10                -5                1
Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu
      5                10                15
Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys Tyr Val Ala Gly Ile
      20                25                30
Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp Asn Val Ser Gly Glu
      35                40                45
Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser Ala Pro Leu Gln Phe
      50                55                60                65
Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His Thr Asn Arg Arg Glu
      70                75                80
Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala
      85                90

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<210> 169

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -73...-1

<400> 169

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Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
      -70                -65                -60
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
      -55                -50                -45
Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
      -40                -35                -30
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
      -25                -20                -15                -10
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
      -5                1                5
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
      10                15                20
Pro Leu Gly Thr Pro
      25

```

<210> 170

<211> 252

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68...-1

<400> 170

```

Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
      -65                -60                -55

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Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50                      -45                      -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
      -35                      -30                      -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
      -20                      -15                      -10                      -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
                        1                      -5                      10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
      15                      20                      25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
      30                      35                      40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
      45                      50                      55                      60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
                        65                      70                      75
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
                        80                      85                      90
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
      95                      100                      105
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
      110                      115                      120
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
      125                      130                      135                      140
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
                        145                      150                      155
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
                        160                      165                      170
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
      175                      180

```

<210> 171

<211> 350

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68...-1

<400> 171

```

Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
      -65                      -60                      -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50                      -45                      -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
      -35                      -30                      -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
      -20                      -15                      -10                      -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
                        1                      5                      10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
      15                      20                      25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
      30                      35                      40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
      45                      50                      55                      60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
                        65                      70                      75
Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala

```

80	85	90
Leu Gln Gln His Arg Pro Ser	Pro Glu Leu Thr Leu Ser	Gln Lys Ile
95	100	105
Arg Thr Lys Leu Gln Asn Pro	Asp Leu Leu Glu Leu Cys	His Ser Val
110	115	120
Pro Lys Glu Val Asp Gln Leu	Gly Gly Arg Gly Tyr Gly	Ser Glu Ser
125	130	135
Gly Glu Glu Asp Phe Ala Ala	Phe Arg Ala Trp Leu Arg	Cys Tyr Gly
145	150	155
Met Pro Gly Met Ser Ser Leu	Gln Asp Arg His Gly Arg	Thr Ile Trp
160	165	170
Phe Gln Gly Asp Pro Gly Pro	Leu Ala Pro Lys Gly Arg	Lys Ser Arg
175	180	185
Lys Lys Lys Ser Lys Ala Thr	Gln Leu Ser Pro Glu Asp	Arg Val Glu
190	195	200
Asp Ala Leu Pro Pro Ser Lys	Ala Pro Ser Lys Thr Arg	Arg Ala Lys
205	210	215
Arg Asp Leu Pro Lys Arg Thr	Ala Thr Gln Arg Pro Glu	Gly Thr Ser
225	230	235
Leu Gln Gln Asp Pro Glu Ala	Pro Thr Val Pro Lys Lys	Gly Arg Arg
240	245	250
Lys Gly Arg Gln Ala Ala Ser	Gly His Cys Arg Pro Arg	Lys Val Lys
255	260	265
Ala Asp Ile Pro Ser Leu Glu	Pro Glu Gly Thr Ser Ala	Ser
270	275	280

<210> 172

<211> 390

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68...-1

<400> 172

Met Pro Glu Gly Pro Glu Leu His	Leu Ala Ser Gln Phe Val Asn Glu
-65	-60 -55
Ala Cys Arg Ala Leu Val Phe Gly	Gly Cys Val Glu Lys Ser Ser Val
-50	-45 -40
Ser Arg Asn Pro Glu Val Pro Phe	Glu Ser Ser Ala Tyr Arg Ile Ser
-35	-30 -25
Ala Ser Ala Arg Gly Lys Glu Leu	Arg Leu Ile Leu Ser Pro Leu Pro
-20	-15 -10 -5
Gly Ala Gln Pro Gln Gln Glu Pro	Leu Ala Leu Val Phe Arg Phe Gly
1	5 10
Met Ser Gly Ser Phe Gln Leu Val	Pro Arg Glu Glu Leu Pro Arg His
15	20 25
Ala His Leu Arg Phe Tyr Thr Ala	Pro Pro Gly Pro Arg Leu Ala Leu
30	35 40
Cys Phe Val Asp Ile Arg Arg Phe	Gly Arg Trp Asp Leu Gly Gly Lys
45	50 55 60
Trp Gln Pro Gly Arg Gly Pro Cys	Val Leu Gln Glu Tyr Gln Gln Phe
65	70 75
Arg Glu Asn Val Leu Arg Asn Leu	Ala Asp Lys Ala Phe Asp Arg Pro
80	85 90
Ile Cys Glu Ala Leu Leu Asp Gln	Arg Phe Phe Asn Gly Ile Gly Asn
95	100 105
Tyr Leu Arg Ala Glu Ile Leu Tyr	Arg Leu Lys Ile Pro Pro Phe Glu
110	115 120

Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
 125 130 135 140
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp
 145 150 155
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
 160 165 170
 Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe
 175 180 185
 Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln
 190 195 200
 Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu
 205 210 215 220
 Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln
 225 230 235
 Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
 240 245 250
 Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
 255 260 265
 Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
 270 275 280
 Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
 285 290 295 300
 His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
 305 310 315
 Glu Gly Thr Ser Ala Ser
 320

<210> 173
 <211> 190
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -82...-1

<400> 173
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
 -15 -10 -5
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
 1 5 10
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile
 15 20 25 30
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
 35 40 45
 Trp Ser Thr Tyr Gln Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu
 50 55 60
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
 65 70 75
 Asp Ala Asp Lys Glu Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His
 80 85 90
 Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu

95

100

105

<210> 174
 <211> 285
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -232...-1

<400> 174
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
 -230 -225 -220
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 -215 -210 -205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 -200 -195 -190 -185
 Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
 -180 -175 -170
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 -165 -160 -155
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 -150 -145 -140
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
 -135 -130 -125
 Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
 -120 -115 -110 -105
 Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
 -100 -95 -90
 Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp
 -85 -80 -75
 Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn
 -70 -65 -60
 Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn
 -55 -50 -45
 Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile
 -40 -35 -30 -25
 Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala
 -20 -15 -10
 Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val
 -5 1 5
 Gly Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile
 10 15 20
 Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu
 25 30 35 40
 Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys Lys
 45 50

<210> 175
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 175
 Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu

```

                20                25                30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
                35                40                45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
                50                55                60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65                70                75                80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
                85                90                95
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
                100                105                110
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
                115                120                125
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
                130                135                140
His His Cys Val Arg Glu Gly Ser Gly
145                150

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<210> 176
 <211> 49
 <212> PRT
 <213> Homo sapiens

```

<400> 176
Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
1                5                10                15
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
                20                25                30
Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe
                35                40                45
Cys

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<210> 177
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

```

<400> 177
Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
                -20                -15                -10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
                -5                1                5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
                10                15                20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
25                30                35                40
Arg Cys Glu Thr Phe Val Phe Ser Gly Cys Asn Gly Asn Leu Asn Asn
                45                50                55
Phe Lys Leu Lys Ile Glu Arg Glu Val Ala Cys Val Ala Lys Tyr Lys
                60                65                70
Pro Pro Arg
                75

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<210> 178
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37...-1

<400> 178
Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu Lys Pro
 -35 -30 -25
Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala Leu Leu
 -20 -15 -10
Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala Thr Lys
-5 1 5 10
Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly Pro Pro
 15 20 25
Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala Phe Ser
 30 35 40
Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met Ile
 45 50 55

<210> 179
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 179
Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
 -20 -15 -10
Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
 -5 1 5
Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
10 15 20 25
Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
 30 35 40
Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
 45 50 55
Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
 60 65 70
Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
 75 80 85
Gln Lys Leu Ala Lys Lys Met Phe Phe
90 95

<210> 180
<211> 59
<212> PRT
<213> Homo sapiens

<400> 180
Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg

```

1           5           10           15
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
                20           25           30
Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu
                35           40           45
Thr Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
        50           55

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<210> 181
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

```

<400> 181
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
                -10           -5           1
Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Pro Arg Ser Ser Ala
                5           10           15
Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
        20           25           30
Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
        35           40           45           50
Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
                55           60           65
Tyr Arg Ile Cys Asp Leu
                70

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<210> 182
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

```

<400> 182
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
                -55           -50           -45
Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
                -40           -35           -30
Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
                -25           -20           -15
Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
        -10           -5           1           5
Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
                10           15           20
Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg
        25           30           35
Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly
        40           45           50
Gln Gln Glu Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu
        55           60           65           70
Ser Leu Gln Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu

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75 80 85
 Leu Arg Ala Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys
 90 95 100
 Leu His Pro Trp Ala
 105

<210> 183
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 183
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
 -35 -30 -25 -20
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
 -15 -10 -5
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
 1 5 10
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
 15 20 25
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 30 35 40 45

<210> 184
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 184
 Met Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu
 -20 -15 -10
 Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile
 -5 1 5 10
 Lys Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Cys
 15 20 25
 Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys Ile Cys Cys Ser Ala Phe
 30 35 40
 Cys Gly Asn Ile Cys Met Ser Ile Leu
 45 50

<210> 185
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 185
 Met Leu Gly Ala Glu Thr Glu Glu Lys Leu Phe Asp Ala Pro Leu Ser
 1 5 10 15

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Ile Ser Lys Arg Glu Gln Leu Glu Gln Gln Val Pro Glu Asn Tyr Phe
      20      25      30
Tyr Val Pro Asp Leu Gly Gln Val Pro Glu Ile Asp Val Pro Ser Tyr
      35      40      45
Leu Pro Asp Leu Pro Gly Ile Ala Asn Asp Leu Met Tyr Ile Ala Asp
      50      55      60
Leu Gly Pro Gly Ile Ala Pro Ser Ala Pro Gly Thr Ile Pro Glu Leu
      65      70      75      80
Pro Thr Phe His Thr Glu Val Ala Glu Pro Leu Lys Thr Tyr Lys Met
      85      90      95
Gly Tyr

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<210> 186
<211> 112
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -21...-1

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<400> 186
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu
      -20      -15      -10
Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val
      -5      1      5      10
Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val
      15      20      25
Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro
      30      35      40
Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys
      45      50      55
Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr
      60      65      70      75
His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg
      80      85      90

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<210> 187
<211> 70
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -44...-1

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<400> 187
Met Cys Cys Tyr Cys Arg Ile Phe Cys Leu Arg Cys Thr Tyr Phe Pro
      -40      -35      -30
Val His Cys Gly Met Cys Asn Leu Arg Tyr Phe Glu Phe Ser Thr Phe
      -25      -20      -15
Leu Leu Ser Leu Ser Leu Ile Thr Tyr Cys Phe Trp Asp Pro Pro His
      -10      -5      1
Arg Gly Ser His Ser Leu Ser Leu Glu His Thr Pro Leu Asp Phe Leu
      5      10      15      20
Glu Trp Gly Leu Leu Arg
      25

```

<210> 188
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 188
 Met Leu Phe Ser Leu Ser Leu Leu Ser Asn Leu Asn Gln Ile Gly Ser
 -10 -5 1
 Ser His Leu Asp Arg Pro His Ile Pro Gly Gln Ser Ala Gln Leu Phe
 5 10 15
 Ile Tyr Gln Met Ser Ser Gln Gln Leu Gln Gln Pro Ser Ala Asn
 20 25 30 35
 Lys Lys Ala Gly Lys Ile His Asn Thr Pro Phe Ala Asn Gln Leu Asn
 40 45 50
 Pro Thr Gln His Leu Ala Lys Pro Phe Gln Gln Ile Leu Pro Gly Arg
 55 60 65
 Gln Ser Gly Ser Leu Thr Ser Pro Phe Leu Ala Cys
 70 75

<210> 189
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 189
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile
 -10 -5 1 5
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
 Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
 25 30 35
 Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
 40 45 50
 Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu
 55 60 65 70
 Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile
 75 80 85
 Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu
 90 95 100
 Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys
 105 110 115
 Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro
 120 125 130
 Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu
 135 140 145 150
 Ala Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr

155

160

165

<210> 190
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala Leu Lys Glu Lys Phe
 1 5 10 15
 Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe Gln Glu Ile Pro Lys
 20 25 30
 Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln Leu Glu Lys Ile Glu
 35 40 45
 Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile Asn Ile Thr Glu Met
 50 55 60
 Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val Asn His Leu Lys Ala
 65 70 75 80
 Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu Pro Thr Thr Val Glu
 85 90 95
 Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn Thr Leu Asn Ser Val
 100 105 110
 His Leu Ala Val Glu Ala Leu Gln Lys Thr Val Asp Glu His Lys Lys
 115 120 125
 Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln His Phe Leu Lys Glu
 130 135 140
 Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro Ser Ala Thr Ser Glu
 145 150 155 160
 Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys Gln Met Gly Asp Arg
 165 170 175
 Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln Val Thr Asn Arg Thr
 180 185 190
 Asp Thr Val Lys Ile Gln Lys Lys Lys
 195 200

<210> 191
 <211> 379
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 191
 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
 -35 -30 -25
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
 -20 -15 -10
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
 -5 1 5 10
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
 15 20 25
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
 30 35 40
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
 45 50 55
 Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

60				65				70				75			
Val	Gly	Pro	Pro	Phe	Thr	Trp	Met	Leu	Ala	Leu	Leu	Gly	Leu	Ser	Gln
				80					85					90	
Ala	Leu	Asn	Ile	Leu	Leu	Gly	Leu	Lys	Gly	Leu	Ala	Pro	Ala	Glu	Ile
		95						100					105		
Ser	Ala	Val	Cys	Glu	Lys	Gly	Asn	Phe	Asn	Val	Ala	His	Gly	Leu	Ala
		110					115					120			
Trp	Ser	Tyr	Tyr	Ile	Gly	Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln
	125					130					135				
Ala	Arg	Ile	Arg	Thr	Tyr	Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly
140					145				150					155	
Ala	Val	Ser	Gln	Arg	Leu	Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val
			160						165					170	
Pro	Asp	Asn	Leu	Ser	Met	Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys
		175						180					185		
Leu	Pro	Gln	Gln	Thr	Gly	Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr
	190					195					200				
Ser	Asn	Ser	Ile	Tyr	Glu	Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr
	205					210					215				
Cys	Val	Leu	Glu	Tyr	Ala	Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser
220					225				230					235	
Gln	Tyr	Ser	Gln	Ala	Gly	Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala
			240						245					250	
Lys	Leu	Phe	Cys	Arg	Thr	Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu
		255					260					265			
Ser	Gln	Asn	Asn	Cys	Arg	Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp
	270					275					280				
Ser	Ser	Phe	Ser	Leu	Ser	Gln	Glu	Val	Leu	Arg	His	Leu	Arg	Gln	Glu
	285					290				295					
Glu	Lys	Glu	Glu	Val	Thr	Val	Gly	Ser	Leu	Lys	Thr	Ser	Ala	Val	Pro
300					305				310					315	
Ser	Thr	Ser	Thr	Met	Ser	Gln	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Gly	Met
			320						325					330	
Gly	Lys	Pro	Leu	Pro	Leu	Arg	Thr	Asp	Phe	Ser					
		335						340							

<210> 192
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 192

Met	Pro	Ser	Glu	Gly	Arg	Cys	Trp	Glu	Thr	Leu	Lys	Ala	Leu	Arg	Ser
1				5					10					15	
Ser	Asp	Lys	Gly	Arg	Leu	Cys	Tyr	Tyr	Arg	Asp	Trp	Leu	Leu	Arg	Arg
		20						25				30			
Glu	Asp	Val	Leu	Glu	Glu	Cys	Met	Ser	Leu	Pro	Lys	Leu	Ser	Ser	Tyr
	35					40					45				
Ser	Gly	Trp	Val	Val	Glu	His	Val	Leu	Pro	His	Met	Gln	Glu	Asn	Gln
	50					55				60					
Pro	Leu	Ser	Glu	Thr	Ser	Pro	Ser	Ser	Thr	Ser	Ala	Ser	Ala	Leu	Asp
65					70				75					80	
Gln	Pro	Ser	Phe	Val	Pro	Lys	Ser	Pro	Asp	Ala	Ser	Ser	Ala	Phe	Ser
			85						90					95	
Pro	Ala	Ser	Pro	Ala	Thr	Pro	Asn	Gly	Thr	Lys	Gly	Lys	Lys	Lys	Lys
		100						105					110		

<210> 193

<211> 43
 <212> PRT
 <213> Homo sapiens

<400> 193
 Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly Ser
 1 5 10 15
 Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg Asn
 20 25 30
 Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys
 35 40

<210> 194
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 194
 Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 195
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 195
 Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
 -15 -10 -5
 Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
 1 5 10
 Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile
 15 20 25 30
 Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys
 35 40 45
 Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala Asp
 50 55 60
 Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly
 65 70 75
 Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala
 80 85 90
 Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe
 95 100 105 110
 Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr

[illegible]

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<210> 196
<211> 353
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -34...-1
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<400> 196																
Met	Glu	Arg	Gly	Leu	Lys	Ser	Ala	Asp	Pro	Arg	Asp	Gly	Thr	Gly	Tyr	
				-30					-25					-20		
Thr	Gly	Trp	Ala	Gly	Ile	Ala	Val	Leu	Tyr	Leu	His	Leu	Tyr	Asp	Val	
			-15					-10					-5			
Phe	Gly	Asp	Pro	Ala	Tyr	Leu	Gln	Leu	Ala	His	Gly	Tyr	Val	Lys	Gln	
		1				5					10					
Ser	Leu	Asn	Cys	Leu	Thr	Lys	Arg	Ser	Ile	Thr	Phe	Leu	Cys	Gly	Asp	
15					20					25				30		
Ala	Gly	Pro	Leu	Ala	Val	Ala	Ala	Val	Leu	Tyr	His	Lys	Met	Asn	Asn	
				35					40					45		
Glu	Lys	Gln	Ala	Glu	Asp	Cys	Ile	Thr	Arg	Leu	Ile	His	Leu	Asn	Lys	
			50					55					60			
Ile	Asp	Pro	His	Ala	Pro	Asn	Glu	Met	Leu	Tyr	Gly	Arg	Ile	Gly	Tyr	
		65					70					75				
Ile	Tyr	Ala	Leu	Leu	Phe	Val	Asn	Lys	Asn	Phe	Gly	Val	Glu	Lys	Thr	
	80					85					90					
Pro	Gln	Ser	His	Ile	Gln	Gln	Ile	Cys	Glu	Thr	Ile	Leu	Thr	Ser	Gly	
95					100					105					110	
Glu	Asn	Leu	Ala	Arg	Lys	Arg	Asn	Phe	Thr	Ala	Lys	Ser	Pro	Leu	Met	
				115					120					125		
Tyr	Glu	Trp	Tyr	Gln	Glu	Tyr	Tyr	Val	Gly	Ala	Ala	His	Gly	Leu	Ala	
			130					135					140			
Gly	Ile	Tyr	Tyr	Tyr	Leu	Met	Gln	Pro	Ser	Leu	Gln	Val	Ser	Gln	Gly	
		145					150					155				
Lys	Leu	His	Ser	Leu	Val	Lys	Pro	Ser	Val	Asp	Tyr	Val	Cys	Gln	Leu	
	160					165					170					
Lys	Phe	Pro	Ser	Gly	Asn	Tyr	Pro	Pro	Cys	Ile	Gly	Asp	Asn	Arg	Asp	
175					180					185				190		
Leu	Leu	Val	His	Trp	Cys	His	Gly	Ala	Pro	Gly	Val	Ile	Tyr	Met	Leu	
				195					200					205		
Ile	Gln	Ala	Tyr	Lys	Val	Phe	Arg	Glu	Lys	Tyr	Leu	Cys	Asp	Ala		
		210						215					220			
Tyr	Gln	Cys	Ala	Asp	Val	Ile	Trp	Gln	Tyr	Gly	Leu	Leu	Lys	Lys	Gly	
		225					230					235				

Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr
 240 245 250
 Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys
 255 260 265 270
 Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro
 275 280 285
 Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe
 290 295 300
 Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu
 305 310 315
 Leu

<210> 197
 <211> 30
 <212> PRT
 <213> Homo sapiens

<400> 197
 Met Gln Met Asp Thr Phe Phe Met Ser Glu Lys His Thr His Thr His
 1 5 10 15
 Thr His Ile His Thr His Thr Arg Lys Thr Lys Lys Lys Lys
 20 25 30

<210> 198
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 198
 Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
 -45 -40 -35
 Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
 -30 -25 -20
 Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
 -15 -10 -5
 Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
 1 5 10 15
 Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe
 20 25 30
 Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser
 35 40 45
 Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
 50 55 60

<210> 199
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 199
 Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
 1 5 10 15

Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
 20 25 30
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
 35 40 45
 Ser Ser Gly His Leu Pro
 50

<210> 200
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 200
 Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr Ala Ala Val
 -20 -15 -10
 Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
 -5 1 5 10
 Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
 15 20 25
 Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
 30 35 40
 Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
 45 50 55
 Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
 60 65 70 75
 Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ser Lys
 80 85 90
 Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
 95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 201
 <211> 228
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 201
 Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
 -25 -20 -15 -10
 Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
 -5 1 5
 Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu Asn Leu
 10 15 20
 Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys Trp Glu
 25 30 35
 Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys Arg Ala
 40 45 50 55

Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu Leu Gly
 60 65 70
 Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu Ser Arg
 75 80 85
 Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro His Ile Leu Ala Gly
 90 95 100
 Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile Thr Arg
 105 110 115
 Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro
 120 125 130 135
 Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu Gly Gly
 140 145 150
 Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp Pro Ala
 155 160 165
 Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met Pro Val
 170 175 180
 Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg
 185 190 195
 Asn Ala Tyr Val
 200

<210> 202
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 202
 Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
 -45 -40 -35
 Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
 -30 -25 -20
 Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
 -15 -10 -5 1
 Pro Asp Leu Pro Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
 5 10 15

<210> 203
 <211> 146
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 203
 Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly
 -30 -25 -20
 Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile
 -15 -10 -5 1
 Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys
 5 10 15
 Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu
 20 25 30

Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn
 35 40 45
 Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile Pro Val Ser Gly Ser
 50 55 60 65
 Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser Arg Gly Gly Pro Phe
 70 75 80
 Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu Lys Asp Gly Gln
 85 90 95
 Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly Asp Glu Val Lys
 100 105 110
 Lys Glu
 115

<210> 204
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 204
 Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser Leu
 1 5 10 15
 Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His Leu
 20 25 30
 Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro Glu
 35 40 45
 Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln Ser
 50 55 60
 Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu Leu
 65 70 75 80
 Glu Val Asp Asp Trp Glu Phe
 85

<210> 205
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 205
 Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5
 Leu Ser Leu Arg Ser Ala Met Ser
 10

<210> 206
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg


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1           5           10           15
Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
20           25           30
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
35           40           45
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
50           55           60
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
65           70           75           80
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
85           90           95
Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val
100          105          110
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
115          120          125
His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
130          135          140
Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
145          150

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<210> 207
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 207
Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
1           5           10           15
Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
20           25           30
Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
35           40           45
Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
50           55           60
Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
65           70           75           80
Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
85           90           95
Lys Gln Thr Ser Val
100

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<210> 208
 <211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

```

<400> 208
Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly
-20          -15          -10
Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn
-5           1           5           10
Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg Ala Leu Glu
15           20           25
Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile Ser Asp Ser

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<220>
<221> SIGNAL
<222> -17...-1
```

<400> 209

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Met Pro Ser Ser Phe Phe Leu Leu Leu Gln Phe Phe Leu Arg Ile Asp
      -15                -10                -5
Gly Val Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp
  1          5          10          15
Lys Thr Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser
      20          25          30
Ser Leu Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile
      35          40          45
Ser Gln Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe
      50          55          60
Pro Glu Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln
      65          70          75
Val Glu
80

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<210> 210

<211> 83

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29...-1

<400> 210

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Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu
      -25                -20                -15
Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe
      -10                -5          1
Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr
  5          10          15
Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro
20          25          30          35
Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg
      40          45          50
Asn Ala Ser

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<210> 211

<211> 229

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 211

```

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
      -20                -15                -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
      -5          1          5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10          15          20          25
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
      30          35          40
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

```

```

          45          50          55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
          60          65          70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
          75          80          85
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
          90          95          100          105
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
          110          115          120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
          125          130          135
Ser Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
          140          145          150
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
          155          160          165
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
          170          175          180          185
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
          190          195          200
Arg Lys Ser Arg Thr
          205

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<210> 212
 <211> 152
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

```

<400> 212
Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
-20          -15          -10
Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
-5          1          5          10
Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly
          15          20          25
Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr
          30          35          40
Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly
          45          50          55
Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val
          60          65          70          75
Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp
          80          85          90
Lys Ala Leu Ile Phe Asn Lys Ile His His Glu Leu Asn Gln Phe Cys
          95          100          105
Ser Val His Thr Leu Gln Glu Val Tyr Ile Glu Leu Phe Gly Leu Glu
          110          115          120
Asn Asp Phe Ser Gln Glu Ser Ser
          125          130

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<210> 213
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -54...-1

<400> 213

Met	Ala	Ala	Ser	Glu	Ala	Ala	Val	Val	Ser	Ser	Pro	Ser	Leu	Lys	Thr
				-50					-45					-40	
Asp	Thr	Ser	Pro	Val	Leu	Glu	Thr	Ala	Gly	Thr	Val	Ala	Ala	Met	Ala
			-35					-30					-25		
Ala	Thr	Pro	Ser	Ala	Arg	Ala	Ala	Ala	Ala	Val	Val	Ala	Ala	Ala	Ala
		-20				-15						-10			
Arg	Thr	Gly	Ser	Glu	Ala	Arg	Val	Ser	Lys	Ala	Ala	Leu	Ala	Thr	Lys
	-5				1				5					10	
Leu	Leu	Ser	Leu	Ser	Gly	Val	Phe	Ala	Val	His	Lys	Pro	Lys	Gly	Pro
			15					20						25	
Thr	Ser	Ala	Glu	Leu	Leu	Asn	Arg	Leu	Lys	Glu	Lys	Leu	Leu	Ala	Glu
			30					35					40		
Ala	Gly	Met	Pro	Ser	Pro	Glu	Trp	Thr	Lys	Arg	Lys	Lys	Gln	Thr	Leu
		45				50						55			
Lys	Ile	Gly	His	Gly	Gly	Thr	Leu	Asp	Ser	Ala	Ala	Arg	Gly	Val	Leu
	60				65						70				
Val	Val	Gly	Ile	Gly	Ser	Gly	Thr	Lys	Met	Leu	Thr	Ser	Met	Leu	Ser
	75				80				85					90	
Gly	Ser	Lys	Arg	Tyr	Thr	Ala	Ile	Gly	Glu	Leu	Gly	Lys	Ala	Thr	Asp
			95					100						105	
Thr	Leu	Asp	Ser	Thr	Gly	Lys	Val	Thr	Glu	Glu	Lys	Pro	Tyr	Gly	Met
			110					115						120	
Asn	Leu	Ile													
			125												

<210> 214

<211> 269

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -92...-1

<400> 214

Met	Ile	Thr	His	Val	Thr	Leu	Glu	Asp	Ala	Leu	Ser	Asn	Val	Asp	Leu
		-90					-85					-80			
Leu	Glu	Glu	Leu	Pro	Leu	Pro	Asp	Gln	Gln	Pro	Cys	Ile	Glu	Pro	Pro
	-75					-70					-65				
Pro	Ser	Ser	Ile	Met	Tyr	Gln	Ala	Asn	Phe	Asp	Thr	Asn	Phe	Glu	Asp
	-60			-55					-50					-45	
Arg	Asn	Ala	Phe	Val	Thr	Gly	Ile	Ala	Arg	Tyr	Ile	Glu	Gln	Ala	Thr
			-40					-35						-30	
Val	His	Ser	Ser	Met	Asn	Glu	Met	Leu	Glu	Glu	Gly	His	Glu	Tyr	Ala
		-25				-20						-15			
Val	Met	Leu	Tyr	Thr	Trp	Arg	Ser	Cys	Ser	Arg	Ala	Ile	Pro	Gln	Val
	-10				-5						1				
Lys	Cys	Asn	Glu	Gln	Pro	Asn	Arg	Val	Glu	Ile	Tyr	Glu	Lys	Thr	Val
	5			10					15					20	
Glu	Val	Leu	Glu	Pro	Glu	Val	Thr	Lys	Leu	Met	Lys	Phe	Met	Tyr	Phe
			25					30						35	
Gln	Arg	Lys	Ala	Ile	Glu	Arg	Phe	Cys	Ser	Glu	Val	Lys	Arg	Leu	Cys
			40				45						50		
His	Ala	Glu	Arg	Arg	Lys	Asp	Phe	Val	Ser	Glu	Ala	Tyr	Leu	Leu	Thr
			55				60					65			

Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn
 70 75 80
 Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala
 85 90 95 100
 Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln
 105 110 115
 Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys Leu
 120 125 130
 His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala Asp
 135 140 145
 Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu Thr
 150 155 160
 Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro
 165 170 175

<210> 215
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 215
 Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val
 -20 -15 -10
 Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala
 -5 1 5 10
 Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser
 15 20 25
 Phe Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile
 30 35 40
 Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe
 45 50 55
 His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu
 60 65 70
 Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile
 75 80 85 90
 Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn
 95 100 105
 Ser Ala Pro Lys Ser Asn Val
 110

<210> 216
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 216
 Met Asn Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 -35 -30 -25
 Val Lys Gly His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr
 -20 -15 -10

Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 -5 1 5 10
 Phe Asn Pro Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 15 20 25
 Glu Val Leu

<210> 217
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 217
 Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
 -50 -45 -40
 Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
 -35 -30 -25
 Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
 -20 -15 -10
 Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
 -5 1 5 10
 Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
 15 20 25
 Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
 30 35 40
 Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
 45 50 55
 Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr
 60 65 70

<210> 218
 <211> 376
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 218
 Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
 -20 -15 -10
 Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
 -5 1 5 10
 Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg Ile Gly
 15 20 25
 Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys Ala Leu
 30 35 40
 Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg Thr Arg
 45 50 55
 Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val Gly Gly
 60 65 70 75
 Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg Ser Phe
 80 85 90
 Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln Thr Lys

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      95              100              105
Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys Leu Leu
      110              115              120
Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly Thr Leu
      125              130              135
Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala Val Asp
140              145              150              155
Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala Leu Thr
      160              165              170
Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp Asn His
      175              180              185
Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp Leu Val
      190              195              200
Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser Trp Leu
      205              210              215
Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe Gln Val
220              225              230              235
Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys Pro Trp
      240              245              250
Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro Val Ala
      255              260              265
Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg Ile Gln
      270              275              280
Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro Leu Pro
      285              290              295
Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val Ser Gly
300              305              310              315
Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly Gly His
      320              325              330
Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu Ala Gln
      335              340              345
Arg Ser Tyr Leu Pro Gln Ile Ser
      350              355

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<210> 219
 <211> 211
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

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<400> 219
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
-30              -25              -20              -15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
      -10              -5              1
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
      5              10              15
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
      20              25              30
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
35              40              45              50
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
      55              60              65
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val Pro Arg Met
      70              75              80
Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe
      85              90              95

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His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro
 100 105 110
 Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser
 115 120 125 130
 Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly
 135 140 145
 Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser
 150 155 160
 Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser
 165 170 175
 Arg Gln Leu
 180

<210> 220
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 220
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
 -60 -55 -50 -45
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
 -40 -35 -30
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
 -25 -20 -15
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
 -10 -5 1
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
 5 10 15 20
 Ala Leu Leu Arg Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu
 25 30 35
 Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
 40 45 50
 Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe
 55 60 65
 Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
 70 75 80
 Pro Glu Phe His Ile Glu Ile Leu Ser Ile
 85 90

<210> 221
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 221
 Met Lys Gly Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala
 -40 -35 -30
 Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro
 -25 -20 -15

Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met
 -10 -5 1 5
 Lys Ser Ser Gln Ala Ala Arg Lys Asp Asp Phe Leu Arg Ser Leu Ser
 10 15 20
 Asp Gly Asp Ser Gly Thr Ser Glu His Ile Ser Ala Val Val Thr Ser
 25 30 35
 Pro Arg Ile Ser Cys His Gly Ala Ala Ile Pro Thr Ala Arg Ala Leu
 40 45 50
 Cys Leu Gly Cys Ser Cys Cys Thr Glu Arg Leu Leu Leu Pro Pro Pro
 55 60 65 70
 Ser Leu Leu Ser Leu Glu Ala Pro Ala Ser Thr
 75 80

<210> 222

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 222

Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln
 -15 -10 -5
 Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr
 1 5 10
 Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr
 15 20 25
 Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr
 30 35 40 45
 Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu
 50 55 60
 Ala Ala Leu Val Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val
 65 70 75
 Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu
 80 85 90
 Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln
 95 100 105
 Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val
 110 115 120 125
 Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
 130 135 140
 Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
 145 150 155
 Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
 160 165 170
 Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
 175 180 185
 Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
 190 195 200 205
 Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
 210 215 220
 His Lys Cys Gln Val Val Phe Phe Leu Ala Ala Ala Phe Phe Ser
 225 230 235
 Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
 240 245 250
 Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
 255 260 265
 Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr

270		275		280		285									
Glu	Pro	Leu	His	Thr	His	Trp	Pro	His	Asn	Phe	Ser	Gly	Leu	Phe	Leu
				290					295					300	
Leu	Thr	Val	Gly	Ser	Ser	Ile	Leu	Thr	Ala	Phe	Leu	Leu	Ser	Gln	Leu
			305					310					315		
Val	Gln	Arg	Lys	Leu	Asp	Gln	Lys	Thr	Lys						
		320					325								

<210> 223
 <211> 210
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 223

Met	Asp	Asn	Arg	Phe	Ala	Thr	Ala	Phe	Val	Ile	Ala	Cys	Val	Leu	Ser
-20					-15					-10					-5
Leu	Ile	Ser	Thr	Ile	Tyr	Met	Ala	Ala	Ser	Ile	Gly	Thr	Asp	Phe	Trp
			1					5					10		
Tyr	Glu	Tyr	Arg	Ser	Pro	Val	Gln	Glu	Asn	Ser	Ser	Asp	Leu	Asn	Lys
		15				20						25			
Ser	Ile	Trp	Asp	Glu	Phe	Ile	Ser	Asp	Glu	Ala	Asp	Glu	Lys	Thr	Tyr
	30					35					40				
Asn	Asp	Ala	Leu	Phe	Arg	Tyr	Asn	Gly	Thr	Val	Gly	Leu	Trp	Arg	Arg
45					50					55					60
Cys	Ile	Thr	Ile	Pro	Lys	Asn	Met	His	Trp	Tyr	Ser	Pro	Pro	Glu	Arg
				65					70					75	
Thr	Glu	Ser	Phe	Asp	Val	Val	Thr	Lys	Cys	Val	Ser	Phe	Thr	Leu	Thr
			80					85					90		
Glu	Gln	Phe	Met	Glu	Lys	Phe	Val	Asp	Pro	Gly	Asn	His	Asn	Ser	Gly
		95					100					105			
Ile	Asp	Leu	Leu	Arg	Thr	Tyr	Leu	Trp	Arg	Cys	Gln	Phe	Leu	Leu	Pro
	110					115					120				
Phe	Val	Ser	Leu	Gly	Leu	Met	Cys	Phe	Gly	Ala	Leu	Ile	Gly	Leu	Cys
125					130					135					140
Ala	Cys	Ile	Cys	Arg	Ser	Leu	Tyr	Pro	Thr	Ile	Ala	Thr	Gly	Ile	Leu
				145					150					155	
His	Leu	Leu	Ala	Val	Thr	Lys	Glu	Ser	Met	Leu	Pro	Ala	Gly	Ala	Glu
			160					165					170		
Ser	Lys	His	Thr	Ala	Thr	Pro	Ala	His	Ala	Cys	Val	Gln	Thr	Gly	Lys
		175					180						185		
Pro	Lys														
	190														

<210> 224
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 224

Met	Asp	Asn	Arg	Phe	Ala	Thr	Ala	Phe	Val	Ile	Ala	Cys	Val	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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-20          -15          -10          -5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
      1          5          10
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
      15          20          25
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
      30          35          40
Asn Asp Ala Pro Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg
      45          50          55          60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
      65          70          75
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr
      80          85          90
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly
      95          100          105
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro
      110          115          120
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
      125          130          135          140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
      145          150          155
His Leu Leu Ala Asp Thr Met Leu
      160

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<210> 225
<211> 227
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -22...-1

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<400> 225
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
      -20          -15          -10
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
      -5          1          5          10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
      15          20          25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
      30          35          40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
      45          50          55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
      60          65          70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
      75          80          85          90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
      95          100          105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
      110          115          120
Ser Gly Phe His Arg Tyr Gln Phe Val Tyr Leu Gln Glu Gly Lys
      125          130          135
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
      140          145          150
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
      155          160          165          170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
      175          180          185

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Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
 190 195 200
 Ala Ala Cys
 205

<210> 226
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 226
 Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu
 -40 -35 -30
 Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
 -25 -20 -15 -10
 Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
 -5 1 5
 Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile
 10 15 20
 Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
 25 30

<210> 227
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 227
 Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly
 1 5 10 15
 Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile
 20 25 30
 Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met Val Lys Lys Ile Ala
 35 40 45
 Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val
 50 55 60
 Asn Leu Leu Glu Val Cys Lys Lys Lys
 65 70

<210> 228
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 228
 Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
 -15 -10 -5
 Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp

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1           5           10           15
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr
           20           25           30
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe
           35           40           45
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg
           50           55           60
Lys Asn
65

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<210> 229
<211> 119
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -56...-1

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<400> 229
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
Ile Leu Ala Lys Lys Lys
60

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<210> 230
<211> 54
<212> PRT
<213> Homo sapiens

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<400> 230
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
Gly Arg Gly Arg Pro His
50

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<210> 231
<211> 210
<212> PRT
<213> Homo sapiens

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<220>
 <221> SIGNAL
 <222> -14...-1

<400> 231
 Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val
 -10 -5 1
 Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr
 5 10 15
 Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
 20 25 30
 Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile
 35 40 45 50
 Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
 55 60 65
 Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met
 70 75 80
 Thr Ala Tyr Leu Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu
 85 90 95
 Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly
 100 105 110
 Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu
 115 120 125 130
 Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile
 135 140 145
 Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg
 150 155 160
 Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp
 165 170 175
 Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys
 180 185 190
 Gln Glu
 195

<210> 232
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
 100 105

<210> 233
 <211> 43

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<400> 233
Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
 -15 -10 -5
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
 1 5 10
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
15 20 25

<210> 234
<211> 36
<212> PRT
<213> Homo sapiens

<400> 234
Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg Leu
1 5 10 15
Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys Thr
 20 25 30
Phe Phe Gln Ile
 35

<210> 235
<211> 307
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 235
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
 -10 -5 1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
 5 10 15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20 25 30 35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
 55 60 65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
 70 75 80
Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
 85 90 95
Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys Lys Gly Leu
100 105 110 115
Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser
 120 125 130
Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr
 135 140 145

Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
 150 155 160
 Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp
 165 170 175
 Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
 180 185 190 195
 Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
 200 205 210
 Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
 215 220 225
 Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
 230 235 240
 Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
 245 250 255
 Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
 260 265 270 275
 Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Ala
 280 285 290
 Lys Lys Lys

<210> 236
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 236
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 237
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 237
 Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5
 Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro

1 5 10
 Gln Leu Ser Asp Lys Val His Asn Asp Ile
 15 20

<210> 238
 <211> 117
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 238
 Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser
 -20 -15 -10 -5
 Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
 1 5 10
 Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
 15 20 25
 Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr
 30 35 40
 Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Gly Arg
 45 50 55 60
 Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg
 65 70 75
 Thr Gly Ile Ser Leu Ile Leu Thr Ser Val Phe Phe Thr Trp Leu Ile
 80 85 90
 Ile Asp Lys Thr Thr
 95

<210> 239
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 239
 Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
 -35 -30 -25
 Gln His Xaa Xaa Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile
 -20 -15 -10
 Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
 -5 1 5 10
 Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu
 15 20 25
 Ile Ser Arg Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val
 30 35 40
 Cys Asp Cys Val Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn
 45 50 55
 Val Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
 60 65 70 75
 His Asn Ile Asn Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr
 80 85 90
 Phe Asp Pro Glu Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe

95 100 105
 His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly
 110 115 120
 Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val
 125 130 135
 Ile Gly
 140

<210> 240
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 240
 Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val
 -25 -20 -15
 Val Leu Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser
 -10 -5 1 5
 Met Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Ile Phe Ile
 10 15 20
 Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr Met Ala
 25 30 35
 Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr
 40 45 50
 Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met Lys Gly
 55 60 65
 Leu Lys Cys Arg Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro
 70 75 80 85
 Tyr Phe Lys Met His Lys Pro Val Thr Met Lys Lys Lys Lys
 90 95

<210> 241
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -115...-1

<400> 241
 Met Arg Trp Ser Cys Glu His Leu Val Met Val Trp Ile Asn Ala Phe
 -115 -110 -105 -100
 Val Met Leu Thr Thr Gln Leu Leu Pro Ser Lys Tyr Cys Asp Leu Leu
 -95 -90 -85
 His Lys Ser Ala Ala His Leu Gly Lys Trp Gln Lys Leu Glu His Gly
 -80 -75 -70
 Ser Tyr Ser Asn Ala Pro Gln His Ile Trp Ser Glu Asn Thr Ile Trp
 -65 -60 -55
 Pro Gln Gly Val Leu Val Arg His Ser Arg Cys Leu Tyr Arg Ala Met
 -50 -45 -40
 Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg Phe
 -35 -30 -25 -20
 Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu Asn Leu Leu Ile Leu

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      -15      -10      -5
Ile Glu Gly Gly Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg Ser
      1      5      10
Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys Asn
      15      20      25
Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Ile Val Leu Gly Arg
      30      35      40      45
Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn
      50      55

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<210> 242

<211> 896

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 18..173

<221> sig_peptide

<222> 18..77

<223> Von Heijne matrix

score 6.5

seq GLCVLQLTTAVTS/AF

<221> polyA_signal

<222> 864..869

<221> polyA_site

<222> 882..893

<400> 242

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aaccttcaca gtgtgag atg cct agt gtg aac agt gct gga tta tgt gtc      50
                Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val
      -20      -15      -10
ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg      98
Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
      -5      1      5
aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc      146
Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala
      10      15      20
cat cat ttc att cat cct tgc ctg gat tgagacgtgt tcttgattca      193
His His Phe Ile His Pro Cys Leu Asp
      25      30
aagtgttacc tcaagaagca gaagaagaaa acagactcct gatagttcag gatgcttcag      253
agagggcagc acttatacct ggtggtcttt ctgatggtca gttttattcc cctcctgaat      313
ccgaagcagg atctgaagaa gctgaagaaa aacaggacag tgagaaacca cttttagaac      373
tatgagtact acttttgtaa aatgtgaaaa accctcacag aaagtcacg aggcaaaaag      433
aggcaggcag tggagtctcc ctgtcgacag taaagttgaa atggtgacgt cactgtctgg      493
ctttattgaa cagctaataa agatttattt attgtaatac ctcacagacg ttgtaccata      553
tccatgcaca tttagttgcc tgccgtgtggc tggtaaggta atgtcatgat tcatcctctc      613
ttcagtgaga ctgagcctga tgtgttaaca aatagggtgaa gaaagtcttg tgctgtattc      673
ctaatacaaaa gacttaatat attgaagtaa cactttttta gtaagcaaga taccttttta      733
tttcaattca cagaatggaa tttttttgtt tcatgtctca gattttattt gtatttcttt      793
tttaacactc tacatttccc ttgtttttta actcatgcac atgtgctctt tgtacagttt      853
taaaaagtgt aataaaatct gacatgtcaa araaaaaaa mcy      896

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<210> 243

<211> 851
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..595

<221> sig_peptide
 <222> 17..85
 <223> Von Heijne matrix
 score 3.70000004768372
 seq FLPPLXRAFACRG/CQ

<221> polyA_signal
 <222> 820..825

<221> polyA_site
 <222> 840..851

<400> 243
 aagggggcgt gggggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc 52
 Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
 -20 -15
 ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg 100
 Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
 -10 -5 1 5
 gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga 148
 Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg
 10 15 20
 ttc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat 196
 Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp
 25 30 35
 aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa 244
 Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu
 40 45 50
 tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa 292
 Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu
 55 60 65
 tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa 340
 Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu
 70 75 80 85
 aaa gaa gaa ttt att cac tca aga cta aaa act aaa ggc ctg ggc ctg 388
 Lys Glu Glu Phe Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu
 90 95 100
 aga act gaa tca ggt cag aaa gca aca ttg aat gca gaa gaa atg gcg 436
 Arg Thr Glu Ser Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala
 105 110 115
 gac ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cac atg tat 484
 Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr
 120 125 130
 tat aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg 532
 Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met
 135 140 145
 gga aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa 580
 Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln
 150 155 160 165
 aag aag agg agc aac taggagtcca ctctgaccca gccagagtcc aggtttccac 635
 Lys Lys Arg Ser Asn
 170
 aggaagcara tggagctcct ttcacagggg ctctgagaaa aactggagct gatctcaaga 695
 agccccacat cttcctaagg ggccccatgg cctgtttggg ggcagggttag gtcctggggc 755

actgtggggc gcctgcctgc tgatgtgggc tctaggccag cttgttgtca cgtacgtggt 815
 gtgaaataaa gcccaagcac tgggaaaaaa aaaaaa 851

<210> 244
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..334

<221> sig_peptide
 <222> 89..130
 <223> Von Heijne matrix
 score 3.59999990463257
 seq AFTLXSLQLQAALL/CV

<221> polyA_signal
 <222> 462..467

<221> polyA_site
 <222> 484..495

<400> 244
 agtaggaasg cgccgscctg ggaggcgcca cgtcccttgc sgcggcgggga gagamatcgc 60
 ttggacttcg gggcggcctc ggacggcc atg gcc ttt acc ctg tas tca ctg 112
 Met Ala Phe Thr Leu Xaa Ser Leu
 -10
 ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag 160
 Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu
 -5 1 5 10
 gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt 208
 Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly
 15 20 25
 gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att 256
 Gly Phe Gly Glu Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile
 30 35 40
 cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca 304
 Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser
 45 50 55
 att gca att gtg tta ctt tta tta ttt gga tgaatwtcat tggagaaaat 354
 Ile Ala Ile Val Leu Leu Leu Leu Phe Gly
 60 65
 ggakactcag aaraggacat gccaktaraa kttattactt tggtcattat tggaatatatt 414
 atatcttagc tggctgacct tgcacttgtc aaaaatgtaa agctgaaaat aaaaccaggg 474
 tttctattta aaaaaaaaaa a 495

<210> 245
 <211> 884
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..614

<221> sig_peptide

<222> 21..83
 <223> Von Heijne matrix
 score 10
 seq LWALAMVTRPASA/AP

<221> polyA_signal
 <222> 849..854

<221> polyA_site
 <222> 873..884

<400> 245
 aataaccttag accctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc 53
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala
 -20 -15
 ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca 101
 Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro
 -10 -5 1 5
 gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg 149
 Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu
 10 15 20
 cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga cgg 197
 Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg
 25 30 35
 ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa 245
 Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
 40 45 50
 ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt 293
 Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu
 55 60 65 70
 cgg gca agc ctg ttg gaa act car atg gag gag gat att ctg cas ctg 341
 Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu
 75 80 85
 cag gca rag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca car 389
 Gln Ala Xaa Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln
 90 95 100
 aag gtg cta cgg gac agc gtg cag cgg cta daa ktc cag ctg arg asc 437
 Lys Val Leu Arg Asp Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa
 105 110 115
 gcc tgg ctg ggc cct gcc tac cga aaa ttt gar gtc tta aag gcy ccc 485
 Ala Trp Leu Gly Pro Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro
 120 125 130
 cck gam aar car aac cac atc cta tgg gcc ctc aca ggc cac gtg cak 533
 Pro Xaa Lys Gln Asn His Ile Leu Trp Ala Leu Thr Gly His Val Xaa
 135 140 145 150
 cgg car arg cgg gar atg gtg gca cag cag cwt ckg ctg cna car atc 581
 Arg Gln Xaa Arg Glu Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile
 155 160 165
 cag gar aaa ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac 634
 Gln Glu Lys Leu His Thr Ala Ala Leu Pro Ala
 170 175
 tgaggaccaa tcatgctgca aggaacactt ccacgccccg tgaggcccct gtgcagggag 694
 gagctgcctg ttcactggga tcagccaggg cgccggggcc cacttctgag cacagagcar 754
 agacagacgc aggcggggac aaaggcagag gatgtagccc cattggggag ggggtggagga 814
 aggacatgta ccctttcatr mctacacacc cctcattaaa gcavagtcgt ggcattctcaa 874
 aaaaaaaaaa 884

<210> 246
 <211> 897
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 94..573

<221> sig_peptide

<222> 94..258

<223> Von Heijne matrix

score 4.69999980926514

seq IGILCSLLGTVLL/WV

<221> polyA_signal

<222> 862..867

<221> polyA_site

<222> 886..897

<400> 246

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aagggcggct gcctagcacc cggaagagcc gtcaacttag cgagcgcaac aggctgccgc      60
tgaggagctg gagctggtgg ggactgggcc gca atg gac aag ctg aag aag gtg      114
                               Met Asp Lys Leu Lys Lys Val
                               -55                               -50
ctg agc ggg cag gac acg gag gac cgg agc ggc ctg tcc gag gtt gtt      162
Leu Ser Gly Gln Asp Thr Glu Asp Arg Ser Gly Leu Ser Glu Val Val
                               -45                               -40                               -35
gag gca tct tca tta agc tgg agt acc agg ata aaa ggc ttc att gcg      210
Glu Ala Ser Ser Leu Ser Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala
                               -30                               -25                               -20
tgt ttt gct ata gga att ctc tgc tca ctg ctg ggt act gtt ctg ctg      258
Cys Phe Ala Ile Gly Ile Leu Cys Ser Leu Leu Gly Thr Val Leu Leu
                               -15                               -10                               -5
tgg gtg ccc agg aag gga cta cac ctc ttc gca gtg ttt tat acc ttt      306
Trp Val Pro Arg Lys Gly Leu His Leu Phe Ala Val Phe Tyr Thr Phe
1                               5                               10                               15
ggg aat atc gca tca att ggg agt acc atc ttc ctc atg gga cca gtg      354
Gly Asn Ile Ala Ser Ile Gly Ser Thr Ile Phe Leu Met Gly Pro Val
                               20                               25                               30
aaa cag ctg aag cga atg ttt gag cct act cgt ttg att gca act atc      402
Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile
                               35                               40                               45
atg gtg ctg ttg tgt ttt gca ctt acc ctg tgt tct gcc ttt tgg tgg      450
Met Val Leu Leu Cys Phe Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp
                               50                               55                               60
cat aac aag gga ctt gca ctt atc ttc tgc att ttg cag tct ttg gca      498
His Asn Lys Gly Leu Ala Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala
65                               70                               75                               80
ttg acg tgg tac agc ctt tcc ttc ata cca ttt gca agg gat gct gtg      546
Leu Thr Trp Tyr Ser Leu Ser Phe Ile Pro Phe Ala Arg Asp Ala Val
                               85                               90                               95
aaa aad tgt ttt gcc gtg tgt ctt gca taattcatgg ccagttttat      593
Lys Xaa Cys Phe Ala Val Cys Leu Ala
                               100                               105
gaagcttttg aaggcactat ggacagaagc tgggtggacag ttttgtwact atcttcgaaa      653
cctctgtctt acagacatgt gcctttttatc ttgcagcaat gtgttgcttg tgattcgaac      713
atttgagggt tactttttgga agcaacaata cattctcgaa cctgaatgtc agtagcacag      773
gatgagaagt gggttctgta tcttgtggag tggaatcttc ctcatgtacc tgtttcctct      833
ctggatgttg tcccactgaa ttcccatgaa tacaaaccta ttcagcaaca gcaaaaaaaaa      893
aaaaa
                               897

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<210> 247
 <211> 518
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..397

<221> sig_peptide
 <222> 74..127
 <223> Von Heijne matrix
 score 7.69999980926514
 seq LLLLPVLGLLVSS/KT

<221> polyA_signal
 <222> 472..477

<221> polyA_site
 <222> 507..518

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<400> 247
aaagaaagag ctgcsgtgca ggaattcgtg tgccggattt ggtagctga gcccaccgag      60
aggcgcctgc agg atg aaa gct ctc tgt ctc ctc ctc ctc cct gtc ctg      109
              Met Lys Ala Leu Cys Leu Leu Leu Pro Val Leu
              -15                               -10

ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc      157
Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
      -5                               1                               5                               10
aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata      205
Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
              15                               20                               25
agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg      253
Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
              30                               35                               40
gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc      301
Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
              45                               50                               55
gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag      349
Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
              60                               65                               70
tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt cgt gtg cag ccc      397
Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
              75                               80                               85                               90
tgaggctcgcg cgcagcgcgt gcacagcgcg ggcggaggcg gctccaggtc cggagggggtt      457
gcggggggagc tggaaataaa cctggagatg atgatgatga tgatgatgga aaaaaaaaaa      517
a                                                                                   518
  
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<210> 248
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 51..242

<221> sig_peptide
 <222> 51..116
 <223> Von Heijne matrix

score 6.5
seq SCLCPALFPGTSS/FI

<221> polyA_signal
<222> 319..324

<221> polyA_site
<222> 339..350

<400> 248
acgtcattcc aaaaccacac ccttgcaaag ctttgtactc cgcaccccag atg atc 56
Met Ile
tcc agg cag ctg aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc 104
Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro
-20 -15 -10 -5
ggg act tcc tcc ttt att gta gca ctg agc tcc cca gcc gat ctg tac 152
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr
1 5 10
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa 200
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys
15 20 25
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta 242
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
30 35 40
tgattttgct gaatttttaa taaaatgaaa accataaatt acatratgct tttattgach 302
cttgacmact ggcctaaata aaaaractct gactccaaaa aaaaaaaaa 350

<210> 249
<211> 996
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..191

<221> sig_peptide
<222> 111..155
<223> Von Heijne matrix
score 5.80000019073486
seq FLXLMTLTTHVHS/SA

<221> polyA_signal
<222> 965..970

<221> polyA_site
<222> 986..996

<400> 249
atccgataca gaacatgcag taatgtggac tgcccaccag aagcaggtga tttccgagct 60
cagcaatgct cagctcataa tgatgtcaag caccatggcc agttttatga atg ggy 116
Met Gly
-15
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag 164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys
-10 -5 1
cca aat gaa caa ccc tgg ttg ttg aac tagcacctaa ggtcttarat 211
Pro Asn Glu Gln Pro Trp Leu Leu Asn
5 10
ggtacgcgtt gctatacaga atctttggat atgtgcatca gtgggtttatg ccaaattggt 271

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ggctgcgac accagctggg aagcacgcgc aaggaarata actgtgggggt ctgcaacrga 331
natgggtcca cctgccgggt ggtccgaggg cartataaat cccakctctc cgcaacccaaa 391
tcrgatgata ctgtgggtgc aattccctat ggaagtakac atattcgctt tgtcttaaaa 451
ggtcctgata acttatactt ggaarccawa accctccagg ggactaawgg tgaaaacagt 511
ctcasctcca caggaacttt ccttgtggac aattctagtg tggacttcca gaawtttcca 571
gacwdagaga tactgagaat ggctggacca ctacacagcag atttcattgt caawattcgt 631
aactcgggct ccgctgacag tacagtccag kkcattctct atcaacccat catccaccga 691
tggagggara cggatttctt tccttgctca gcaacctgtg gaggagggtta tcagctgaca 751
tcggctgagt gctacgatct gaggagcaac cgtgtgggtg ctgaccaata ctgtcactat 811
taccagaga acatcaaacc caaacccaag cttcaggagt gcaacttgga tccttgtcca 871
gccaggtcag tcaaatttgc tagttcattt gtcataaaca taactcaagt tccaaatagg 931
ttatttaaata taaaatgaaa cgttttaatt aaaaataaaa tgaaattaaa catcaaaaaa 991
aaaaa 996

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<210> 250

<211> 860

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 45..602

<221> sig_peptide

<222> 45..107

<223> Von Heijne matrix

score 8.5

seq LLTIVGLILPTRG/QT

<221> polyA_signal

<222> 828..833

<221> polyA_site

<222> 850..860

<400> 250

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acctctctcc acgaggctgc cggcttagga cccccagctc cgac atg tcg ccc tct 56
                                     Met Ser Pro Ser
                                     -20
ggt cgc ctg tgt ctt ctc acc atc gtt ggc ctg att ctc ccc acc aga 104
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg
-15 -10 -5
gga cag acg ttg aaa gat acc acg tcc agt tct tca gca gac tca act 152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr
1 5 10 15
atc atg gac att cag gtc ccg aca cga gcc cca gat gca gtc tac aca 200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
20 25 30
gaa ctc cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca 248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
35 40 45
cca caa ccc cag acc cag acc cag caa ctg gaa gga acg gat ggg cct 296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
50 55 60
cta gtg aca gat cca gag aca cac wak agc mcc aaa gca gct cat ccc 344
Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys Ala Ala His Pro
65 70 75
act gat gac acc acg acg ctc tct gag aga cca tcc cca agc aca kac 392
Thr Asp Asp Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Xaa
80 85 90 95

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gtc cat dac aga ccb cba kda ccc tca akc cat ctg gtt ttc atg agg      440
Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu Val Phe Met Arg
                               100                               105                               110
atg acc cct tct tct atg atg aac aca ccc tcc gga aac sgg ggc tgt      488
Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly Asn Xaa Gly Cys
                               115                               120                               125
tgg tcg cag ctg tgc tgt tca tca cag gca tca tca tcc tca cca gtg      536
Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser Ser Ser Pro Val
                               130                               135                               140
gca agt gca ggc agc tgt ccc ggt tat gcc gga atc att gca ggt gag      584
Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile Ile Ala Gly Glu
                               145                               150                               155
tcc atc aga aac agg agc tgacaacctg ctgggcaccc gaagaccaag      632
Ser Ile Arg Asn Arg Ser
                               160                               165
ccccctgcc gctcaccgtg cccagcctcc tgcacccct cgaagagcct ggccagagag      692
ggaagacaca gatgatgaag ctggagccag ggctgccggt ccgagtctcc tacctcccccc      752
aaccctgccc gccctgaag gctacctggc gccttggggg ctgtccctca agttatctcc      812
tctgctaaga caaaaagtaa agcactgtgg tctttgcaaa aaaaaaaaaa      860

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<210> 251
 <211> 593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..560

<221> sig_peptide
 <222> 24..101
 <223> Von Heijne matrix
 score 10.3999996185303
 seq LLLLLCGPSQDQC/RP

<221> polyA_signal
 <222> 563..568

<221> polyA_site
 <222> 583..593

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<400> 251
aanccagctg csgccggcca gcc atg gag act gga gcg ctg cgg cgc ccg caa      53
                               Met Glu Thr Gly Ala Leu Arg Arg Pro Gln
                               -25                               -20
ctt ctc ccg ttg ctg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc      101
Leu Leu Pro Leu Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys
                               -15                               -10                               -5
cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc      149
Arg Pro Val Leu Gln Asn Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser
1                               5                               10                               15
ttg gaa gtg ccc act ggg aga gaa gga aag gaa ggt ggg gat cgg gga      197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Asp Arg Gly
                               20                               25                               30
cca ggg cta akt ggg gcc act cca gcc agg agc cct cag ggc aag gag      245
Pro Gly Leu Xaa Gly Ala Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu
                               35                               40                               45
atg ggg aga caa agg acc aga aag gtg aag ggc cct gct tgg akt cac      293
Met Gly Arg Gln Arg Thr Arg Lys Val Lys Gly Pro Ala Trp Xaa His
50                               55                               60

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aca gca aat cag gaa cta aac agg atg agg tct ctg tct tct ggc tcc      341
Thr Ala Asn Gln Glu Leu Asn Arg Met Arg Ser Leu Ser Ser Gly Ser
65                               70                               75                               80
gtg cca gtg ggg cat ctg gag ggt ggc acg gtc aag ctt cag aag gac      389
Val Pro Val Gly His Leu Glu Gly Gly Thr Val Lys Leu Gln Lys Asp
85                               90                               95
acg ggc ctc cat tcc tgc ara gat ggt atg gct tct ctt gaa ggg acg      437
Thr Gly Leu His Ser Cys Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr
100                            105                            110
cca gct tca gtc ctg gct gat gct tgc cca gga ttc cat gat gtg aan      485
Pro Ala Ser Val Leu Ala Asp Ala Cys Pro Gly Phe His Asp Val Xaa
115                            120                            125
gtt car arg gcc cta ttt ggg tta agt ggg ana rta ctg tgg ctg aaa      533
Val Gln Xaa Ala Leu Phe Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys
130                            135                            140
acc cac ttc tgc ctt tct att ana ctt taaataaact ctgaaracct      580
Thr His Phe Cys Leu Ser Ile Xaa Leu
145                            150
gtaaaaaaaaaaaa aaa      593

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<210> 252
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 109..558

<221> sig_peptide
 <222> 109..273
 <223> Von Heijne matrix
 score 3.70000004768372
 seq VAFMLTLPILVCK/VQ

<221> polyA_site
 <222> 1104..1114

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<400> 252
attagctstc caaggtctcc cccagcactg aggagctcgc ctgctgccct cttgcgcgcg      60
ggaagcagca ccaagttcac ggccaacgcc ttggcactag ggtccaga atg gct aca      117
                               Met Ala Thr
                               -55
aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga      165
Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg
-50                               -45                               -40
ctt tgt gat aag gct gaa gct tgg ggc atc gtc cta gaa acg gtg gcc      213
Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu Thr Val Ala
-35                               -30                               -25
aca gcc ggg gtt gtg acc tcg gtg gcc ttc atg ctg act ctc ccg atc      261
Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile
-20                               -15                               -10                               -5
ctc gtc tgc aag gtg cag gac tcc aac agg cga aaa atg ctg cct act      309
Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met Leu Pro Thr
1                               5                               10
cag ttt ctc ttc ctc ctg ggt gtg ttg ggc atc ttt ggc ctc acc ttc      357
Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly Leu Thr Phe
15                               20                               25
gcc ttc atc atc gga ctg gac ggg agc aca ggg ccc aca cgc ttc ttc      405
Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr Arg Phe Phe

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      30              35              40
ctc ttt ggg atc ctc ttt tcc atc tgc ttc tcc tgc ctg ctg gct cat      453
Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His
45              50              55              60
gct gtc agt ctg acc aag ctc gtc cgg ggg agg aaa gcc cct ttc cct      501
Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala Pro Phe Pro
      65              70              75
gtt ggt gat tct ggg tct ggc cgt ggg ctt cag cct agt cca gga tgt      549
Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser Pro Gly Cys
      80              85              90
tat cgc tat tgaatatatt gtccctgacca tgaataggac caacgtcaat      598
Tyr Arg Tyr
      95
gtctttttctg agcttttccgc tctctcgtcgc aatgaaaact ttgtcctcct gctcacctac      658
ktcctctttct tgatggcgct gaccttcctc wtgtcctcct tcaccttctg tggtkccttc      718
acgggctgga avagacatgg ggcccacatc tacctcasga tgctcskctc cattgccatc      778
tgggtggcct ggatcaccct gctcatgctt cctgactttg accgcragggtg ggatgacacc      838
atcmtcarct ccgccttggs trcsaatggc tgggtgttcc tgttggctta tgttagtccc      898
gagttttggc tgctcacaaa gcaackaaac cccatggatt atcctgttga ggatgctttc      958
tgtaaaccctc aactcgtgaa gaagagctat ggtgtggrga acagagccta skctcaagag      1018
gaaatcactc aaggttttga agagacaggg gacacgctct atgcccccta ttccacacat      1078
tttcagctgc agaascagcc tccccaaaaa aaaaaa      1114

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<210> 253

<211> 1182

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..835

<221> sig_peptide

<222> 128..220

<223> Von Heijne matrix

score 4.69999980926514

seq LAVDSWWLDPGHA/AV

<221> polyA_signal

<222> 1145..1150

<221> polyA_site

<222> 1170..1181

<400> 253

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aagaactgcg tctcgcgacc caggcgcgagg ttcccggagg acagccaaca agcgatgctg      60
ccgccgccgt ttcctgattg gttgtgggtg gctacctctt cgttctgatt ggccgctagt      120
gagcaag atg ctg agc aag ggt ctg aag cgg aaa cgg gag gag gag gag      169
      Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
      -30              -25              -20
gag aag gaa cct ctg gca gtc gac tcc tgg tgg cta gat cct ggc cac      217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
      -15              -10              -5
gca gcg gtg gca cag gca ccc ccg gcc gtg gcc tct agc tcc ctc ttt      265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
      1              5              10              15
gac ctc tca gtg ctc aag ctc cac cac agc ctg cag vrr agt rag ccg      313
Asp Leu Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro
      20              25              30
gac ctg cgg cac ctg gtg ctg gtc atr aac act ctg cgg cgc atc cag      361

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Asp Leu Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln
      35              40              45
gcg tcc atg gca ccc gcg gct gcc ctg cca cct gtg cct acc cca cct      409
Ala Ser Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro
      50              55              60
gca gcc ccc ant gtg gct gac aac tta ctg gca agc tcg gac gct gcc      457
Ala Ala Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala
      65              70              75
ctt tca gcc tcc atg gcc arm ctc ctg gar gac ctc agc cac att gag      505
Leu Ser Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu
      80              85              90              95
ggc ctg agt cag gct ccc caa ccc ttg gca gac gag ggg cca cca ggc      553
Gly Leu Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly
      100              105              110
cgt agc atc ggg gga wca ccg ccc amc ctg ggt gcc ttg gac ctg ctg      601
Arg Ser Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu
      115              120              125
ggc cca gcc act ggc tgt cta ctg gac aat ggg ctt gag ggc ctg ttt      649
Gly Pro Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe
      130              135              140
gag gat att gac acc tct atg tat gac aat gaa ctt tgg gca cca gcc      697
Glu Asp Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala
      145              150              155
tct gag ggc ctc aaa cca ggc cct gag gat ggg ccg ggc aag gag gaa      745
Ser Glu Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu
      160              165              170              175
gct ccg gag ctg gac gag gcc gaa ttg gac tac ctc atg gat gtg ctg      793
Ala Pro Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu
      180              185              190
gtg ggc aca cag gca ctg gag cga ccg ccg ggg cca ggg cgc      835
Val Gly Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
      195              200              205
tgagccctcg tgctggaatg gttgtctggt atctgaactg agcctgctgg ctggaccaac      895
tgctcctcgaa aagacacagc tggcttccct agtacagaga acagggcttg ggccactttg      955
gagagacaga atctagtctt gggcaacttc acatccgtcc tcctgtctca gggctggcag      1015
ggggagcctg gaattacccc ctagtgatgg aatgacaggg tctggtgggg actgaattcc      1075
ctggccctgg ggtcatagct tgggctgttc cttctctgat acgggaagag acccaatcag      1135
atttttcaaaa ttaaagccag tctgggaaaa tctcaaaaaa aaaaaaac      1182

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<210> 254

<211> 1073

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..505

<221> sig_peptide

<222> 59..358

<223> Von Heijne matrix

score 3.70000004768372

seq LASSFLFTMGGLG/FI

<221> polyA_signal

<222> 1042..1047

<221> polyA_site

<222> 1062..1073

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<400> 254
actgttttng ggagggcggt ggggcttgag gccgagaacg gcccttgctg ccaccaac      58
atg gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac      106
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100                               -95                               -90                               -85
ctg aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act      154
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80                               -75                               -70
gtg tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata      202
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65                               -60                               -55
att tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat      250
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50                               -45                               -40
gaa cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat      298
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35                               -30                               -25
gga caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg      346
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20                               -15                               -10                               -5
gga ggt tta ggt ttc ata atc ctg gac gga tcg aat gca cca aat atc      394
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
1                               5                               10
cca aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc      442
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
15                               20                               25
cta twr agt ttt tkc ayg gct aga gta ttc atg aga atg aaa ctg ccg      490
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
30                               35                               40
ggc tat ctg atg ggt tagagtgcct ttgasaagaa atcagtggat actggatttg      545
Gly Tyr Leu Met Gly
45
ctcctgtcaa wgaastttta aaggctgtmc caatcctcta atatgaaatg tggaaaagaa      605
tgaagagcag cagtaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga      665
ctagaatttc ttcttggtat taaagagaca agtttatcac agaatttttt ttcttgctgg      725
cctattgcta taccaatgat gttgagtggc attttctttt tagtttttca ttaaaatata      785
ttccatatct acaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat      845
tttttgagaga tgacattttct gatttttcaga aattaacata aaatccagaa gcaagattcc      905
gtaagctgag aactctggac agttgatcag ctttacctat ggtgctttgc ctttaactag      965
agtgtgtgat ggtagattat ttcagatatg tatgtaaaac tgtttcctga acaataagat      1025
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<210> 255

<211> 818

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..207

<221> sig_peptide

<222> 1..147

<223> Von Heijne matrix

score 7.59999990463257

seq HLPFLLLLSCVGX/XP

<221> polyA_signal

<222> 784..789

<221> polyA_site
<222> 807..818

<400> 255
atg cct ttc cat ttt ccg ttc ctt ggg ttt gtg tgt ctg cat ctc cat 48
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
-45 -40 -35
ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg 96
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
-30 -25 -20
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg 144
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
-15 -10 -5
gkc www ccc tcc tgt ctg cct tct tcc tcc act tgt gtc agc ttg cat 192
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
1 5 10 15
ttt ttt att cct gac tgagtcacca caccctctc ccctgatcaa agggaatatk 247
Phe Phe Ile Pro Asp
20
artttttaat ttggatcgac tgagggtgccca ggagaaactg cagkcccagg tatccmvaca 307
gccaccagga tggccctctg cccaccccc accgcctctk cccaccttt tccaacgtgt 367
tgcatgctgg gaactggggg gtgtggggga aggggctgcc ggcttctttc aggangctga 427
rgtttggar caaaatcaac ctgggaracc accccggccg cggcgccctca gtggacaggt 487
gggargaaaa gaaaacttct taccttggar garggacatc ccgcttctt atccttagct 547
tttttgttgc tctccccac tgcccctttt aatttatattg gttgtttgcg gaaggagggg 607
ggaagggggg aagctggggc gggaactgtc cgaggtgctg agctggggcg ggaccggaat 667
cctcccggta gggtaccagg gactgagttg ggccctggggc cgtgtccaag gtgccaatga 727
tgccgggccga cagarcgggc cgcactgtct gtctgtccgt ctgtcccga aagaactata 787
aagcgctgga agcgcctgca aaaaaaaaaa a 818

<210> 256
<211> 971
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..734

<221> sig_peptide
<222> 12..101
<223> Von Heijne matrix
score 4.80000019073486
seq ILFCVGAVGACTL/SV

<221> polyA_signal
<222> 914..919

<221> polyA_site
<222> 961..971

<400> 256
aatacacaga a atg ggg act gcg agc aga agc aac atc gct cgc cat ctg 50
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu
-30 -25 -20
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act 98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr
-15 -10 -5
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag 146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu

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      1           5           10           15
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag      194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu
      20           25           30
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac      242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn
      35           40           45
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg      290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg
      50           55           60
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act      338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr
      65           70           75
tca aat gac agt gca att tac atc tgt gga ata gca ttc ccc agt gtg      386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val
      80           85           90           95
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta      434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val
      100           105           110
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct      482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala
      115           120           125
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc      530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe
      130           135           140
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata      578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile
      145           150           155
aaa gaa gac tca caa aag aag aag agt gct cgg cgt att ttt cag gaa      626
Lys Glu Asp Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu
      160           165           170           175
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa      674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln
      180           185           190
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac      722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn
      195           200           205
tat gaa agg cca tagaaacggt ttaattttca atgaagtcac tgaaaatcca      774
Tyr Glu Arg Pro
      210
actccaggag ctatggcagt gttaatgaac atatatcacc aggtctttaa aaaaaataaa      834
ggtaaaactga aaagacaact ggctacaaag aaggatgccaa raatgtaagg aaactataac      894
taataktcat taccaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa      954
tttgccaaaa aaaaaaw                                         971

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<210> 257

<211> 640

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 378..518

<221> sig_peptide

<222> 378..467

<223> Von Heijne matrix

score 5.5

seq SLMTCTTLINASA/IS

Thr	Arg	Val	Glu	Ser	Glu	Lys	Cys	Asn	Asn	Leu	Trp	Leu	Phe	Leu	Glu		
		10					15					20					
acc	gga	cag	ctc	ccc	aaa	gac	agg	agc	aca	gat	cag	ara	agc				304
Thr	Gly	Gln	Leu	Pro	Lys	Asp	Arg	Ser	Thr	Asp	Gln	Xaa	Ser				
		25				30					35						
taggagagct	ccagcagggg	cacagargat	tgggggcagg	argartctgg	aacacakcct												364
tcatgcccc	tgaccccagg	cgcacctcc	ccacacccta	gggtaccca	gtcgtatcct												424
ctgtccgcat	gtgtggccag	gcctgacaaa	cmctgcaga	tggctgctgc	cccaacctgg												484
gacctgcca	ggaggttgga	gcagaaaggg	ctctccctgg	ggtggtgttt	ctcctctagg												544
gtattgggat	gcatgttctg	cactgccagc	agagaggggtg	tgtctggggg	ccaccaccta												604
tgggacacgg	ggtcgaaggg	gcctgtacac	tctgtcattt	cctttctagc	ccctgcatct												664
ccaacaagtc	caaggtgaca	gctggtgcta	ggggcggtggg	gttaataaat	ggcttatcct												724
tctctccaaa	araaaaaaam	c															745

<210> 259

<211> 637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 201..419

<221> sig_peptide

<222> 201..272

<223> Von Heijne matrix

score 6.40000009536743

seq LSYLPLWLGPiWP/CS

<221> polyA_signal

<222> 601..606

<221> polyA_site

<222> 627..637

<400> 259

acaaaatata	attgcctcts	ccctctccca	ttttctctct	tgggagcaat	ggtcacagtc												60
cctggtagct	gaaaaggtac	ctaggtctag	gcccttcttc	cctttccctt	cctctcccct												120
accccagaac	tttggctccc	tttcccttct	ctctctggta	gctccaggag	gcctgtgatc												180
cagctccctg	cctagcatcc	atg acc	tgt tgg	atg tta	cct cca	atc agt	ttc										233
		Met Thr	Cys Trp	Met Leu	Pro Pro	Ile Ser	Phe										
				-20			-15										
ctg tcc	tac ctg	cct ctt	tgg ctt	gga cct	ata tgg	cca tgc	tct ggc										281
Leu Ser	Tyr Leu	Pro Leu	Trp Leu	Gly Pro	Ile Trp	Pro Cys	Ser Gly										
		-10			-5		1										
tct acc	ctt ggg	aag cct	gat ccc	ggt gtg	tgg ccc	agc ttg	ttc agg										329
Ser Thr	Leu Gly	Lys Pro	Asp Pro	Gly Val	Trp Pro	Ser Leu	Phe Arg										
	5		10		15												
ccc tgg	gat gct	gca tct	cca ggc	aac tat	gca ctt	tcc cgg	gga rar										377
Pro Trp	Asp Ala	Ala Ser	Pro Gly	Asn Tyr	Ala Leu	Ser Arg	Gly Xaa										
	20		25		30		35										
aac cak	tat gav	aak tgg	ggg cag	ggc aca	cat tca	tct ttg											419
Asn Xaa	Tyr Xaa	Xaa Trp	Gly Gln	Gly Thr	His Ser	Ser Ser	Leu										
		40		45													
targaaggtc	tggcctgggg	tcrggtgaag	gagggcccag	gtcagttctg	gggtcccagt												479
gacctgcttt	gccattctcc	tgggtgccgt	gctgctccct	gtttctggag	ctggatgttc												539
cccacctggc	agttgagctg	cctgagccaa	tgtgtctgtc	tttggttaact	gagtgaaacca												599
taataaaggg	gaacatttgg	ccctgtgaaa	aaaaaaaa														637

<210> 260
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 123..302

<221> sig_peptide
 <222> 123..176
 <223> Von Heijne matrix
 score 4.30000019073486
 seq WTCLKSFPSPTSS/HA

<221> polyA_signal
 <222> 1279..1284

<221> polyA_site
 <222> 1301..1312

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<400> 260
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cgccgcagag ccagtgcaga atacagaaac tgcagccatg accacgcacg tcaccctgga      120
ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg      167
    Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro
          -15                      -10                      -5
acc agc agc cat gca tcg agc ctc cac ctt cct cca tca tgt acc agg      215
Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg
          1                      5                      10
cta act ttg aca caa act ttg agg aca gga atg cat ttg tca cgg gca      263
Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala
          15                      20                      25
ttg caa ggt aca ttg acc agg cta cag tcc act cca gca tgaatgarat      312
Leu Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
          30                      35                      40
gctggaggaa ggacatgakt atgcggtcat gctgtacacc tggcgcagct gttccccgggc      372
cattccccag gtgaaatgca acragcagcc caaccgakta raratctatg araaracagt      432
aragggtgctg gagccggagg tcaccaagct catgaagttc atgtattttc arcgcaaggc      492
catcgagcgg ttctgcascg aggtgaagcg gctgtgccat gccgagcgca ggaaggactt      552
tgtctctgag gcctacctcc tgacccttgg caagttcac aacatgtttg ctgtcctgga      612
tgagctaaag aacatgaast gcagcgtcaa raatgaccac tctgcctaca agagggcagc      672
acagttcctg cggaagatgg cagatcccca gtctatccag gagtgcgaga acctttccat      732
gttcctggcc aaccacaaca ggatcaccca gtgtctccac cagcaacttg aagtgatccc      792
aggctatgag gagctgctgg ctgacattgt caacatctgt gtggattact acgagaacaa      852
gatgtacctg actcccagtg agaaacatat gtcctcaag gtaaaactcc cctgaggccg      912
cacccatgga gcctgggctt accctctcac cttcttctta ttaaaaatcc gttttaaaaa      972
acaatgtttc ttttttctta aacattgata cagatcttac ggcacataat gggttgtaac     1032
ctgttccttt cctgtaatat aatataccgt agtcaccttt ccagatgtca ttaaggctat     1092
ttctacaatg ttatgtgtaa tgactgccaa gtattctgtt gtattggaac attgtcatgt     1152
aacatatccc ctgtggttgg atatttgcta aacttcattg aacacccttg tagcagtttt     1212
tgtgcacatc tttttgtcaa ggcaaacttc ctagaagaga aattgctggc tcaaagggaa     1272
aaacagaata aatcgttttt tttatttcaa aaaaaaaaaa ccc                        1315

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<210> 261
 <211> 1035
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 98..673

<221> sig_peptide

<222> 98..376

<223> Von Heijne matrix

score 5.59999990463257

seq VLLLRQLFAQAEK/WY

<221> polyA_site

<222> 1025..1035

<400> 261

aattttcygt ggtccaacta ccctcggcga tcccaggctt ggcggggcac cgcctggcct 60
 ctcccgttcc tttaggctgc cgccgtgcc tgccgcc atg gca gag ttg ggc cta 115
 Met Ala Glu Leu Gly Leu
 -90

aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt 163
 Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg
 -85 -80 -75

tca aag aga ggc ttg aga ctc aaa act gta gat tcc tgc ttc caa gac 211
 Ser Lys Arg Gly Leu Arg Leu Lys Thr Val Asp Ser Cys Phe Gln Asp
 -70 -65 -60

ctc aag gag agc agg ctg gtg gag gac acc ttc acc ata gat gaa gtc 259
 Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val
 -55 -50 -45 -40

tct gaa gtc ctc aat gga tta caa gct gtg gtt cat agt gag gtg gaa 307
 Ser Glu Val Leu Asn Gly Leu Gln Ala Val Val His Ser Glu Val Glu
 -35 -30 -25

tct gag ctc atc aac act gcc tat acc aat gtg tta ctt ctg cga cag 355
 Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn Val Leu Leu Leu Arg Gln
 -20 -15 -10

ctg ttt gca caa gct gag aag tgg tat ctt aag cta cag aca gac atc 403
 Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu Lys Leu Gln Thr Asp Ile
 -5 1 5

tct gaa ctt gaa aac cga gaa tta tta gaa caa ktt gca gaa ttt gaa 451
 Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu Gln Xaa Ala Glu Phe Glu
 10 15 20 25

aaa gca rav att aca tct tca aac aaa aag ccc atc tta dat gtc aca 499
 Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys Pro Ile Leu Xaa Val Thr
 30 35 40

aas cca aaa ctt gct cca ctt aat gaa ggt gga aca gca aaa ctc cta 547
 Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly Gly Thr Ala Lys Leu Leu
 45 50 55

aac aag gta ata tgt att att ttg aga aac gga aag tct ctc att ctg 595
 Asn Lys Val Ile Cys Ile Ile Leu Arg Asn Gly Lys Ser Leu Ile Leu
 60 65 70

tcc tgt cat tgc cta ggg tgg aga aac aaa agt gga agg ttt gtt tca 643
 Ser Cys His Cys Leu Gly Trp Arg Asn Lys Ser Gly Arg Phe Val Ser
 75 80 85

ggt cct ctg agg ata att agt cca ttg cag tagttttact tgatgggtacc 693
 Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
 90 95

ccatggggcca gaagagggca tacttaacct tctagagagc ctgaagtagc tcttgatcac 753

acctttttcaa ggtaaagtga agagcatgaa atttttggaca gcgtttattg atggacattt 813

aaagttttgtg atctgcggtg acaaggagaa ggggttttttaa gtttataaaa attattttatc 873

aattagccgg gtgtgggtgt acgtgcctat agtcagagct actcgggagg ctgaggcagg 933

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tagcctgggc gacagagcga gactccatct caaaaaaaaa aa 1035

<210> 262
 <211> 696
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..463

<221> sig_peptide
 <222> 17..232
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LMGLALAVYKCQS/MG

<221> polyA_signal
 <222> 657..662

<221> polyA_site
 <222> 684..696

<400> 262
 actcaaacag attccc atg aat ctc ttc atc atg tac atg gca ggc aat act 52
 Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr
 -70 -65
 atc tcc atc ttc cct act atg atg gtg tgt atg atg gcc tgg cga ccc 100
 Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro
 -60 -55 -50 -45
 att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt 148
 Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser
 -40 -35 -30
 tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg 196
 Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu
 -25 -20 -15
 atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta 244
 Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu
 -10 -5 1
 cct aca cat gca tcg gat tgg tta gcc ttc att gag ccc cct gag aga 292
 Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
 5 10 15 20
 atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg 340
 Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
 25 30 35
 cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca 388
 Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
 40 45 50
 gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac 436
 Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn
 55 60 65
 caa aaa act ctt ttc tcc atg gtg ggg tgacaggtcc taaaaggaca 483
 Gln Lys Thr Leu Phe Ser Met Val Gly
 70 75
 atgtgcatat tacgacaaac acaaaaaaaaaac tataccataa cccagggttg aaaataatgt 543
 aaaaaacttt atttttgttt ccagtagaca gcaaaacaac acaaaaaaaaa cataactatg 603
 taaacaaaaa aataactgct gctaaatcaa aaactgttgc agcatctcct ttcaataaat 663
 taaatggttg araacaatgc aaaaaaaaaaa aaa 696

<210> 263
 <211> 868

<212> DNA
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<220>
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<222> 263..481

<221> sig_peptide
<222> 263..322
<223> Von Heijne matrix
score 11.1999998092651
seq ILVVLMGLPLAQA/LD

<221> polyA_site
<222> 858..868

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caggagctcc gggaggcagg gccggcccca cgctctctgc gcaccaccct gagttggatc      180
ctctgtgcgc caccctgag ttggatccag ggctagctgc tgttgacctc cccactccca      240
cgctgccctc ctgcctgcag cc atg acg ccc ctg ctc acc ctg atc ctg gtg      292
                Met Thr Pro Leu Leu Thr Leu Ile Leu Val
                -20                               -15
gtc ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt      340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10                -5                1                5
gcc tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg      388
Ala Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met
                10                15                20
gtt gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg      436
Val Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met
                25                30                35
aag gtc agt aag tcc tgc gtg ccc cgc tgc ttc gar nac tgt gta      481
Lys Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Xaa Cys Val
                40                45                50
tgatgggtac tccaagcacg cgtccaccac ctctgtctgc cagtacgacc tctgcaacgg      541
cacgggcctt gccaccccg ccaccctggc cctggccccc atcctccttg ccaccctctg      601
gggtctcttc taaagccccc gaggcagacc cactcaagaa caaagctctc gagacacact      661
gctayacctt ckcaccckac tcaccctgcc tcaccctcca cactccctgc gacctctca      721
gccatgcccc gggtcaggac tgtgggcaag aagacaccgg acctcccca accaccacac      781
gacctcactt cgaggccttg acctttcgat gctgtgtggg atcccaaaaag tgtccggctt      841
tgatgggctg atcagcaaaa aaaaaaa      868

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<210> 264
<211> 775
<212> DNA
<213> Homo sapiens

<220>
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<222> 42..299

<221> sig_peptide
<222> 42..101
<223> Von Heijne matrix
score 5.40000009536743
seq WFFVHSSALGLVLA/PP

<221> polyA_site

<222> 762..775

<400> 264

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                                     Met Asn Leu His Phe
                                     -20
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca      104
Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro
-15          -10          -5          1
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt      152
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys
          5          10          15
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc      200
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr
          20          25          30
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa      248
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys
          35          40          45
aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cgg      296
Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg
50          55          60          65
cag tgaaactwkk ttcwcttcta aagcccttca tttcccacaa ggttaagctc      349
Gln
tcgaaacccc atttgatcct tggttcctat ttcgatccctc ctttggaatc tgaaaatcgg      409
tctccatggt gtatgcaa ataaaakttgc cttgtttgtt actcttccaa cacaggggtat      469
cagggaraaa gaggccttat ctgttcctcc atccccctg ttttgacaga ctgctaagaa      529
ttcctcagga cttccttttg ttggggattt tactttccca aaagtctgat ctgatttctt      589
tcaggggtag acaagcttgt cctagtgtct tgcttcaggt cttatcagaa gaaacccagg      649
aatagaaaag gtatagtcct tgacttttgt ccctgttgtg gggactaaag tgttttttgc      709
cagaattgtc aaaagctccg gttcaaacctc tgtagagttt catggaaaaa caaaacaaaa      769
aaaaaa      775

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<210> 265

<211> 1075

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 198..431

<221> sig_peptide

<222> 198..260

<223> Von Heijne matrix

score 6.90000009536743

seq LLACGSLLPGLWQ/HL

<221> polyA_site

<222> 1064..1074

<400> 265

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atatatttct gaggcagtac ccattctcact tgtaaacctta aaagacaccg cagagatttg      60
agggactcag aagtcaaata gagtaggtta aaaacctctt atttttcaaa ttaattgttt      120
taagaaaacaa gcatacctgt gtaagtgaata tatcttaatt tgtgttgaat caagtttagga      180
gacagagatt ctcatga atg tgt cct gtg ttc tca aag cag ctg cta gcc      230
                                     Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala
                                     -20          -15
tgt ggg tct ctc cta cct ggg tta tgg cag cac ctc aca gcc aat cac      278
Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His
-10          -5          1          5

```

```

tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca      326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
          10                      15                      20
gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt      374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg
          25                      30                      35
tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac      422
Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr
          40                      45                      50
tct atc acc tagccattgt akccatacca agccgggctt cctacttccc      471
Ser Ile Thr
55
tctgctcccc ttggtttcct cctgtraart aaatctcact gacccttgat gcasctccaa      531
gcatatataa tatatatata ataaaacccat abtctaaaaa attcaaacca ggawaaataa      591
asccaraaat ttgtatggga aaaatctgca caaatttatt tggccagcat gggtatcatg      651
gctctattga atttatcctt gaccgtcttt aaagccaaag caaacgggat aaagtgatca      711
actacttacc tctcaatacc aaaaargaag caggaggcaa aatctctcaw taatttcata      771
aaaacaattc ttakctgggc gcggtggctc wcacctgtar tcccaacact ttgggaggcc      831
saggtgggag gatcatgagg tcgggagatc aamaccatcc tggctaacad ggtgaaaccc      891
catctctact aaaattacaa aaaattrgct gggcgagggtg gcgggcacct gtggtcccag      951
ctactcggga ggctgaggca agagaatggt gtgaacccca gggggcggag cctgcagtga     1011
gctgagatcg caccactgca ctccagcctg ggcgacagtg agactccgtc tcaaaaaaaaa     1071
aaah                                                                    1075

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<210> 266

<211> 981

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 279..473

<221> sig_peptide

<222> 279..362

<223> Von Heijne matrix

score 4.40000009536743

seq SCFLVALIIWCYL/RE

<221> polyA_signal

<222> 944..949

<221> polyA_site

<222> 970..981

<400> 266

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agaatcgtgt cttgtgtgcc ccggcgggccc ggtgagctcc tcaaggtctc ggagggccga      60
gggcagacac cggcggggcgg gcggasgctt actgctctct ctcttccagg gccgtccggg      120
cgctgagggt cataggctgg gcttcccga gacctcatcc gttgcccggg tcccgggatc      180
gggcccaccc tgccgccgag gaagaggacg accctgaccg cccattgag ttttctccca      240
gcaaagccaa cctcaccgc tggtcggtgg gccatacc atg gga aag gga cat cag      296
                               Met Gly Lys Lys Gly His Gln
                               -25
cgg ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg      344
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu
          -20                      -15                      -10
atc atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg      392
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu
          -5                      1                      5                      10
aga cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag      440

```

Arg	Gln	Val	Trp	Gly	Glu	Val	Pro	Glu	Pro	Ser	Asp	Arg	Ser	Glu	Glu	
				15					20					25		
cct	gag	act	cca	gct	gcc	tac	aga	gcg	aga	act	tgacgggggtg	cccgtg	gggg			493
Pro	Glu	Thr	Pro	Ala	Ala	Tyr	Arg	Ala	Arg	Thr						
			30					35								
ctggcaggaa	gggagccgac	asccgcccctt	cggatttgat	ktcacgtttg	cccgtgactg											553
tccctggctat	gcktgcgctcc	tcagcactra	argacttggc	tggtggatgg	ggcacttggc											613
tatgctgatt	cgcgtagaagg	cggavcaaaa	tctcagcaaa	tcggaaactg	ctcctcscct											673
ggctccttgat	ktccaaggat	tccatcgga	aaacttctca	ratccttggg	gaaggtttca											733
gttgactgt	atgctgttgg	atttgccaag	tctttgtata	acataatcat	gtttccaaag											793
cacttctggt	gacacttgtc	atccagtgtt	agtttgcagg	taatttgctt	tctgagatag											853
aatatctggc	agaagtgtga	aactgtattg	catgctgcgg	cctgtgcaag	gaacacttcc											913
acatgtgagt	tttacacaac	aacaaatgaa	aataaatttt	aattttataa	tatgggaaaa											973
aaaaaaaa																981

<210> 267

<211> 1031

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..644

<221> sig_peptide

<222> 12..92

<223> Von Heijne matrix

score 4

seq LTFFSGVYGTICIG/AT

<221> polyA_signal

<222> 1002..1007

<221> polyA_site

<222> 1020..1031

<400> 267

acaccaagga	g	atg	ctc	ctt	ctt	agt	att	aca	act	gct	tat	aca	ggg	ctg		50
	Met	Leu	Leu	Leu	Ser	Ile	Thr	Thr	Ala	Tyr	Thr	Gly	Leu			
			-25				-20					-15				
gaa	tta	act	ttc	ttc	tct	ggg	gta	tat	gga	acc	tgt	att	ggg	gct	aca	98
Glu	Leu	Thr	Phe	Phe	Ser	Gly	Val	Tyr	Gly	Thr	Cys	Ile	Gly	Ala	Thr	
			-10				-5					1				
aat	aaa	ttt	gga	gca	gaa	gag	ara	agc	ctt	att	gga	ctt	tct	ggc	att	146
Asn	Lys	Phe	Gly	Ala	Glu	Glu	Xaa	Ser	Leu	Ile	Gly	Leu	Ser	Gly	Ile	
	5					10					15					
ttc	atc	ggc	att	gga	gaa	att	tta	ggg	gga	agc	ctc	ttc	ggc	ctg	ctg	194
Phe	Ile	Gly	Ile	Gly	Glu	Ile	Leu	Gly	Gly	Ser	Leu	Phe	Gly	Leu	Leu	
	20				25				30							
agc	aag	aac	aat	cgt	ttt	ggg	aga	aat	cca	ggt	gtg	ctg	ttg	ggc	atc	242
Ser	Lys	Asn	Asn	Arg	Phe	Gly	Arg	Asn	Pro	Val	Val	Leu	Leu	Gly	Ile	
	35			40				45				50				
ctg	gtg	cac	ttc	ata	gct	ttt	tat	cta	ata	ttt	ctc	aac	atg	cct	gga	290
Leu	Val	His	Phe	Ile	Ala	Phe	Tyr	Leu	Ile	Phe	Leu	Asn	Met	Pro	Gly	
			55				60				65					
gat	gcc	ccg	att	gct	cct	gtt	aaa	gga	act	gac	agc	agt	gct	tac	atc	338
Asp	Ala	Pro	Ile	Ala	Pro	Val	Lys	Gly	Thr	Asp	Ser	Ser	Ala	Tyr	Ile	
			70				75					80				
aaa	tcc	agc	aaa	raa	ttt	gcc	att	ctc	tgc	akt	ttt	ctg	tkg	ggc	ctt	386
Lys	Ser	Ser	Lys	Xaa	Phe	Ala	Ile	Leu	Cys	Xaa	Phe	Leu	Xaa	Gly	Leu	

85	90	95	
gga aac agc tgc ttt aat acc cas ctg ctt akt atc tkg ggc ttt ctg			434
Gly Asn Ser Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu			
100	105	110	
tat tct gaa rac agc gcc cca kca ttt gcc atc ttc aat ttt gtt cag			482
Tyr Ser Glu Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln			
115	120	125	130
tct att tgc gca gcc gtg gca ttt ttc tac agc aac tac ctt ctc ctt			530
Ser Ile Cys Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu			
	135	140	145
cac tgg caa ctc ctg gtc atg gtk atw ttt ggg ttt ttk gga aca att			578
His Trp Gln Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile			
	150	155	160
tct ttc ttc act gtg gaa tgg gaa sct gcc gcc ttt gta scc cgc ggc			626
Ser Phe Phe Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly			
	165	170	175
tct gac tac cga agt atc tgatctgggtg tccgtgaggg gacacgtatg			674
Ser Asp Tyr Arg Ser Ile			
180			
acctcagaaaa cacagctgga cacagagctt ggtggaagaa gtcgcctttg atcttcacta			734
tatattgggt gatgttcagt atggaaaatc aagggattaa gactgttaaa tcagccagag			794
tkggtgttca agtttacaga tatgagttat ttaaagcaag tagaataagg gaaagctgtt			854
ctgtcaactg taattgttca aagatgttgt ttttcatttc atctatctca attcttataa			914
tcatgttata gaatgtaaat gttttcttct ctctcctgct cttgttgga gacccctgcct			974
tgatttagaa tactaggcca tatgtcatat aaatatTTTT tctggaaaaa aaaaaaa			1031

<210> 268

<211> 1283

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 91..459

<221> sig_peptide

<222> 91..330

<223> Von Heijne matrix

score 7.69999980926514

seq LVLFLSLALLVTP/TS

<221> polyA_site

<222> 1271..1281

<400> 268

tattccttgg agttccacga ctgaattaag actgttgggg grdcccataat tttcaaatac 60

ttgccctata ttcgtgttga gggttcacac atg agc aca tgg tat ttg gca ctt 114

Met Ser Thr Trp Tyr Leu Ala Leu

-80 -75

aat aag tcc tat aag aat aaa gac agc gtt agg att tat ctc agc ttg 162

Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu

-70 -65 -60

tgc aca gtg agc att aaa ttt aca tac ttt cat gat ata cag act aat 210

Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn

-55 -50 -45

tgt ctt aca aca tgg aaa cat tgc aga tgc aga ttt tat tgg gca ttt 258

Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe

-40 -35 -30 -25

ggg ggt tcc att tta cag cac tca gtg gat ccc ctt gtt ttg ttc cta 306

Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Leu Phe Leu

```

          -20          -15          -10
agc ctg gcc ctg tta gtg aca ccc act tcc acc cct tct gct aar ata 354
Ser Leu Ala Leu Leu Val Thr Pro Thr Ser Thr Pro Ser Ala Lys Ile
          -5          1          5
car agc ctt caa att gac ctc cct gga ggc tgg agg ctg gcc act gac 402
Gln Ser Leu Gln Ile Asp Leu Pro Gly Gly Trp Arg Leu Ala Thr Asp
          10          15          20
agg atc ttt acc ctc tcc ccc gta ccc atg gac rgc ccc ctc atc ctt 450
Arg Ile Phe Thr Leu Ser Pro Val Pro Met Asp Xaa Pro Leu Ile Leu
          25          30          35          40
cat cag ttg taaaggtaga tatttgttcc ttggagtcca acatcatgct 499
His Gln Leu
gttcagaata taatgagatc aatagttgaa aaactagata tacatgccac ccwgacaaaag 559
ctattaagtt attaagtgtc agccctggat cttggcttat tgtgaaatgt taattatttt 619
atcactcyat taagaagctg tgggctccat ctcagcattg aaaagggact aatttgctct 679
gttttggaaat tgaattagct ttcaggccas cagggcactg tttggtaaata tgctttttcc 739
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gagggcagat catgaggtca ggagattgar accatcctgg ctaacacggt gaaaccccg 1099
ctctactaaa aatacaaaar aattakccgg gcatggtagt gggcgctgt gtaccagct 1159
actggggagg ctgaggcarg araatcgctt gaacctggga ggcggagggt gcastragct 1219
gagatggtgc caccgcactc tagcctgggt gacagagcga gacttcattt caaaaaaaaaa 1279
aamc 1283

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<210> 269
 <211> 1777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..327

<221> sig_peptide
 <222> 70..147
 <223> Von Heijne matrix
 score 9.60000038146973
 seq WLIALASWSWALC/RI

<221> polyA_signal
 <222> 1741..1746

<221> polyA_site
 <222> 1763..1774

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<400> 269
agccccggttt cgtgcccgcg gccgactgcg casctgtccg cgagtctgag atacttacag 60
agagctaca atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg 111
          Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp
          -25          -20          -15
cta ata gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt 159
Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu
          -10          -5          1
tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt 207
Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu
          5          10          15          20
ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat 255

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Leu Leu Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp
      25              30              35
gta ttg ctt tat ttt ccw kaa cag yya tcc tct tca cgt ctt tat gat      303
Val Leu Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp
      40              45              50
tcc cat gcc cac tgg cmt tgc rca taaaaaaatt ttcattcagaa ccaaagatgg      357
Ser His Ala His Trp Xaa Ser Xaa
      55              60
aatacgtctg aatcttattt tgatacgata cactggagac aattcacctt attccccaac      417
tataatttat tttcatggga atgcaggcaa cataggtcac aggttggcca aatgcattac      477
ttatgttggg taacctcaaa gtaaaccttt tgctgggtga ttatcgagga tatggaaaaa      537
gtgaaggaga agcaagtga gaaggactct acttagattc tgaagctgtg ttagactacg      597
tgatgactag acctgacctt gataaaaaca aaatttttct ttttggccgt tcttgggtg      657
garcagtggc tattcatttg gcttctgaaa attcacatag gatttcagcc attatgggtg      717
agaacacatt ttaagcata ccacatatgg ccagcacttt attttcattc tttccgatgc      777
gttaccttcc tttatgggtg tacaaaaata aatttttgtc ctacagaaaa atctctcagt      837
gtagaatgcc ttcacttttc atctctggac tctcagatca attaatcca ccagtaatga      897
tgaaacaact ttatgaactc tccccatctc ggactaagan attagccatt tttccagatg      957
ggactcacia tgacacatgg cagtgccaa gctatttcac tgcacttgaa cagttcatca      1017
aagaagtcgt aaagagccat tctcctgaag aaatggcaaa aacttcattc aatgtaacaa      1077
ttatataatg tttccctttt tgattattgc attgtatttt aatttgtgca gaatgataaa      1137
gaatgttcct tttagaagtg tgttatgtct gtacctgtct gaagagtgc attaaacttt      1197
gaaaggactt cactgctcct ttacgatatt ccaaatagtt ttttacattg gaaaaactaa      1257
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ttcagtttaa tatgtcagta taatagatat tgttcaaaag tttcttggtg ctaaagtggg      1377
gtaactctgt acacagatga atagctagat gtggaaagag atatgtaaac aagaaacctt      1437
tgggtattgt ttcttaagta aatattggga caatcatggt aagcaaactt agttctgtaa      1497
ctgcattttt caccttaaaa gttaaatgaa atgcatgatg gtattttatt ccttgaatta      1557
tgcaatgcaa cattttacat gtaaatagca ctgggtcatat actgatgtat atggttatct      1617
gggttatatc tatttttatg taaactctat ttttgttttt ggcaagaagt gaaattgaga      1677
cttatgtgca ggttgccatt gaattttgct ctgggtgaatg ctgagatcca gctttttctt      1737
acaaataaat gggaccctgt tttccaaaaa aaaaaamcm      1777

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<210> 270
 <211> 970
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..497

 <221> sig_peptide
 <222> 12..104
 <223> Von Heijne matrix
 score 5.5
 seq LVGVLWFVSVTTG/PW

<221> polyA_signal
 <222> 935..940

<221> polyA_site
 <222> 955..967

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<400> 270
aggtctccaa g atg gcg gcc gcc tgg ccg tct ggt ccg ket gct ccg gag      50
      Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
      -30              -25              -20
gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act      98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr

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-15          -10          -5
aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg      146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
      1          5          10
ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca      194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
      15          20          25          30
aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca      242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
      35          40          45
gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc      290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser
      50          55          60
agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
      65          70          75
ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tcg      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser
      80          85          90
cat gtc tct ttt tct tgg atg gtt ggg agc aga tcg att tta cct tgg      434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
      95          100          105          110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg      482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp
      115          120          125
aat tgg gag cct aat tgatttcaty cttatttcaa tgcagattgt tggaccttca      537
Asn Trp Glu Pro Asn
      130
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact      597
aatgaaacat ttagaaaaac gcaattatat ccataaatat tttttaaaag aaacagattt      657
gagcctcctt gattttaata gagaacttct agtgtatgga tttaaagatt tctctttttc      717
attcatatac cattttatga gttctgtata attttttgtg gtttttggtt tgttgagtta      777
aagtatatta ttgtgagatt tatttaatag gacttccttt gaaagctgta taatagtgtt      837
tctcgggctt ctgtctctat gagagatagc ttattactct gatactcttt aatcttttac      897
aaaggcaagt tgccacttgt catttttggt tctgaaaaat aaaagtataa cttattcaca      957
aaaaaaaaaa mms      970

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<210> 271
 <211> 645
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..383

<221> sig_peptide
 <222> 90..200
 <223> Von Heijne matrix
 score 4.90000009536743
 seq MLIMLGIFNVHS/AV

<221> polyA_signal
 <222> 609..614

<221> polyA_site
 <222> 632..643

<400> 271
 atctctgccc cctgcgagg gcattcctggg ctttctccca ccgctttccg agcccgttg 60

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cacctcggcg atccccgact cccttcttt atg gcg tcg ctc ctg tgc tgt ggg      113
                               Met Ala Ser Leu Leu Cys Cys Gly
                               -35                               -30
ccg aag ctg gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc      161
Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile
                               -25                               -20                               -15
atg ttg ata atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg      209
Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
                               -10                               -5                               1
att gag gac gtt ccc ttc acg gag aaa gat ttt gag aac ggc ccc car      257
Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln
                               5                               10                               15
aac ata tac aac ctt tac rag caa ktc agc tac aac tgt ttc atc gct      305
Asn Ile Tyr Asn Leu Tyr Xaa Gln Xaa Ser Tyr Asn Cys Phe Ile Ala
20                               25                               30                               35
gca ggc ctt tac ctc ctc ctc gga ggc ttc tct ttc tgc caa ktt cgg      353
Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Xaa Arg
                               40                               45                               50
ctc aat aag cgc aag gaa tac atg gtg cgc tagggccccg gcgcgtttcc      403
Leu Asn Lys Arg Lys Glu Tyr Met Val Arg
                               55                               60
ccgctccagc ccctcctcta tttaaaract ccctgcaccg tktcaccag gtcgcgtccc      463
acccttgccg gcgcctctg tgggactggg tttcccgggc rararactga atcccttctc      523
ccatctctgg catccggccc ccgtggarar ggctgaggct ggggggctgt tccgtctctc      583
cacccttcgc tgtgtcccg atctcaataa agagaatctg ctctcttcaa aaaaaaaaaa      643
my                                                                    645

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<210> 272
 <211> 773
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..541

<221> sig_peptide
 <222> 332..376
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FLPCCLLWSVFPN/ES

<221> polyA_signal
 <222> 739..744

<221> polyA_site
 <222> 761..773

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<400> 272
aaaacaattc atgcctttca tagtttatta ttattaaagt ctaaacaaaa ttgcaatttc      60
ttaggtaacc ttatatttac aataaatgaa gattaccctc aaatgctaga agctgtctag      120
gtcgcgtccg tgtgtcagat tttcctcaga ttagatgtgc caataaccaa gtttattcag      180
taaacaactt gtacttggtt catctgggtt tattactctc acccataaac agtaatgact      240
ctctgaccct ctggaaatat gtaatgcttc caatcttgct ttgtgtatct catttaattt      300
gttataaggt agtactgatt ttagcatatt a atg cga ttt ctt cct tgt tgt      352
                               Met Arg Phe Leu Pro Cys Cys
                               -15                               -10
ttg ctt tgg tct gtg ttc aat cca gag agc tta aat tgt cat tat ttt      400
Leu Leu Trp Ser Val Phe Asn Pro Glu Ser Leu Asn Cys His Tyr Phe
                               -5                               1                               5

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ghk ndd gaa amc tgt att ttt gyt agt tta caa tat tat gaa att tca      448
Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser
  10                      15                      20
ctt cag gag aaa ctg ctg ggc ttc ctg tgg ctt tgt ttt ctt agt tac      496
Leu Gln Glu Lys Leu Leu Gly Phe Leu Trp Leu Cys Phe Leu Ser Tyr
  25                      30                      35                      40
ttt ttc cgt gcc gtg tat ttt tta att gat ttt tct tct ttt act      541
Phe Phe Arg Ala Val Tyr Phe Leu Ile Asp Phe Ser Ser Phe Thr
          45                      50                      55
tgaaaagaaa gtgtttttatt ttcaaactctg gtccatattt acattctagt tcagagccaa      601
gccttaaaact gtacagaatt tccactgtaa ttaaaactat ttagtgtag ttataaatag      661
ccttcaaaaa gagagattct ccattacacg atcacctgca tcacagccca tggatgaatgt      721
atgtttctgc atagcgaaat aaaaatggca aatgcactga aaaaaaaaaa aa      773

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<210> 273

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 43..222

<221> sig_peptide

<222> 43..177

<223> Von Heijne matrix

score 4

seq ENFLSLLSKSCSA/DP

<221> polyA_signal

<222> 530..535

<221> polyA_site

<222> 555..566

<400> 273

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aacgagtgga ggtgtggcta gtggctgtga tgagataaat cc atg cat agc ctt      54
                                   Met His Ser Leu
                                   -45
ttc att gcg agc ttg aaa gtt ctt ttc tat tac agt ttt agc ttt agg      102
Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser Phe Ser Phe Arg
  -40                      -35                      -30
ttt aat tgg ttc gac tgc ctt ctc cac aat ttg ggc gag aat ttc ctt      150
Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly Glu Asn Phe Leu
  -25                      -20                      -15                      -10
agc ctt ctc agc aaa agt tgt tct gcg gac ccg tct ggg tca act ttc      198
Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser Gly Ser Thr Phe
          -5                      1                      5
atg agg gac att gag aca aac aaa tgaaatatgg gttaaagtac tctgagcagc      252
Met Arg Asp Ile Glu Thr Asn Lys
  10                      15
tacaaaaaga araccagtct atcctgctgg agacagtggc cacgtgaara aagagctctt      312
gcagtatgaa agaccacatg gaaagagagg ccacatggaa ccaacagtca gcatcttggt      372
ttcggacacg tgaaraaatt catctcarac tgtgtatcct aaatcaggca cttgctgaat      432
ctaactacat gagtgaagacc agttgacaac acatggagca racatgagct gttctcagt      492
artcctacac aaattcctga ctcaacaac tgtgagcaat aaaatgggtt ttattttaag      552
ccaaaaaaaa aaaa      566

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<400> 275
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 agccttagtt tcccatggcc ctgaaacaca cacatttccc ccttcctttc ccagaagcca 180
 ctggccccc atagcaccca gtgcctcctt tttacaagtg gaagaactag g atg gct 237
 Met Ala
 ttc caa agt ctt cta gaa atg aag ttc ttt ctc tgt gca gct ttc ccc 285
 Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro
 -20 -15 -10
 ctt gga gca gga gtg aag atg ttt cat tat ctt ggg cct ggg aaa cca 333
 Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro
 -5 1 5 10
 ctt cyy cag gct tct ccc tcc ccc cac ccc cat agg amc agg att tgg 381
 Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp
 15 20 25
 cct tagcttctgg gcctatcsgc tgccttcctt ctttytctta ccacctcttc 434
 Pro
 tgccttcctt trawctctgt tgggcttggg gatcttagtt ttcttttggt tatttcccat 494
 ctcatttttt tcttctgggc agttttttta aggggggggtg ttgtgggttt ttgtttttgt 554
 tttgcttctg aaaaarcatt tgcctttctt cctctcccaa cataacaatc gtggtaacag 614
 aatgcgactg ctgatttacc gatgtattta atgtaagtaa aaaaaggaaa aaaaraaaa 673

<210> 276

<211> 639

<212> DNA

<213> Homo sapiens

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<222> 143..427

<221> sig_peptide

<222> 143..286

<223> Von Heijne matrix

score 7.5

seq FVILLLFIFTVVS/LV

<221> polyA_signal

<222> 606..611

<221> polyA_site

<222> 628..639

<400> 276
 aatcgcttca gcagcatcct ctcagacaag agccactatt tctgattcag atcacctgtc 60
 atcgaagttt aaagaagggg aaacaggaga cagaaatata ctgaaccaa aagattcaaa 120
 agagcaagtg gaatctctaa ga atg gct tcc agc cac tgg aat gaa acc act 172
 Met Ala Ser Ser His Trp Asn Glu Thr Thr
 -45 -40
 acc tct gtt tat cag tac ctt ggt ttt caa gtt caa aaa att tac cct 220
 Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro
 -35 -30 -25
 ttc cat gac aac tgg aac act gcc tgc ttt gtc atc ctg ctt tta ttt 268
 Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile Leu Leu Leu Phe
 -20 -15 -10
 ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc ctt tat gaa gtg 316
 Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe Leu Tyr Glu Val
 -5 1 5 10
 ctt gam wgc tgc tgc tgt gta aaa aac aaa acc gtg aaa gac ttg aaa 364
 Leu Xaa Xaa Cys Cys Cys Val Lys Asn Lys Thr Val Lys Asp Leu Lys

	15	20	25	
agt gaa ccc aac cct ctt ara akt atg atg gac aac atc aga aaa cgt				412
Ser Glu Pro Asn Pro Leu Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg				
	30	35	40	
gaa act gaa gtg gtc taacactcta taraaaatga acaaaatctc tgaaagcagc				467
Glu Thr Glu Val Val				
	45			
tcaacctctt ctgaraaaaa aaatatattc tgaggccaac tgttgctaca aaacaaattc				527
tgactgaatg gttaaaacat ttctagtara aggggaaaaa aaakttaaac atgcactgtt				587
tgtgtgtata sccatttcat taaatatata gtaaaactyc aaaaaaaaaa aa				639

<210> 277
 <211> 772
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 284..463

<221> sig_peptide
 <222> 284..379
 <223> Von Heijne matrix
 score 3.79999995231628
 seq TFINITLWLGLC/QR

<221> polyA_site
 <222> 762..772

<400> 277	
acagctgggg ctttgtcttc tttattgcta ggagaatgta gcaatagaag ttctcatcgc	60
cctgtattgc acttttggtt ttaaggactg gaccagagt tcctgaaagc caaactccat	120
aagctgctca gtaagttcca agcacatagc cggctkhggg atgcgattcg gtcgaggtct	180
gttgaatgaa ggtagacgca gcaggcagtt tgtccttacc agtgacctgg aagacgggtg	240
cacttctctga gtgagctcac ttaccttccc tgaatggtga ggc atg gat gaa tat	295
	Met Asp Glu Tyr
	-30
tcc tgg tgg tgc cac gtg tta gag gtg gta aag ggt caa atg ttt act	343
Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly Gln Met Phe Thr	
	-25 -20 -15
ttt att aat att aca tta tgg ctt ggt tct ctg tgt cag cga ttt ttc	391
Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys Gln Arg Phe Phe	
	-10 -5 1
tat gcc tcg ggt act tat ttc cta ata tat atc agc aca gta acg cct	439
Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser Thr Val Thr Pro	
5 10 15 20	
agc tgg agg ctt tgt ctt gtt agt tgataaatta gtgtaacag gtagatttgg	493
Ser Trp Arg Leu Cys Leu Val Ser	
	25
ttacctccca aagtgtggg attrcagacg tgagccaccg cgcttgccg aaacaattct	553
tttgaaagag agaagtctcc ctgtgttgcg caggctggct tcagactcct ggggtcaagt	613
gagcctctcg ctttcgcctc ctaaagtgtc gggattacag gcgtgagcca ccgcaccocg	673
acagatgtgt tgattttaaa gtgggtatga ggcttgagcc ctggagtttg agaccagcct	733
ggacaacatg gcaagaccct gtctctccaa aaaaaaaaaa	772

<210> 278
 <211> 840
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 162..671

<221> sig_peptide

<222> 162..398

<223> Von Heijne matrix

score 4.09999990463257

seq QGVLFICFTCARS/FP

<221> polyA_signal

<222> 805..810

<221> polyA_site

<222> 830..840

<400> 278

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ctgcaacgcg cgtgggagggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg      120
atgtttcccg ggaagaactg ggataaaggg gtcccagcac c atg gag gac ccg aac      176
                                         Met Glu Asp Pro Asn
                                         -75

cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt ccc      224
Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
                                         -70          -65          -60

cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc acc      272
Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr
                                         -55          -50          -45

cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac atg      320
Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met
                                         -40          -35          -30

aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc      368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val
                                         -25          -20          -15

ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa gcc      416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys Ala
-10          -5          1          5

ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg      464
Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa Ala Lys Pro Thr Leu
10          15          20

ccg gtt gca acc act act gcc car ccc acc ttc cct tgt cct gac tgt      512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
25          30          35

ggc aaa acc ttt ggg cag gct gtt tct ctg arg cgg cac csc caa atr      560
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa Arg His Xaa Gln Xaa
40          45          50

cat gar gtc cgt gcc cct cct ggc acc ttc gcc tgc aca rad tgc ggt      608
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Xaa Cys Gly
55          60          65          70

cag gac ttt gct car gaa rca ggg ctg cat caa cac tac att cgg cat      656
Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln His Tyr Ile Arg His
75          80          85

gcc cgg ggg gga ctc tgagttcagc ttaagcctct ccacggtgac ggggtggctct      711
Ala Arg Gly Gly Leu
90

gtggctggta ggactacccc atgatatggg gtgcaggaac tctggggggcc ctgaaggatt      771
tgcttccctc ccctgggaag gcagaggggt cttaataaag aggacccaka agattcttaa      831
aaaaaaaaa                                         840

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<210> 279
 <211> 840
 <212> DNA
 <213> Homo sapiens

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 <222> 63..632

<221> sig_peptide
 <222> 63..308
 <223> Von Heijne matrix
 score 4.40000009536743
 seq NLPHLQVVGLTWG/HI

<221> polyA_signal
 <222> 808..813

<221> polyA_site
 <222> 829..840

<400> 279
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 ga atg tat gtd tgg ccc tgt gct gtg gtc ctg gcc cag tac ctt tgg 107
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp
 -80 -75 -70
 ttt cac aga aga tct ctg cca ggc aag gcc atc tta gag att gga gct 155
 Phe His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala
 -65 -60 -55
 gga gtg agc ctt cca gga att ttg gct gcc aaa tgt ggt gca gaa gta 203
 Gly Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val
 -50 -45 -40
 ata ctg tca gac agc tca gaa ctg cct cac tgt ctg gaa gtc tgt cgg 251
 Ile Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg
 -35 -30 -25 -20
 caa agc tgc caa atg aat aac ctg cca cat ctg cag gtg gta gga cta 299
 Gln Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu
 -15 -10 -5
 aca tgg ggt cat ata tct tgg gat ctt ctg gct cta cca cca caa gat 347
 Thr Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp
 1 5 10
 att atc ctt gca tct gat gtg ttc ttt gaa cca gaa rat ttt gaa gac 395
 Ile Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp
 15 20 25
 att ttg gct aca ata tat ttt ttg atg cac aar aat ccc aag gtc caa 443
 Ile Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln
 30 35 40 45
 ttg tgg tct act tat caa gtt agg art gct gac tgg tca ctt gaa gct 491
 Leu Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala
 50 55 60
 tta ctc tac aaa tgg gat atg aaa tgt gtc cac att cct ctt gag tct 539
 Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser
 65 70 75
 ttt gat gca gac aaa gaa rat ata gca gaa tct acc ctt cca gga aga 587
 Phe Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg
 80 85 90
 cat aca gtt gaa atg ctg gtc att tcc ttt gca aag gac agt ctc 632
 His Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
 95 100 105
 tgaattatac ctacaacctg ttctgggaca gatatcaatac tgatgagcaa cctggcacac 692
 aaactatgag cagaccactt cagcttgaga atgcagtggg tctgaagatg gtcaagtctg 752

tttgccttar- attttgatgt cacctagaca acacttaaac tcatatgaaa caaaaattaa 812
 aatacgattt acaagcaaaa aaaaaaaaaa 840

<210> 280
 <211> 849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..362

<221> sig_peptide
 <222> 21..200
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LVILSLKSQTLDA/ET

<221> polyA_signal
 <222> 821..826

<221> polyA_site
 <222> 838..849

<400> 280
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 Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
 -60 -55 -50
 tgg aac cgt gtg aga atc cct aag gcg ggg aac cgc agc gca gtg aca 101
 Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
 -45 -40 -35
 gtg cag aac ccc ggc gcg gcc ctt gac ctt tgc att gca gct gta att 149
 Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
 -30 -25 -20
 aaa gaa tgc cat ctc gtc ata ctg tcg ctg aag agc caa acc tta gat 197
 Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
 -15 -10 -5
 gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga 245
 Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
 1 5 10 15
 atg ggc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt 293
 Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
 20 25 30
 tta aag cgt ttg aaa aac atg aat ttg gag ggc tca att caa gac ctg 341
 Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu
 35 40 45
 ttt gag ttg ttt tct tcc aag taagtaagtg gtccarttgc tttgtgatgt 392
 Phe Glu Leu Phe Ser Ser Lys
 50
 ggtgggctgg gaactcaatg tcttgtgatc kcccttwgga tktctctakg ctygckgttg 452
 gaatataacc aattataccw cagctgtaka aatwttgttt taatgtgggg taccygggtg 512
 ktgtggtaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt 572
 catggtagat tatattaaaa catcagtggg ctgttattgt gcttaactac ctcaagttga 632
 gcttaaagca agtcttcact tgaaaactgc tatagaaatg ctttatattt aaaaatgaaa 692
 gtaatgggar mttgcacata gctgaaaatg tgaagggtcg cccagggagg amatggaagc 752
 tctgtgcttc tttgcccata ccttgcccta tgcattcttt tgtttcaatc ctttgtcata 812
 tcctttataa taaactggta aatgtaaaaa aaaaaaaa 849

<210> 281
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..503

<221> sig_peptide
 <222> 21..344
 <223> Von Heijne matrix
 score 5.30000019073486
 seq ACMTLTASPGVFP/SL

<221> polyA_signal
 <222> 1305..1310

<221> polyA_site
 <222> 1330..1341

<400> 281
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 Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln
 -105 -100
 tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat atc tca gtc tca 101
 Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser
 -95 -90 -85
 atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc 149
 Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg
 -80 -75 -70
 aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt 197
 Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu
 -65 -60 -55 -50
 tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct 245
 Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro
 -45 -40 -35
 aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag 293
 Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln
 -30 -25 -20
 gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc 341
 Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe
 -15 -10 -5
 ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg 389
 Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr
 1 5 10 15
 cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa 437
 Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln
 20 25 30
 aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg 485
 Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu
 35 40 45
 gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag 533
 Glu Lys Ser Ile Met Leu
 50
 atgatgaccg ttcattaata aatttgcac tcatgcacac cagttacttc ctctttgtga 593
 tgggtgataac aatgttttgc tatgtgtgta tcaagggcag acctagcaaa ttgcgtcaga 653
 gcaatcctga attttgtccc gagaagggtgg ctttggctga agcctaattc cacagctcct 713
 tgttttttga gagagactga gagaaccata atccttgcct gctgaaccca gcctgggcct 773
 ggatgctctg tgaatacatt atcttgcgat gttggggttat tccagccaaa gacatttcaa 833
 gtgcctgtaa ctgatttgta catatttata aaaatctatt cagaaattgg tccaataatg 893
 cacgtgcttt gccctgggta cagccagagc ctttcaacce caccttggac ttgaggacct 953


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acctgatggg acgtttccac gtgtctctag agaaggatcc tggatctagc tggtcacgac 1013
gatgttttca ccaaggtcac aggagcattg cgtcgctgat ggggttgaag tttggtttgg 1073
ttcttgtttc agcccaatat gtagagaaca tttgaaacag tctgcacctt tgatacggta 1133
ttgcatttcc aaagccacca atccattttg tggattttat gtgtctgtgg cttaataatc 1193
atagtaacaa caataatacc tttttctcca ttttgcttgc aggaaacata ccttaagttt 1253
tttttgtttt gtttttgttt ttttgttttt tgttttcctt tatgaagaaa aaataaaata 1313
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<210> 282
 <211> 671
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..201

<221> sig_peptide
 <222> 1..63
 <223> Von Heijne matrix
 score 5.09999990463257
 seq LLLKIWLLQRPES/QE

<221> polyA_signal
 <222> 637..642

<221> polyA_site
 <222> 660..671

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Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
-20 -15 -10
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg 96
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
-5 1 5 10
atg gag agg aga gtt aaa aat gac ctc atg tcc ttc ttg tcc acg gtt 144
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
15 20 25
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca 192
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
30 35 40
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtcttttg 241
Leu Arg Met
45
ctcagttcat ttaaaaaaga tatctatttg aaagttctca rarttggtaca tatgtttcac 301
agtacaggat ctgtacataa aagtttcttt cctaaaccat tcaccaagag ccaatatcta 361
ggcattttct tggtagcaca aattttctta ttgcttaraa aattgtctct cttgttattt 421
ctgtttgtaa racttaagtg agttaggtct ttaaggaaa caacgctcct ctgaaatgct 481
tgtctttttt ctgttgccga aatarctggg cctttttcgg gagttaratg tatarartgt 541
ttgtatgtaa acatttcttg taggcacac catgaacaaa gatatatattt ctatttattt 601
attatatgtg cacttcaaga agtcactgtc agagaaataa agaattgtct taaatgtcaa 661
aaaaaaaaa 671

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<210> 283
 <211> 1601
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 39..1034

<221> sig_peptide

<222> 39..134

<223> Von Heijne matrix

score 6.09999990463257

seq LPLLTSAHLGLQQ/QH

<221> polyA_signal

<222> 1566..1571

<221> polyA_site

<222> 1587..1597

<400> 283

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agccccagat cctgaaggag gtgcagagcc cagagggg atg atc kcg ctg agg gac      56
                                   Met Ile Xaa Leu Arg Asp
                                   -30
aca gct gcc tcc ctc cgc ctt gag aga gac aca agg cag ttg cca ctg      104
Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln Leu Pro Leu
-25                               -20                               -15
ctc acc agt gcc ctg cac gga ctg cag cag cag cac cca gcc ttc tct      152
Leu Thr Ser Ala Leu His Gly Leu Gln Gln Gln His Pro Ala Phe Ser
-10                               -5                               1                               5
ggt gtg gca cgg ctg gcc aag cgg tgg gtg cgt gcc cag ctt ctt ggt      200
Gly Val Ala Arg Leu Ala Lys Arg Trp Val Arg Ala Gln Leu Leu Gly
10                               15                               20
gag ggt ttc gct gat gag agc ctg gat ctg gtg gcc gct gcc ctt ttc      248
Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu Val Ala Ala Ala Leu Phe
25                               30                               35
ctg cac cct gag ccc ttc acc cct ccg agt tcc ccc cag gtt ggc ttc      296
Leu His Pro Glu Pro Phe Thr Pro Pro Ser Ser Pro Gln Val Gly Phe
40                               45                               50
ctt cga ttc ctt ttc ttg gta tca acg ttt gat tgg aag aac aac ccc      344
Leu Arg Phe Leu Phe Leu Val Ser Thr Phe Asp Trp Lys Asn Asn Pro
55                               60                               65                               70
ctc ttt gtc aac ctc aat aat gag ctc act gtg gag gag cag gtg gar      392
Leu Phe Val Asn Leu Asn Asn Glu Leu Thr Val Glu Glu Gln Val Glu
75                               80                               85
atc cgc agt ggc ttc ctg gca gct cgg gca cag ctc ccc gtc atg gtc      440
Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala Gln Leu Pro Val Met Val
90                               95                               100
att gtt acc ccc caa rac cgc aaa aac tct gtg tgg aca cag gat gga      488
Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser Val Trp Thr Gln Asp Gly
105                               110                               115
ccc tca gcc car atc ctg cag cag ctt gtg gtc ctg gca gct gaa scc      536
Pro Ser Ala Gln Ile Leu Gln Gln Leu Val Val Leu Ala Ala Glu Xaa
120                               125                               130
ctg ccc atg tta rar aas cag ctc atg gat ccc cgg gga cct ggg gac      584
Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp Pro Arg Gly Pro Gly Asp
135                               140                               145                               150
atc agg aca gkg ttc cgg ccg ccc ttg gac att tac gac gtg ctg att      632
Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp Ile Tyr Asp Val Leu Ile
155                               160                               165
cgc ctg tct cct cgc cat atc ccg cgg cac cgc cag gct gtg gac tcr      680
Arg Leu Ser Pro Arg His Ile Pro Arg His Arg Gln Ala Val Asp Ser
170                               175                               180
cca gct gcc tcc ttc tgc cgg ggc ctg ctc agc cag ccg ggg ccc tca      728
Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu Ser Gln Pro Gly Pro Ser

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      185              190              195
tcc ctg atg ccc gtg ctg ggc tak gat cct cct cag ctc tat ctg acg      776
Ser Leu Met Pro Val Leu Gly Xaa Asp Pro Pro Gln Leu Tyr Leu Thr
      200              205              210
cag ctc arg gag gcc ttt ggg gat ctg gcc ctt ttc ttc tat gac cag      824
Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala Leu Phe Phe Tyr Asp Gln
      215              220              225              230
cat ggt gga gag gtg att ggt gtc ctc tgg aag ccc acc agc ttc cag      872
His Gly Gly Glu Val Ile Gly Val Leu Trp Lys Pro Thr Ser Phe Gln
      235              240              245
ccg cag ccc ttc aag gcc tcc agc aca aag ggg cgc atg gtg atg tct      920
Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys Gly Arg Met Val Met Ser
      250              255              260
cga ggt ggg gag cta gta atg gtg ccc aat gtt gaa gca atc ctg gag      968
Arg Gly Gly Glu Leu Val Met Val Pro Asn Val Glu Ala Ile Leu Glu
      265              270              275
gac ttt gct gtg ctg ggt gaa ggc ctg gtg cag act gtg gag gcc cga      1016
Asp Phe Ala Val Leu Gly Glu Gly Leu Val Gln Thr Val Glu Ala Arg
      280              285              290
agt gag agg tgg act gtg tgatcccagc tctggagcaa gctgtagacg      1064
Ser Glu Arg Trp Thr Val
      295              300
gacagcagga cattggacct ctagagcaag atgtcagtag gatgacctcc accctccttg      1124
gacatgaatc ctccatggag ggctgtctgg ctgaacatgc tgaatcatct ccaacaaaac      1184
ccagccccc aa ctttctctct gatgctccag cattggggca ggggcatggt ggcccatgta      1244
gtctcctggg cctcaccatc ccagaagagg agtgggagcc agctcagaga aggaactgaa      1304
cccaggagat ccatccacct attagccctg ggccctggacc tccctgcatg tccccactcc      1364
tttcttagtc ttcttcaga aacagagaag gggatgtgtg octgggagag gctctgtctc      1424
cttctgtctg ccaggacctg tgcctagact tagcatgccc ttcactgcag tgtcaggcct      1484
ttagatggga cccagcgaaa atgtggccct tctgagtcac atcaccgaca ctgagcagtg      1544
gaaaggggct atatgtgtat gaatagacca cattgaagga gcaaaaaaaaa aaamcch      1601

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<210> 284

<211> 1206

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..263

<221> sig_peptide

<222> 69..125

<223> Von Heijne matrix

score 3.90000009536743

seq ALSMSSFSFHSSS/CS

<221> polyA_signal

<222> 1173..1178

<221> polyA_site

<222> 1196..1205

<400> 284

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acatttgtga ctttaccat accctcccag ttcttgatag acagctgtag gttgctgggt      60
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt      110
      Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser
      -15              -10
ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc      158
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser

```

```

-5          1          5          10
aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta      206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu
          15          20          25
gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa      254
Glu Asn Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys
          30          35          40
att gtg ggc tgatttggtc ttctctcct cctcccactg ttactgcct      303
Ile Val Gly
          45
gcagcccttg ttcaggtgta cagaccctta ttctggcctc tagtgtcctt gtctgtcatg      363
acacaccctt ccgccc aaat acctctgacc ccaaggctgg aatggggctg gtaggarata      423
agtttgctta ctcatartca tgccttttct cttggcacct gcttccctgc ggtgtcctca      483
aatggatttc tgtgtggcag tggartgatt gcatgaattt ttctgtaaca cattaacttt      543
gtattattat taagggarth tgaraaagct ttgcttataa tgtcaaggca aggaggtaaa      603
aactggagcc caaakaaatt cccttagggc aagattatgt tataataraa aattgaattt      663
cctgaggcag tggctgccac cccttttcar atgttttagtc ctgcaaatac catcttttctt      723
gtagtctgtg acatggatgg ggatgctagg gcccttaggg gcaaggggac taaactaaat      783
caakttgagt ttttttccag caggggttar gggaggact cscgtgtgat atttgacact      843
araaagtaat cttttttaca aaactgtttt tctaggtggg tggaaagtga aactgccaca      903
tccttggttg tttagtccaa raratcattt gcaacaacag taratgtccg ggttttgttt      963
ctgtcttttt attatgaaaa actatgttaa gggggaaaat gtggattatg gtaaccarag      1023
gaatccctas ccttgttttc cttaraarac ttgttttagtg ttttatcara cgtctgttgt      1083
agttgtarac aggaaagctt gtgaraaaaa caccacatgg ascctgtaaa tgtttttgca      1143
caacctgtaa agcattcttg gaaktggcca gtaaaaaggg gttttaccat taaaaaaaaa      1203
aat                                                                 1206

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<210> 285

<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..285

<221> sig_peptide

<222> 115..204

<223> Von Heijne matrix

score 3.70000004768372

seq SMMLLTVYGGYLC/SV

<221> polyA_signal

<222> 505..510

<221> polyA_site

<222> 525..536

<400> 285

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acgagtgctg cgttcggctg tgctgggaag ttgcgtagac agtggcctcg agaccctgcc      60
tgcttgagga ggctcgggtt ggatgcgaag gagctgcagc atccagggga caag atg      117
                                                                 Met
                                                                 -30
cca act ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc      165
Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr
          -25          -20          -15
tcc atg atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga      213
Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val Arg
          -10          -5          1
gtc tac cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa      261

```

Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala Glu
 5 10 15
 gaa cag aag dac tca gga atc atg tagaactggg gggctttttc tcctgagcar 315
 Glu Gln Lys Xaa Ser Gly Ile Met
 20 25
 asakgccccaa ggcattgctgt ggagagactt cacctgccac catttccagg tcaacaggac 375
 tagagcggttg atggttttca aaccctgttg gaagaaagt cccatgggtt ctctggttct 435
 gccartttga cagtttatgg argcttttga atcgtaatar caatgtgagg gtgargtaca 495
 cctacagaca ttaaataatt tgctgtgtca aaaaaaaaaa a 536

<210> 286
 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..344

<221> sig_peptide
 <222> 90..140
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLLITAILAVAVG/FP

<221> polyA_signal
 <222> 500..505

<221> polyA_site
 <222> 515..527

<400> 286
 aatatrarak agctacaata ttccagggcc artcacttgc cattttctcat aacagcgtca 60
 gagagaaaga actgactgar acgttttgag atg aag aaa gtt ctc ctc ctg atc 113
 Met Lys Lys Val Leu Leu Leu Ile
 -15 -10
 aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag 161
 Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
 -5 1 5
 gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr 209
 Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
 10 15 20
 wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att 257
 Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
 25 30 35
 cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata 305
 Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile
 40 45 50 55
 cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
 Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
 60 65
 ggaaaagtca crataaacct ggtaacactga aattgaaatt gagccacttc cttgaaraat 414
 caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
 gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aaacc 529

<210> 287
 <211> 493
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..311

<221> sig_peptide

<222> 57..107

<223> Von Heijne matrix

score 8.19999980926514

seq LLLITAILAVAVG/FP

<221> polyA_signal

<222> 467..472

<221> polyA_site

<222> 482..493

<400> 287

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aacttgccat ttctcataac agcgtcagag agaaagaact gactgaaacg tttgag atg      59
                                     Met
aag aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt      107
Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
-15                               -10                               -5
ttc cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac      155
Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp
1                               5                               10                               15
agc gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca      203
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro
20                               25                               30
ttt cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga      251
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg
35                               40                               45
cgt aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt      299
Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu
50                               55                               60
ccg agc gaa aag taaacaagaa ggaaaagtca cgataaacct ggtcacctga      351
Pro Ser Glu Lys
65
aattgaaatt gagccacttc cttgargaat caaaattcct gttaataaaaa gaaaaacaaa      411
tgtaattgaa atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa      471
acatgaaagc aaaaaaaaaa aa                                          493

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<210> 288

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 96..302

<221> sig_peptide

<222> 96..182

<223> Von Heijne matrix

score 5

seq ELSLLPSSLWVLA/TS

<221> polyA_site

<222> 501..514

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<400> 288
aagagacgtc accggctgcg ccccttcagta tcgctggacgg aagatggcgt ccgccaccgc      60
tctcatccag cggctgcgga actgggctgc cgggc atg acc tgc agg gga agc      113
                               Met Thr Cys Arg Gly Ser
                               -25
tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca      161
Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro
          -20          -15          -10
agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca      209
Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala
          -5          1          5
ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt      257
Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg
10          15          20          25
crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg      302
Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Gln Xaa Ala Leu Leu
          30          35          40
tagctgccac tgaaaaaraag gcggtgactc cagctcctcc cataaaagagg tgggagctgt      362
cctcggacca gccttacctg tgacactgca cctcacggc caccgcgacta ctttgctcctc      422
ttggatttcc tccagggaga atgtgaccta atttatgaca aatacgtara gctcaggtat      482
cacttctagt ttacttttaa aaaataaaaa aatagagac      521

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<210> 289
<211> 811
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 161..526

<221> sig_peptide
<222> 161..328
<223> Von Heijne matrix
      score 4.19999980926514
      seq XSPLLTLALLGQC/SL

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<221> polyA_site
<222> 799..811

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<400> 289
aaaaaattgc agtgctgaag aacttgacc cgcaaaaggc tgtccctccc aaacctggga      60
ttctgggctc actgagttca cctgcgagtc agccctacct gcactgctct ggtctagtag      120
aaacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc      175
                               Met Val Pro Trp Pro
                               -55
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc      223
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe
          -50          -45          -40
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct      271
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser
-35          -30          -25          -20
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg      319
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu
          -15          -10          -5
ggg cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa      367
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln
1          5          10
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg      415

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Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp
  15                      20                      25
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaa      463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys
  30                      35                      40                      45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt      511
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val
                      50                      55                      60
caa ttt ttt tta ggg tgaatggagg garagttggg gactgaaaas ccttcaaara      566
Gln Phe Phe Leu Gly
                      65
caatgttatt acagcaktct ccccttatcc aaaktttcct tttcctgadt ttcagttagc      626
tatggtcaac cgcttggaac atakttgaac acagtacaat aaratatttt gaggtggga      686
ktggtggctc atgcctgtaa taatcccagg actttgtgar accaaktttg aaggatcact      746
tgaaccagg aktttgarac cscctgggc aacatrgtra gacctcatct ctacaaaaaa      806
aaaaa                                                                811

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<210> 290
 <211> 625
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 210..332

<221> sig_peptide
 <222> 210..299
 <223> Von Heijne matrix
 score 8.10000038146973
 seq ITCLLAFWVPASC/IQ

<221> polyA_signal
 <222> 594..599

<221> polyA_site
 <222> 613..625

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<400> 290
acaggctsmc ttaacatctc ttgatttgag ccactccac tgtcatcagc tttcacctgg      60
attatcgtga cagcctccta ctgcttctct atcatgtggc cagagctatc ttccttaaaa      120
atgcattgca tagttgatca agtcactctc tggcctaaaa ccttccttgg ctccctgctg      180
ccctcaggat aaagtctgga cccctcagc atg gct tgt gag act cat ggt gtc      233
                                Met Ala Cys Glu Thr His Gly Val
                                -30                      -25
ctt gtc cct gct cac ctc tct ggt ctc atc act tgc ctt ctt gca ttc      281
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe
-20                      -15                      -10
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca      329
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro
-5                      1                      5                      10
ctc tgattcctcc tttcttttgg tcacagagaa agggacttt ctctgtcaaa      382
Leu
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgaccccc      442
accctggcat actacacara tcactctggg ctcaattgcc tgcctaattg tcactctccc      502
agtaaactgt aagctccttg agggcaagga ttgtgttgga atttttgtat taacagtgcc      562
tggcttgggt cctggcacct aaaaagcact caataaatgt ttgtttaatg aaaaaaaaaa      622
aaa                                                                625

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<210> 291
 <211> 684
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 212..361

<221> sig_peptide
 <222> 212..319
 <223> Von Heijne matrix
 score 4.09999990463257
 seq HWLFLASLSGIKT/YQ

<221> polyA_signal
 <222> 650..655

<221> polyA_site
 <222> 673..684

<400> 291
 atccccawns cactctctca cagagactgt tcttttccct ctgagaccct actccagctt 60
 gtatgttctaa atctgtgatt atgcactgtc tgtcttccct ttgaggtcag gggccatttc 120
 ttttgttctc tgctatgtc aggaccaga tcaaaggagc tcagtaacta ttacaggcg 180
 tacatcatat gtggaggaca cttatgtctg g atg gcc cca cac aca gct tcc 232
 Met Ala Pro His Thr Ala Ser
 -35 -30
 ttt ggg gtc tgt ccc ctg ctc tcc gtt acc cgc gtg gta gcc act gag 280
 Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg Val Val Ala Thr Glu
 -25 -20 -15
 cac tgg ctc ttc ctg gct tca ctc tct ggc atc aaa act tat cag tcc 328
 His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile Lys Thr Tyr Gln Ser
 -10 -5 1
 tac atc tca gtc ttt tgc aag gtg aca ctt atc tgattaccta attcacacra 381
 Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile
 5 10
 aggtgttaat ggtggtaatg gcataktatt tattaccca ggggaccak aacggtggta 441
 tcaaaacata tcattcccca gtggtttaaa actctggtag ctttccargg aatccaaagt 501
 ggaatccagt ctcccttagct gawttcacag ggccccgtct gcacaacttg gcttctgtcg 561
 gcttccctan ccctgaacttc ccaagcctta gtcatcacc tctctccac ccagggtca 621
 gcacagtacc tggaacagtc aagccctcaa taaatgttta ctgagtgcac yaaaaaaaaa 681
 aaa 684

<210> 292
 <211> 628
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..482

<221> sig_peptide
 <222> 75..128
 <223> Von Heijne matrix
 score 3.59999990463257
 seq KMLISVAMLGAXA/GV

<221> polyA_signal
<222> 595..600

<221> polyA_site
<222> 618..627

<400> 292
aagtgagacc gcgcggcaac agcttgcggc tgcgggggagc tcccgtgggc gctccgctgg 60
ctgtgcaggc ggcc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
-15 -10
atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg 158
Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
-5 1 5 10
acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg 206
Thr Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
15 20 25
cag gac cca agg agc agg gag gag gcg gcc agg acc cag cag cta ttg 254
Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
30 35 40
ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg 302
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
45 50 55
agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac 350
Arg Lys Asn Trp Met Val Gly Gly Glu Gly Ala Thr Gly Xaa His
60 65 70
cgt gag acc gga ctt gcc tcc gtg ggc gcc gga cct tgg ctt ggg cgc 398
Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
75 80 85 90
agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg 446
Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
95 100 105
amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg 492
Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
110 115
tcgggtgagc acgtgtcccc caaacctgg actgactgct ttaagggtccg caaggcgggc 552
cagggccgag acgcgagtcg gatgtggtga actgaaagaa ccaataaaat catgttcctc 612
cammcaaaaa aaaaah 628

<210> 293
<211> 813
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..631

<221> sig_peptide
<222> 50..244
<223> Von Heijne matrix
score 8
seq LTLIGCLVTGVES/KI

<221> polyA_signal
<222> 777..782

<221> polyA_site
<222> 801..812

<400> 293

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aaggaaagga ttactcgagc cttgttagaa tcagacatgg cttcagggg atg cag gac      58
                                   Met Gln Asp
                                   -65
gct ccc ctg agc tgc ctg tca ccg act aag tgg agc agt gtt tct tcc      106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
      -60                               -55                               -50
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg      154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
      -45                               -40                               -35
cct ttt cag ttc tgt ctc cgg cag gct ttg agg atg aag gct gcg ggc      202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
      -30                               -25                               -20                               -15
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc      250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
      -10                               -5                               1
tac act cgt tgc aaa ctg gca aaa ata ttc tcg agg gct ggc ctg gac      298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
      5                               10                               15
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat      346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr
      20                               25                               30
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc      394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser
      35                               40                               45                               50
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc      442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg
      55                               60                               65
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg      490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu
      70                               75                               80
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt      538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val
      85                               90                               95
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt      586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys
      100                               105                               110
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc      631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser
      115                               120                               125
taaactggaa ctggacccag gatgctttgc ascaacgccc taggggtttgc agtgaatgtc      691
caaatgcctg tgtcatcttg tcccgtttcc tcccaatatt ccttctcaaa cttggagagg      751
gaaaattaag ctatactttt aagaaaataa atatttccat ttaaattgtca amaaaaaaaa      811
ah                                                                                   813

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<210> 294

<211> 778

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 154..576

<221> sig_peptide

<222> 154..360

<223> Von Heijne matrix

score 4.80000019073486

seq MMVLSLGIILASA/SF

<221> polyA_signal
<222> 737..742

<221> polyA_site
<222> 763..775

<400> 294

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agtaaaaaaaaa cactggaata aggaaggggct gatgactttc agaagatgaa ggtaagtaga      60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag      120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc      174
                               Met Thr Ser Gln Pro Val Pro
                               -65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa      222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
                               -60                               -55                               -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa      270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
                               -45                               -40                               -35
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt      318
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
                               -30                               -25                               -20                               -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc      366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
                               -10                               -5                               1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac      414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
                               5                               10                               15
cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg      462
Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg
                               20                               25                               30
atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct      510
Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa
                               35                               40                               45                               50
gcc agc ttg cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa      558
Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu
                               55                               60                               65
tct tgt tct cct gtc ggg targataaca ggggttgctt ratttttagat      606
Ser Cys Ser Pro Val Gly
                               70
caattttctta tcagactcaa ataaacattt cttttgaaaa tcatcttatt cttcacatta      666
tcatcttgag ctatgatgga aactagtgas ktctctccag gtttaggcga aaaaaaaatc      726
catgaattag gataaagttg ggaaggaaca ttttatacaa aaaaaaaaah cc      778

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<210> 295
<211> 1060
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 154..897

<221> sig_peptide
<222> 154..360
<223> Von Heijne matrix
score 4.80000019073486
seq MMVLSLGIILASA/SF

<221> polyA_signal
<222> 1017..1022

<221> polyA_site

<222> 1044..1054

<400> 295

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agtaaaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga      60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag      120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc      174
                                Met Thr Ser Gln Pro Val Pro
                                -65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa      222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
                                -60                                -55                                -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa      270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
                                -45                                -40                                -35
cat cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt      318
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
                                -30                                -25                                -20                                -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc      366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
                                -10                                -5                                1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac      414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
                                5                                10                                15
cca ttc ata gga ccc ttt ttt ttt atc atc tct ggc tct cta tca atc      462
Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile
                                20                                25                                30
gcc aca aaa aaa agg tta acc aac ctt ttg gtg cat acc acc ctg gtt      510
Ala Thr Lys Lys Arg Leu Thr Asn Leu Leu Val His Thr Thr Leu Val
                                35                                40                                45                                50
gga agc att ctg agt gct ctg tct gcc ctg gtg ggt ttc att ayc ctg      558
Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Xaa Leu
                                55                                60                                65
tct gtc aaa cag gcc acc tta aat cct gcc tca ctg cak tgt gag ttg      606
Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Xaa Cys Glu Leu
                                70                                75                                80
gmc aaa aat aat ata cca aca ara akt tat gtt yct tac ttt tat cat      654
Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa Tyr Val Xaa Tyr Phe Tyr His
                                85                                90                                95
gat tca ctt tat acc acg gac kgc tat aca gcc aaa gcc akt ctg gct      702
Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr Thr Ala Lys Ala Xaa Leu Ala
                                100                                105                                110
gga act ctc tct ctg atg ctg att tgc act ctg ctg gaa ttc tgc cwa      750
Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Xaa
                                115                                120                                125                                130
sct gtg ctc act gct gtg ctg cgg tgg aaa cag gct tac tct gac ttc      798
Xaa Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe
                                135                                140                                145
cct ggg agt gta ctt ttc ctg cct cam agt tac att ggw aat tct ggm      846
Pro Gly Ser Val Leu Phe Leu Pro Xaa Ser Tyr Ile Gly Asn Ser Gly
                                150                                155                                160
atg tcc tca aaa atg acy cat gac tgt gga tat gaa gaa cta ttg act      894
Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr
                                165                                170                                175
tct taagaaaaaa gggagaaata ttaatcagaa agttgattct tatgataata      947
Ser
tggaaaagtt aaccattata gaaaagcaaa gcttgagttt cctaaatgta agcttttaaa      1007
gtaatgaaca ttaaaaaaaaa ccattatttc actgtcaaaa aaaaaaamcc nkt      1060

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<210> 296
 <211> 444
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 146..292

<221> sig_peptide
 <222> 146..253
 <223> Von Heijne matrix
 score 5.5
 seq FTSMCILFHCLLS/FQ

<221> polyA_signal
 <222> 395..400

<221> polyA_site
 <222> 433..444

<400> 296
 aacttgggac aagaratcaa actttaaaaga tgggtctaaag cccctcttaa aggtctgact 60
 gtgtcggacc tctagagcta atctcactag atgtgagcca ttgtttatat tctagccatc 120
 ctttcatttc attctagaag accccc atg caa gtt ccc cac cta agg gtc tgg 172
 Met Gln Val Pro His Leu Arg Val Trp
 -35 -30
 aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca 220
 Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
 -25 -20 -15
 agt atg tgc ata ttg ttc cac tgt ctt ctt agc ttt cag gtt ttc aaa 268
 Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
 -10 -5 1 5
 aag aaa aga aaa ctt ara ctt ttc tgatgttctt ttttacgtaa ataaccattt 322
 Lys Lys Arg Lys Leu Xaa Leu Phe
 10
 tattgttggt ttgctttttc tgccttcaaa ctactcccac aggccaaata tavctggctg 382
 cttcttttctg taaataaagt tttattgggc cacagccatg gccatctttt aaaaaaaaaa 442
 aa 444

<210> 297
 <211> 754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..383

<221> sig_peptide
 <222> 126..167
 <223> Von Heijne matrix
 score 7.5
 seq VALNLIILVPCCAA/WC

<221> polyA_signal
 <222> 726..731

<221> polyA_site
 <222> 743..754

<400> 297
aattgtatgt tacgatgttg tattgatttt taagaaagta attkratttg taaaacttct 60
gctcgttttac actgcacatt gaatacaggt aactaattgg wgggagaggg gaggtcactc 120
ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg 170
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp
-10 -5 1
tgt gac cca cgg agg atc cac tcc cag gat gac gtg ctc cgt agc tct 218
Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser
5 10 15
gct gct gat act ggg tct gcg atg cag cgg cgt gag gcc tgg gct ggt 266
Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly
20 25 30
tgg aga agg tca caa ccc ttc tct gtt ggt ctg cct tct gct gaa aga 314
Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg
35 40 45
ctc gag aac caa cca ggg aag ctg tcc tgg agg tcc ctg gtc gga gag 362
Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu
50 55 60 65
gga cat aga atc tgt gac ctc tgacrrctgt gaasccaccc tgggctacar 413
Gly His Arg Ile Cys Asp Leu
70
aaaccacagt cttcccagca attattacaa ttcttgaatt ccttggggat tttttactgc 473
cctttcaaag cacttaaktg tkrratctaa cgktktccag tgtctgtctg aggtgactta 533
aaaaatcaga acaaaacttc tattatccag agtcatggga gagtacaccc tttccaggaa 593
taatgttttg ggaaacactg aaatgaaatc ttcccagtat tataaattgt gtattttaaaa 653
aaaagaaact ttcttgaatg cctacctggc ggtgtatacc aggcagtgtg ccagtttaaa 713
aagatgaaaa agaataaaaa cttttgagga aaaaaaaaaa a 754

<210> 298
<211> 629
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..497

<221> sig_peptide
<222> 66..239
<223> Von Heijne matrix
score 5.40000009536743
seq QL LDSVLWL GALG/LT

<221> polyA_signal
<222> 594..599

<221> polyA_site
<222> 618..629

<400> 298
aactcccaga atgctgacca aagtgggagg agcactaggt cttcccgta cctccacctc 60
tctcc atg acc cgg ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg 110
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro
-55 -50 -45
atc cca gtt cct cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt 158
Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser
-40 -35 -30
cca gtg cgt cca cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc 206
Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu

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      -25      -20      -15
ctg gac agt gtc cta tgg ctg ggg gca cta gga ctg aca atc cag gca      254
Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala
      -10      -5      1      5
gtc ttt tcc acc act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc      302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe
      10      15      20
ctc acc ttt gac ctg ctc cat agg ccc gca gtc aca ctc tgc cac agc      350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser
      25      30      35
gca aac ttc tca cca ggg gcc aga gtc agg ggg ccg gtg aag gtc ctg      398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu
      40      45      50
gac agc agg agg ctc tac tcc tgc aaa tgg gta cag tct cag gac aac      446
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn
      55      60      65
tta gcc tcc agg aag cac tgc tgc tgc tgc tca tgg ggc tgg gcc cgc      494
Leu Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg
      70      75      80      85
tcc tgaaaacctg tggcatgccc ttgwaccctg cttggcctgg ctttctgcct      547
Ser
ccatccttgg gcctgakanc cctccccac aactcagtgt ccttcaaata tacaatgacc      607
acccttcttc aaaaaaaaaa aa      629

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<210> 299
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..411

<221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix
 score 10.1000003814697
 seq LVLTLCTLPLAVA/SA

<221> polyA_signal
 <222> 732..737

<221> polyA_site
 <222> 750..763

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<400> 299
aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg      57
                                         Met Glu Arg
                                         -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10      -5      1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5      10      15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
      20      25      30      35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt agt gag tcy ccc      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser Glu Ser Pro

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      40      45      50
ccg ggc aga ggg cas gtg cca bgt gcc ggg gaa kgg ccg gtg ccc ccg      297
Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro Val Pro Pro
      55      60      65
cct ctc wkc gac tta bct atg act cct cgg ckc ycc agg gcc tgg ggc      345
Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg Ala Trp Gly
      70      75      80
cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tgc      393
Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser
      85      90      95
ggc gag cat ccs rva btg tgaatkkkga cttttttctc ckccatttga      441
Gly Glu His Pro Xaa Xaa
100      105
agtgtcacta ggaactgtca gcaggacaaa ggctctgatg tcaactgaatt tacaaaraca      501
gcaggaacrs ackggtgggg atgggcagct gttcrargcr atgggkacg tgcccttctc      561
ggcacagcac artacacctg ccatacaacc carcatcagg cakgctgcac tggaaatcgat      621
acagtgtatg acaatgtcat atagtataac acaacataat gaatataacg tgtatattgc      681
aacttaatat aatacgtatg aatataatgc tacataatac aacataatat aataaaatag      741
aatgcaacac aaaaaaaaaa aacc      765

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<210> 300
 <211> 623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..534

<221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix
 score 10.1000003814697
 seq LVLTLCTLPLAVA/SA

<221> polyA_signal
 <222> 593..598

<221> polyA_site
 <222> 612..623

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<400> 300
aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg      57
                                   Met Glu Arg
                                   -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10      -5      1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
      5      10      15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20      25      30      35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
      40      45      50
cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
      55      60      65

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atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
      70                      75                      80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
      85                      90                      95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
      100                      105                      110                      115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
      120                      125                      130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
      135                      140                      145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcacctc ttggaracaa      594
taaactctca tgcccccaaa aaaaaaaaaa      623

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<210> 301
 <211> 571
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..415

<221> sig_peptide
 <222> 86..145
 <223> Von Heijne matrix
 score 9.80000019073486
 seq FTIGLTLLLGXQA/MP

<221> polyA_signal
 <222> 540..545

<221> polyA_site
 <222> 560..571

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<400> 301
aaaaactcac ccagtgagtg tgagcattta agaagcatcc tctgccaaga ccaaaaggaa      60
agaagaaaaa bggccaaaag ccaaa atg ara ctg atg gta ctt gtt ttc acc      112
                        Met Xaa Leu Met Val Leu Val Phe Thr
                        -20                      -15
att ggg cta act ttg ctg cta gga rtt caa gcc atg cct gca aat cgc      160
Ile Gly Leu Thr Leu Leu Leu Gly Xaa Gln Ala Met Pro Ala Asn Arg
      -10                      -5                      1                      5
ctc tct tgc tac aga aag ata cta aaa gat cac aac tgt cac aac ctt      208
Leu Ser Cys Tyr Arg Lys Ile Leu Lys Asp His Asn Cys His Asn Leu
      10                      15                      20
ccg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat      256
Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp
      25                      30                      35
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc      304
His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe
      40                      45                      50
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat      352
Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp
      55                      60                      65
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct      400

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Leu Phe Arg Asp Ser Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser
 70 75 80 85
 ggc gaa cac cat tcc tgatttccca caaactgcac tacatcagta taactgcatt 455
 Gly Glu His His Ser

90
 tctagtttct ataatgtgca atagagcata gattctataa attcttactt gtctaagaaa 515
 gttaaactctgt gttaaacaag tagtaataaa agttaattca atccaaaaaa aaaaaa 571

<210> 302
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..268

<221> sig_peptide
 <222> 56..100
 <223> Von Heijne matrix
 score 4.59999990463257
 seq LLTHNLLSSHVRG/VG

<221> polyA_signal
 <222> 584..589

<221> polyA_site
 <222> 601..612

<400> 302
 ctaatcgaaa aggggggattt tccgggtccg gcctggcgag agtttgtgcg gcgac atg 58
 Met
 -15

aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg 106
 Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly
 -10 -5 1

tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc 154
 Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys
 5 10 15

cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg 202
 Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val
 20 25 30

gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag 250
 Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln
 35 40 45 50

gtg ccg aga agg gcc ggt tgagggatat gaggagaatg aggagtttct 298
 Val Pro Arg Arg Ala Gly
 55

gaggaccatg caccacctgc tgctggaggt ggamstgaka gagggcaccc tgcagtgccc 358
 ggaatctgga cgtatgttcc ccatcagccg cgggatcccc aacatgctgc tgagtgaaga 418
 ggaaactgag agttgattgt gccaggcgcc agtttttctt gttatgactg tgtatttttg 478
 ttgatctata ccctgtttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac 538
 accaaacaca gtgtttttga gctcggtatt atatattttt ttctcattaa aggtttaaaa 598
 ccaaaaaaaaa aaaa 612

<210> 303
 <211> 539
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..328

<221> sig_peptide

<222> 32..103

<223> Von Heijne matrix

score 4.59999990463257

seq FFIFCSLNTLLLG/GV

<221> polyA_signal

<222> 508..513

<221> polyA_site

<222> 528..539

<400> 303

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aacaactatc ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga      52
                                   Met Lys Ser Ala Lys Leu Gly
                                   -20
ttt ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg      100
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu
      -15                               -10                               -5
ggg ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat      148
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp
      1                               5                               10                               15
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt      196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe
      20                               25                               30
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc      244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe
      35                               40                               45
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt      292
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg
      50                               55                               60
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg      338
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg
      65                               70                               75
tgaactcatg aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcaractg      398
atttwgaaat ctttgttwta tttccmymak ggcgwktaag cttccatattg tttgctatgt      458
tcctgacctt agttttgtct ttcttggaat ttaactgtat gakkattasa atgaaagagt      518
ctttctgtca aaaaaaaaaa a
                                   539

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<210> 304

<211> 964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..527

<221> sig_peptide

<222> 21..95

<223> Von Heijne matrix

score 8.5

seq LKVLPLLPLAPAAA/QD

<221> polyA_signal
<222> 921..926

<221> polyA_site
<222> 953..963

<400> 304

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agggcggatc ttctccggcc atg agg aag cca gcc gct ggc ttc ctt ccc tca      53
                Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
                -25                -20                -15
ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat      101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp
                -10                -5                1
tcg act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac      149
Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr
                5                10                15
caa cgc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc      197
Gln Arg Phe Phe Ala Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr
                20                25                30
tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag      245
Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln
                35                40                45                50
ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc      293
Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys
                55                60                65
tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act      341
Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr
                70                75                80
cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt      389
His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys
                85                90                95
tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa      437
Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu
                100                105                110
sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc      485
Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Leu Pro His Leu Thr
                115                120                125                130
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc      527
Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala
                135                140
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccttgctccc tgggaggcca      587
ggagcaagcg ccagagcaca agcaggagca aggagtggag cacaggcagg agccgacaca      647
agaacacaag caggaagagg ggcagaaaca ggaagagcaa gaagaggaac aggaagagga      707
gggaaagcag gaagaaggac aggggactaa ggagggacgg gaggctgtgt ctcagctgca      767
gacagactca gagcccaagt ttcactctga atctctatct tctaaccctt cctcttttgc      827
tccccgggta cganaagtag agtctactcc tatgataatg gagaacatcc aggagctcat      887
tcgatcagcc caggaaatag atgaaatgaa tgaaatatat gatgagaact cctactggag      947
aaaccaaaaa aaaaaaak      964

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<210> 305
<211> 684
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..647

<221> sig_peptide
<222> 147..374

<223> Von Heijne matrix
score 3.5
seq LASASELPLGSRP/AP

<221> polyA_site

<222> 668..681

<400> 305

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aacttcctgt gagcccgccg gtgacaacgg caacatggcc cgtgaacgga gctgaagtcg      60
acgacttctc ctrgrarmcc cgcactgagg cggagacgaa ggtgctgcag gcgcgacggg      120
agcggcaaga tcgcatctcc cggctc atg ggc gac tat ctg ctg cgc ggt tac      173
                               Met Gly Asp Tyr Leu Leu Arg Gly Tyr
                               -75                               -70

cgc atg ctg ggc gag acg tgt gcg gac tgc ggg acg atc ctc ctc caa      221
Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln
-65                               -60                               -55

gac aaa cag cgg aaa atc tac tgc gtg gct tgt cag gaa ctc gac tca      269
Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser
-50                               -45                               -40

gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc      317
Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser
-35                               -30                               -25                               -20

caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc      365
Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly
-15                               -10                               -5

tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag      413
Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu
1                               5                               10

gga gct gca gca gga ctc aag gca gcc cag ggg cca cct gct cct gct      461
Gly Ala Ala Ala Gly Leu Lys Ala Ala Gln Gly Pro Pro Ala Pro Ala
15                               20                               25

gtg cct cca aat aca rat gtc atg gcc tgc aca cag aca gcc ctc ttg      509
Val Pro Pro Asn Thr Xaa Val Met Ala Cys Thr Gln Thr Ala Leu Leu
30                               35                               40                               45

caa aag ctg acc tgg gcc tct gct gaa ctg ggc tct anc acc tcc cyg      557
Gln Lys Leu Thr Trp Ala Ser Ala Glu Leu Gly Ser Xaa Thr Ser Xaa
50                               55                               60

gga aaa mta gca tcc agc tgt gtg gcc tta tcc gcg cat gtg cgg agg      605
Gly Lys Xaa Ala Ser Ser Cys Val Ala Leu Ser Ala His Val Arg Arg
65                               70                               75

ccc tgc gca gcc tgc agc agc tac agc act aag aga agc ccc      647
Pro Cys Ala Ala Cys Ser Ser Tyr Ser Thr Lys Arg Ser Pro
80                               85                               90

tgagaaaaaac ctctagaaaa acaaaaaaaaaaaa aaaaccc      684

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<210> 306

<211> 693

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 262..471

<221> sig_peptide

<222> 262..306

<223> Von Heijne matrix
score 3.5
seq LCFLLPHHRLQEA/RQ

<221> polyA_signal
<222> 663..668

<221> polyA_site
<222> 682..693

<400> 306

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atttcgcggc gctcgcgbgma cyhsgwtgtt cagcaccttc ggtccggttg aggttggtcaa      60
gtcggmccaa acaggttggtt tctctgcagt ttccaacatg gcagggmsgt ttaatagaca      120
tggataagaa gtccactcac agaaatcctg aagatgccag ggctggcaaa tatgaaggta      180
aacacaaacg aaagaaaaga agaaagcaaa accaaaacca gcaccgatcc cgacatagat      240
cagtgcgctc tttttcttca g atg atc cta tgt ttc ctt ctt cct cat cat      291
                               Met Ile Leu Cys Phe Leu Leu Pro His His
                               -15                               -10

cgt ctt cag gaa gcc aga cag att caa gta ttg aag atg ctt cca agg      339
Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro Arg
-5                               1                               5                               10
gaa aaa tta aga aga aga gaa gag aga aaa caa ata aat ggg aaa aaa      387
Glu Lys Leu Arg Arg Arg Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys
                               15                               20                               25
raa agg aca aaa tat gaa aca cca aga aaa rga raa gga aaa aaa gga      435
Xaa Arg Thr Lys Tyr Glu Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly
                               30                               35                               40
gga aac mac cmc wtw tkt cmc ctt tcc aar agg gac tgaaactggg      481
Gly Asn Xaa Xaa Xaa Xaa Xaa Leu Ser Lys Arg Asp
                               45                               50                               55
ctgacccttt tgattttcaa vctcascgtt ttggtgtaag gcggccaaar aaggatgcgg      541
ascccagcac tgtgaagcct acaaaaacat tgatgcgctg gcttggggat ttgaatttga      601
acatctttca cactaagttc agactcatga aaccaatctt cagatgctct gtaaaccaca      661
taataaagag tttggaaaatt aaaaaaaaaa aa      693

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<210> 307
<211> 1656
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..1216

<221> sig_peptide
<222> 74..172
<223> Von Heijne matrix
score 5.80000019073486
seq XLCLGMALCPRQA/TR

<221> polyA_signal
<222> 1627..1632

<221> polyA_site
<222> 1640..1652

<400> 307

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atctcttggc gtctcaacgt tcggatcagc agcttttttc cattctctct ctcactttct      60
tcagtgcgca gcc atg agt tgg act gtg cct gtt gtg cgg gcc agc cag      109
                               Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln
                               -30                               -25

aga gtg agc tcg gtg gga gcg aat ktc cta tgc ctg ggg atg gcc ctg      157
Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu
-20                               -15                               -10

```

tgt	ccg	cgt	caa	gca	acg	cgc	atc	ccg	ctc	aac	ggc	acc	tgg	ctc	ttc	205
Cys	Pro	Arg	Gln	Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	
-5					1			5						10		
acc	ccc	gtg	agc	aag	atg	gcg	act	gtg	aar	agt	gag	ctt	att	gag	cgt	253
Thr	Pro	Val	Ser	Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	
		15						20					25			
ttc	act	tcc	gar	aag	ccc	gtt	cat	cac	agt	aag	gtc	tcc	atc	ata	gga	301
Phe	Thr	Ser	Glu	Lys	Pro	Val	His	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	
		30					35					40				
act	gga	tcg	gtg	ggc	atg	gcc	tgc	gct	atc	agc	atc	tta	tta	aaa	ggc	349
Thr	Gly	Ser	Val	Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	
	45					50					55					
ttg	agt	gat	gaa	ctt	gcc	ctt	gtg	gat	ctt	gat	gaa	rac	aaa	ctg	aag	397
Leu	Ser	Asp	Glu	Leu	Ala	Leu	Val	Asp	Leu	Asp	Glu	Xaa	Lys	Leu	Lys	
60					65					70				75		
ggg	gag	acr	atg	gat	ctt	caa	cat	ggc	agc	cct	ttc	acg	aaa	atg	cca	445
Gly	Glu	Thr	Met	Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro	
			80					85						90		
aat	att	gtt	tgt	agc	aaa	rat	tac	ttt	gtc	aca	gca	aac	tcc	aac	cta	493
Asn	Ile	Val	Cys	Ser	Lys	Xaa	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu	
		95						100					105			
gtg	att	atc	aca	gca	ggg	gca	cgc	caa	raa	aag	gga	gaa	acg	cgc	ctt	541
Val	Ile	Ile	Thr	Ala	Gly	Ala	Arg	Gln	Xaa	Lys	Gly	Glu	Thr	Arg	Leu	
	110						115						120			
aat	tta	stc	cag	cga	aat	gtg	gcc	atc	ttc	aag	tta	atg	att	tcc	agt	589
Asn	Leu	Xaa	Gln	Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser	
	125					130					135					
att	gtc	cag	tac	agc	ccc	cac	tgc	aaa	ctg	att	att	gtt	tcc	aac	cca	637
Ile	Val	Gln	Tyr	Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro	
140					145					150				155		
gtg	gat	atc	tta	act	tat	gta	gct	tgg	aag	ttg	agt	gca	ttt	ccc	aaa	685
Val	Asp	Ile	Leu	Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys	
			160					165					170			
aac	cgt	att	att	gga	agc	ggc	tgt	aat	ctg	ata	mhg	gct	cgt	ttt	cgt	733
Asn	Arg	Ile	Ile	Gly	Ser	Gly	Cys	Asn	Leu	Ile	Xaa	Ala	Arg	Phe	Arg	
		175						180					185			
ttc	ttg	att	gga	caa	aag	ctt	ggg	atc	cat	tct	gaa	agc	tgc	cat	gga	781
Phe	Leu	Ile	Gly	Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly	
	190						195					200				
tgg	atc	ctc	gga	gag	cat	gga	gac	tca	agt	gtt	cct	gtg	tgg	agt	gga	829
Trp	Ile	Leu	Gly	Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	
	205					210					215					
gtg	aac	ata	gct	ggg	gtc	cct	ttg	aag	gat	ctg	aac	tct	gat	ata	gga	877
Val	Asn	Ile	Ala	Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly	
220					225					230				235		
act	gat	aaa	gat	cct	gag	caa	tgg	aaa	aat	gtc	cac	aaa	gaa	gtg	act	925
Thr	Asp	Lys	Asp	Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr	
			240					245					250			
gca	act	gcc	tat	gag	att	att	aaa	atg	aaa	ggg	tat	act	tct	tgg	gcc	973
Ala	Thr	Ala	Tyr	Glu	Ile	Ile	Lys	Met	Lys	Gly	Tyr	Thr	Ser	Trp	Ala	
		255					260					265				
att	ggc	cta	tct	gtg	gcc	gat	tta	aca	gaa	agt	att	ttg	aag	aac	ctt	1021
Ile	Gly	Leu	Ser	Val	Ala	Asp	Leu	Thr	Glu	Ser	Ile	Leu	Lys	Asn	Leu	
		270					275					280				
agg	aga	ata	cat	cca	gtt	tcc	acc	ata	act	aag	ggc	ctc	tat	gga	ata	1069
Arg	Arg	Ile	His	Pro	Val	Ser	Thr	Ile	Thr	Lys	Gly	Leu	Tyr	Gly	Ile	
	285					290					295					
rat	gaa	gaa	gta	ttc	ctc	agt	att	cct	tgt	atc	ctg	gga	gag	aac	ggg	1117
Xaa	Glu	Glu	Val	Phe	Leu	Ser	Ile	Pro	Cys	Ile	Leu	Gly	Glu	Asn	Gly	
300					305					310				315		
att	acc	aac	ctt	ata	aag	ata	aag	ctg	acc	cct	gaa	gaa	gag	gcc	cat	1165
Ile	Thr	Asn	Leu	Ile	Lys	Ile	Lys	Leu	Thr	Pro	Glu	Glu	Glu	Ala	His	


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          320          325          330
ctg aaa aaa agt gca aaa aca ctc tgg gaa att cag aat aag ctt aag      1213
Leu Lys Lys Ser Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys
          335          340          345
ctt taaagttgcc taaaactacc attccgaaat tattgaagag atcatagata      1266
Leu
caggattata taacgaaatt ttgaataaac ttgaattcct aaaagatgga aacaggaaag      1326
taggtagagt gattttccta tttatttagt cctccagctc ttttattgag catccacgtg      1386
ctggacgata cttatttaca attcckaagt atttttggta cctctgatgt agcagcactt      1446
gccatgttat atatatgtag ttgrmathtt gttcccaaaa agtaggatgt aggtatttat      1506
tgtgttctag aaattccgac tcttttcatt agatatatgc tatttctttc attcttgctg      1566
gtttatacct atgttcattt atatgctgta aaaaagtagt agcttcttct acaatgtaaa      1626
aataaatgta catacaaaaa aaaaaamcmc                                1656

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<210> 308
 <211> 517
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..164

<221> sig_peptide
 <222> 48..89
 <223> Von Heijne matrix
 score 4
 seq YYMVCLFFRLIFS/EH

<221> polyA_signal
 <222> 482..487

<221> polyA_site
 <222> 505..517

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<400> 308
aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac      56
                                   Met Tyr Tyr
atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att      104
Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile
-10          -5          1          5
ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca      152
Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro
          10          15          20
aca tct gct ggc taaataaaga catgatcttc accttttggg attgttaatt      204
Thr Ser Ala Gly
          25
taaaatgggt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctggtg      264
atttatatgg ctcttcacaa ggtgttattt tggggatatca aggtatggat gcttaaatca      324
gctgcaggaa gtaagaaaga agaaaaaagg agtgataaag ataaaaaaaa atcaaccttg      384
gtccttcac caaaacccat taatttccat atcatcatct gcataararg gaaaattcct      444
acwtgaccag gttactgcaa ggatktkaat tttgaatatt aaaatattat mcmcaattgg      504
aaaaaaaaaa aaa                                              517

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<210> 309
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 185..334

<221> sig_peptide

<222> 185..295

<223> Von Heijne matrix

score 5.90000009536743

seq LSYASSALSPCLT/AP

<221> polyA_signal

<222> 355..360

<221> polyA_site

<222> 392..405

<400> 309

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atcaccttct tctccatcct tstctgggcc agtcccccac ccagtccttc tctgacctg      60
cccagcccaa gtcagccttc agcacgcgt tttctgcaca cagatattcc aggcctacct      120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg      180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg      229
    Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
          -35          -30          -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
          -20          -15          -10
ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg      325
Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met
          -5          1          5          10
cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc      374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaaa a      405

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<210> 310

<211> 1087

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 195..347

<221> sig_peptide

<222> 195..272

<223> Von Heijne matrix

score 7.09999990463257

seq LASLQWSLTLAWC/GS

<221> polyA_signal

<222> 1037..1042

<221> polyA_site

<222> 1071..1082

<400> 310

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aaagtgtaga acacggacct ctgagttatg ctcttgagag gtgccaaagc tgggctgttt      60
acctacctta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg      120
gaattttatc tagaaaagaa gactaagcag cttttgttct tctgtgaccc agttgctggc      180
ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg      230

```

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      Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg
      -25                -20                -15
cct ctc gct tct ttg cag tgg agc ctg aca ctg gcg tgg tgt ggc tcc 278
Pro Leu Ala Ser Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser
      -10                -5                1
ggc agc cac tgg aca gag aga cca akt cag akt tca ccg tgg akt tct 326
Gly Ser His Trp Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser
      5                10                15
ctg tca gcg acc acc agg ggg tgatcacacg gaaggtgaac atccaggtcg 377
Leu Ser Ala Thr Thr Arg Gly
      20                25
gggatgtgaa tgacaacgcg cccacatttc acaatcagcc ctacagcgtc cgcateccctg 437
araatacacc agtgggggacg cccatcttca tcgtgaatgc cacagacccc gacttggggg 497
caggggggcag cgtcctctac tccttccagc ccccctccca attcttcgcc attgacagcg 557
cccgcggtat cktcacagtg atccgggagc tggactacga taccacrcmg gcctaccagc 617
tcwcggtcwa cgccacagat caagacaara ccaggcctct gtccaccstg gccaaacttg 677
ccatcatcat cacagatgtc caggacatgg accccatctt catcaacctg ccttacagca 737
ccaacatcta cgagcattct cctccgggca cgacggtgcg catcatcacc gccatagacc 797
aggataaagg acgtcccccg ggcattgggt acaccatcgt ttcagggcat ctgtgtttac 857
aagaacccaa gatctctcag gagctcagga aaaggggctt gctgtgaggc tcagggttcc 917
catggacatt ctgagctgac cctcctcagc attggatctc ctggctcagg aactaggaac 977
gaagcttggg tgttttctcc tttcctacag catctgtatt catttcctat agttgccata 1037
ataaaatgcc actaacttag tggcttaaaa accaaaaaaa aaaaaccctt 1087

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<210> 311
 <211> 916
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..815

<221> sig_peptide
 <222> 90..179
 <223> Von Heijne matrix
 score 13.1999998092651
 seq LLLLSTLVIPSAA/AP

<221> polyA_signal
 <222> 883..888

<221> polyA_site
 <222> 905..916

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<400> 311
aaaacagtac gtgggcgggc ggaatccggg agtccggtga cccgggctgt ggtctagcat 60
aaaggcggag ccagaagaag gggcggggt atg gga gaa gcc tcc cca cct gcc 113
      Met Gly Glu Ala Ser Pro Pro Ala
      -30                -25
ccc gca agg cgg cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg 161
Pro Ala Arg Arg His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu
      -20                -15                -10
gtg atc ccc tcc gct gca gct cct atc cat gat gct gac gcc caa gag 209
Val Ile Pro Ser Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu
      -5                1                5                10
agc tcc ttg ggt ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc 257
Ser Ser Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser
      15                20                25
cga ctt ttc ctg aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc 305

```

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Arg Leu Phe Leu Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe
      30                      35                      40
tct gcc ccc atg gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag      353
Ser Ala Pro Met Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu
      45                      50                      55
gag aac cag gag cac cag ctg ggg aac aac acc ctc tcc agc cac ctc      401
Glu Asn Gln Glu His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu
      60                      65                      70
cag atc gac aag atg acc gac aac aag aca gga gag gtg ctg atc tcc      449
Gln Ile Asp Lys Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser
      75                      80                      85                      90
gag aat gtg gtg gca tcc att caa cca vcg gag ggg anc ttc gag ggt      497
Glu Asn Val Val Ala Ser Ile Gln Pro Xaa Glu Gly Xaa Phe Glu Gly
      95                      100                      105
gat ttg aag gth ccc agg atg gag gar aag gag gcc ctg gta ccc mtc      545
Asp Leu Lys Val Pro Arg Met Glu Lys Glu Ala Leu Val Pro Xaa
      110                      115                      120
car aag gcc acg gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc      593
Gln Lys Ala Thr Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala
      125                      130                      135
ttc tgg atc att aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg      641
Phe Trp Ile Ile Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu
      140                      145                      150
gag ggc ggc cac tgg ctc anc gar aag cga cac cgc ctg cag gcc atc      689
Glu Gly Gly His Trp Leu Xaa Glu Lys Arg His Arg Leu Gln Ala Ile
      155                      160                      165                      170
cgg gat gga ctc cgc aag ggg acc cac aag gac rtc cta daa rag ggg      737
Arg Asp Gly Leu Arg Lys Gly Thr His Lys Asp Xaa Leu Xaa Xaa Gly
      175                      180                      185
acc gar agc tcc tcc cac tcc agg ctg tcc ccc cga aar amm cac tta      785
Thr Glu Ser Ser Ser His Ser Arg Leu Ser Pro Arg Lys Xaa His Leu
      190                      195                      200
ctg tac atc ctc arg ccc tct cgg cag ctg targgggtggg gaccgggggar      835
Leu Tyr Ile Leu Xaa Pro Ser Arg Gln Leu
      205                      210
macctgcctg tagcccccat caraccctgc cccaagcacc atatggaaat aaagttcttt      895
cttacatcca aaaaaaaaaa a      916

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<210> 312

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..513

<221> sig_peptide

<222> 52..231

<223> Von Heijne matrix

score 4

seq LVRRTLLVAALRA/WM

<221> polyA_signal

<222> 553..558

<221> polyA_site

<222> 572..583

<400> 312

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aaggaaacag caaccagagg gagatgatca cctgaaccac tgctccaaac c atg ggc      57
                                   Met Gly
                                   -60
agt aaa tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag      105
Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln
                                   -55
agg cgg cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg      153
Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val
                                   -40
aarg gca gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc      201
Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg
                                   -25
agg acc ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg      249
Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp
                                   -10
tgg agg acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg      297
Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu
                                   10
ttr ggg gtc tac gtc atc cag gag cag gcg gcg gtc aag ctc cag tcc      345
Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu Gln Ser
                                   25
tgc atc cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat      393
Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn
                                   40
gct ctc tgc ttg ttc cag gtc cca aaa agc agc ctt gcc ttc caa act      441
Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe Gln Thr
                                   55
gat ggc ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag      489
Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu
                                   75
ttc cac att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg      543
Phe His Ile Glu Ile Leu Ser Ile
                                   90
cactacccta ataaatgtct gaccaggtaa aaaaaaaaaa      583

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<210> 313
 <211> 697
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..438

<221> sig_peptide
 <222> 172..354
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LLPCNLHCSWLHS/SP

<221> polyA_signal
 <222> 682..687

<221> polyA_site
 <222> 685..697

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<400> 313
agattggctg ggcagatggg ctgactggct gggcagatgg gtgggtgagt tccctctccc      60
cagagccatc ggccagggtac caaagctcag ctgtatggat tcccaacagg aggacctgag      120
cttccctggg acccattgtt gtactggatt aacaagcgac ggcgctacgg c atg aat      177

```

Met Asn
-60

gca gcc atc aac acg ggc cct gcc cct gct gtc acc aag act gag act 225
Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr Glu Thr
-55 -50 -45

gag gtc cag aat cca gat gtt ctg tgg gat ttg gac atc ccc gaa gcc 273
Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro Glu Ala
-40 -35 -30

agg agc cat gct gac caa gac agc aac ccc aag gcg gaa gcc ctg ctc 321
Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala Leu Leu
-25 -20 -15

ccc tgc aac ctg cac tgc agc tgg ctc cac agc agc ccc agg cca gat 369
Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg Pro Asp
-10 -5 1 5

ccc cat tcc cac ttc cca tct ktc agg agg tgc cct ttg ccc cac cct 417
Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro His Pro
10 15 20

tgt gca acc tac ccc ccs kgc tgaaccactc tgtctcctat cctttggcca 468
Cys Ala Thr Tyr Pro Pro Xaa
25

cctgtcctga aaggaatggt ctcttccatt cctctctgaa tctggcccag gaagaccata 528
gcttcaatgy caagcctttt ccttcaaaaac tgtagcctcc tctcactgaa ggtgggagct 588
gcaggaatca ggtgcagagt aggaaatgga actaacctca ggaagggtggt attgacagag 648
gtcaggaccc acctggatgt catgctatga aacattaaaa gaaaaaaaaa 697

<210> 314
<211> 803
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..366

<221> sig_peptide
<222> 148..225
<223> Von Heijne matrix
score 5.5
seq LFTLLFLIMLVLK/LD

<221> polyA_signal
<222> 770..775

<221> polyA_site
<222> 792..803

<400> 314
aaatggggggg aaaaggcgcg aaaaggacaa ggatccaaac tggcgaattt gctgatcttc 60
gcgtccctct ccgctttccg gccggcagcg ctgccagggt atatttcctt tttccgatc 120
ctgcaacagc ctctttaaac tgttttaa atg aga atg tcc ttg gct cag aga gta 174
Met Arg Met Ser Leu Ala Gln Arg Val
-25 -20

cta ctc acc tgg ctt ttc aca cta ctc ttc ttg atc atg ttg gtg ttg 222
Leu Leu Thr Trp Leu Phe Thr Leu Leu Phe Leu Ile Met Leu Val Leu
-15 -10 -5

aaa ctg gat gag aaa gca cct tgg aac tgg ttc ctc ata ttc att cca 270
Lys Leu Asp Glu Lys Ala Pro Trp Asn Trp Phe Leu Ile Phe Ile Pro
1 5 10 15

gtc tgg ata ttt gat act atc ctt ctt gtc ctg ctg att gtg aaa atg 318
Val Trp Ile Phe Asp Thr Ile Leu Leu Val Leu Leu Ile Val Lys Met

	20	25	30	
gct ggg cgg tgt aag tct ggc ttt gac ctc gac atg gat cac aca ata				366
Ala Gly Arg Cys Lys Ser Gly Phe Asp Leu Asp Met Asp His Thr Ile				
	35	40	45	
taaaaaaaaa aacctggtac ctcattgcac tgtkacttaa attasccttc tgcctcgcac				426
tctgtgctaa actggaacag tttactacca tgaatctatc ctatgtcttc attcctttat				486
gggccttgct ggctggggct ttaacagaac tcggatataa tgtctttttt gtgaaagact				546
gacttctaag tacatcatct cctttctatt gctgttcaac aagttaccat taaagtgttc				606
tgaatctgtc aagcttcaag aataccagag aactgagggg aaataccaaa ttagtattta				666
tactacttcc ataaaacagg attggtgaat cacggacttc tagtcaacct acagcttaat				726
tattcagcat ttgagttatt gaaatcctta ttatctctat gtaaataaag tttgttttgg				786
acctcaaaaa aaaaaaa				803

<210> 315

<211> 823

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 175..336

<221> sig_peptide

<222> 175..276

<223> Von Heijne matrix

score 3.70000004768372

seq SVLNVGHLLFSSA/CS

<221> polyA_site

<222> 812..823

<400> 315

aaggcgcgcg cgaccggcgg ctctttggcg cggattaggg ggtctcggcg agggagtcac	60
caagctttgg tgtatgtgtt ggccggttct gaagtcttga agaagctctg ctgaggaaga	120
ccaaagcagc actcgttgcc aattagggaa tggaccgttt gggttccttt agca atg	177
	Met
atc cct ctg ata agc cac ctt gcc gag gct gct cct cct acc tca tgg	225
Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser Trp	
	-30 -25 -20
agc ctt ata tca agt gtg ctg aat gtg ggc cac ctc ctt ttt tcc tct	273
Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser Ser	
	-15 -10 -5
gct tgc agt gtt tca ctc gag gct ttg agt aca aga aac atc aaa gcg	321
Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys Ala	
1 5 10 15	
atc ata ctt atg aaa taatggcttc agattttcct gtccttgatc ccagctggac	376
Ile Ile Leu Met Lys	

tgctcaagaa raaatggccc ttttagaasc tgtgatggac tgtggctttg gaaattggca	436
ggatgtagcc aatcaaagt gcaccaarac caaggaggag tgtgagaagc actatatgaa	496
gcatttcac aataaccyc tgtttgcac trscctgctg aacctgaaac aascagrnga	556
agcaaaaact gctgacacag ccattccatt tcaactetaca ratgaccctc cccgacckac	616
ctttgactcc ttgctttctc gggacatggc cgggtacwtg ccmgctcgag cagatttcat	676
tgaggaattt gacaattatg cagaatggga cttgagagac attgattttg ttgaagatga	736
ctcggacatt ttacatgctc tgaagatggc tgtggtagat atctatcatt ccagggttaa	796
ggagagacaa agacgaaaa aaaaaaa	823

<210> 316

<211> 823
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 191..553

<221> sig_peptide
 <222> 191..304
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LAFLSCLAFLVLVD/TQ

<221> polyA_signal
 <222> 766..771

<221> polyA_site
 <222> 804..817

<400> 316
 aactctgcag ggcctccaag gccaggcttc agggctggga ctcaagtctg aggcactggg 60
 gagccatgag gggctgtggc agggaggggc aggggtgtgga aagactcccc tggggccatg 120
 gtggagatgt gctgaggtct tctccctgat cgtcttctcc tccctgctga ccgacggcta 180
 ccagaackag atg gag tct ccg cag ctc cac tgc att ctc aac agc aac 229
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn
 -35 -30
 agc gtg gcc tgc agc ttt gcc gtg gga gcc ggc ttc ctg gcc ttc ctc 277
 Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
 -25 -20 -15 -10
 agc tgc ctg gcc ttc ctc gtc ctg gac aca cag gag acc cgc att gcc 325
 Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
 -5 1 5
 ggc acc cgc ttc aag aca gcc ttc cag ctc ctg gac ttc atc ctg gct 373
 Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala
 10 15 20
 gtt ctc tgg gca gtt gtc tgg ttc atg ggt ttc tgc ttc ctg gcc aac 421
 Val Leu Trp Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn
 25 30 35
 caa tgg cag cat tcg ccg ccc aaa gar kkc ctc ctg ggg agc agc agt 469
 Gln Trp Gln His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser
 40 45 50 55
 gcc cag gca gcc atc ggc stt cac ctt ctt ctc cat cct tgt ctg gat 517
 Ala Gln Ala Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp
 60 65 70
 att cca rgc cta cct ggc akk cca gga cct ccg aaa tgatgctcca 563
 Ile Pro Xaa Leu Pro Gly Xaa Pro Gly Pro Pro Lys
 75 80
 gtcccttacm arcgcttccct ggatgaaggt ggcattggtgs kkaacaccct ccccttgccc 623
 tctgccaaaca gcctgtgaac atgcccacca ctggcccca cagcctgagt tatgctagct 683
 ctgccttgct cccctgtctg accgctcmaa agtccccccg gcttgctatg atgcctgaca 743
 actaaatatc cttatccaaa tcaataaaga gagaatcctc cctccagaag ggttttctaaa 803
 aacaaaaaaa aaaahncctt 823

<210> 317
 <211> 1112
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 106..603

<221> sig_peptide
<222> 106..216
<223> Von Heijne matrix
score 4.30000019073486
seq LWEKLTLLSPGIA/VT

<221> polyA_site
<222> 1102..1112

<400> 317

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agcgattgcg aatcctccgc tgaggtgatt tggatatccc tagaacgttg agggcacgag      60
tcgggtcctg agaccaggtc ctcagccagc agagccacgt tcctt atg agc acc gtg      117
                                     Met Ser Thr Val
                                     -35
ggt tta ttt cat ttt cct aca cca ctg acc cga ata tgc ccg gcg cca      165
Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile Cys Pro Ala Pro
                                     -30               -25           -20
tgg gga ctc cgg ctt tgg gag aag ctg acg ttg tta tcc cca gga ata      213
Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu Ser Pro Gly Ile
                                     -15               -10           -5
gct gtc act ccg gtc cag atg gca ggc aag aag gac tac cct gca ctg      261
Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp Tyr Pro Ala Leu
1               5               10               15
ctt tcc ttg gat gag aat gaa ctc gaa gag cag ttt gtg aaa gga cac      309
Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe Val Lys Gly His
                                     20               25           30
ggt cca ggg ggc cag gca acc aac aaa acc agc aac tgc gtg gtg ctg      357
Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn Cys Val Val Leu
                                     35               40           45
aar mac atc ccc tca ggc atc gtt gta aag tgc cat cag aca aga tca      405
Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His Gln Thr Arg Ser
                                     50               55           60
gtt gat cag aac aga aag cta gct cgg aaa atc cta caa gag aaa gta      453
Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu Gln Glu Lys Val
65               70               75
rat gtt ttc tac aat ggt gaa aac agt cct gtt cac aaa gaa aaa cga      501
Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His Lys Glu Lys Arg
80               85               90               95
gaa gcg gcg aag aaa aaa car gaa agg aaa aaa aga gca aag gaa acc      549
Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg Ala Lys Glu Thr
100               105               110
ctg gaa aaa aag aas ctm ctt aaa raa ctg tgg gag tca agt aaa aag      597
Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu Ser Ser Lys Lys
115               120               125
gtc cac tgagaaaaga attagagatt ccaactgaca gaatctgcca gaagctccca      653
Val His
gggaataatg gtggcgagtt ccatcaccag cattattata gtgcttcaaa agaaatattt      713
ttgatgaact taaaagacaa caaatattatt taaatggtgc actaaactgt agtgaacaga      773
gacatgcacg attcaagaat aaaactcggc cgggcacggt ggacggtgcc tcacatctgt      833
aatcccagca ctttgggagg ccgagggcggg cggatcactt gaggtcagga gtttgagacc      893
agcctggcca acatggtgaa acccgcgtctc tactaaaaat acaaaaaatt agccaggcat      953
ggtggcgggc acctgtaatc ccagctactc gggaggccga ggcaggagaa ttgcgtgaac      1013
ctgggaggcg gaggttcgag tgagctgaga tcgcgccact gcactcaagc ctgggcaaca      1073
cctgggtgac agagcaagac cccatcycaa aaaaaaaaaa      1112

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<210> 318
<211> 1623

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..586

<221> sig_peptide
<222> 47..124
<223> Von Heijne matrix
score 6.30000019073486
seq GVGLVTLLGLAVG/SY

<221> polyA_signal
<222> 1583..1588

<221> polyA_site
<222> 1614..1623

<400> 318
agggatctgt cggcttgtca ggtggtggag gaaaaggcgc tccgtc atg ggg atc 55
Met Gly Ile
-25
cag acg agc ccc gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act 103
Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr
-20 -15 -10
ctg ctc ggc ctg gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg 151
Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg
-5 1 5
cct cag gtc act ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg 199
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu
10 15 20 25
cta gac aag acg act gtg agc cac aac acc aag agg ttc cgc ttt gcc 247
Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala
30 35 40
ctg ccc acc gcc cac cac act ctg ggg ctg cct gtg ggc aaa cat atc 295
Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly Lys His Ile
45 50 55
tac ctc tcc acm mga att gat ggc agc ctg gtc atc agg cca tac act 343
Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr
60 65 70
cct gtc acc agt gat gag gat caa ggc tat gtg gat ctt gtc mtc aag 391
Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Xaa Lys
75 80 85
gtc tac ctg aag ggt gtg cac ccc aaa ttt cct gag gga ggg aar atg 439
Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met
90 95 100 105
tct cak tac ctg gat asc ctg aaa gtt ggg gat btg gtg gaa ttt csg 487
Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val Glu Phe Xaa
110 115 120
ggg cca agc ggg ttg ctc act tac act gga aaa ggg cat ttt aac att 535
Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile
125 130 135
cag ccc aac aag aat ctc cac cag aac ccc gag tgg cga aga aac tgg 583
Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg Arg Asn Trp
140 145 150
gaa tgattgccgg cgggacagga atcaccccaa tgctacagct gatccggggc 636
Glu
atcctgaaag tccctgaaga tccaaccag tgctttctgc tttttgccaa ccagacagaa 696
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aagctctggg tcaactctgga tcatccccc aaagrttggg cctacagcaa gggctttgtg 816
actgccgacw tgatccggga acacctgccc gctccagggg atgatgtgct ggtactgctt 876

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tgtggggccmc- ccccaatggt gcagctggcc tgccatccca acttggacaa actgggctac 936
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gataatcgaa aactgctgtt tgtgggcarg aaccctggc tgtgcaaata atggggctga 1596
ngccctgtgt gatattgaaa aaaaaaa 1623

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<210> 319

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 99..371

<221> sig_peptide

<222> 99..290

<223> Von Heijne matrix

score 3.79999995231628

seq LFIVVCVICVTLN/FP

<221> polyA_signal

<222> 491..496

<221> polyA_site

<222> 513..524

<400> 319

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attggattag tagaattgct tttgtcattc cattgttttc atatatttgt ttgggacatt 60
ttactttttt ctgttaacgc ttaccctagr aattagaa atg aca cca cgt att ctt 116
                                Met Thr Pro Arg Ile Leu
                                -60

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agc gaa gtc cag ttt tca gca ttt tgt cct tat tgg aca ata gca agg 164
Ser Glu Val Gln Phe Ser Ala Phe Cys Pro Tyr Trp Thr Ile Ala Arg

```

-55

-50

-45

```

ata tta gaa cgt gtt ggt tcc gcg tgc ttc cgt ctt gag tta tgt gct 212
Ile Leu Glu Arg Val Gly Ser Ala Cys Phe Arg Leu Glu Leu Cys Ala

```

-40

-35

-30

```

gct att gtc gga tat ttt gtc tta gat gta cgt act ttc ctg ttc att 260
Ala Ile Val Gly Tyr Phe Val Leu Asp Val Arg Thr Phe Leu Phe Ile

```

-25

-20

-15

```

gtg gta tgt gta att tgc gtt act ttg aat ttt cca cgt ttt tac ttt 308
Val Val Cys Val Ile Cys Val Thr Leu Asn Phe Pro Arg Phe Tyr Phe

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-10

-5

1

5

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ctt tgt ctc tca tca ctt acc gct ttt ggg acc ccc ccc atc ggg gtt 356
Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly Thr Pro Pro Ile Gly Val

```

10

15

20

```

cac att ccc tct ccc tararcacac tcccttgat ttcctcradt ggggtctgct 411
His Ile Pro Ser Pro

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25

```

gcgggtgaagc tttcccatTTt tatgtgcaga ttattttcag agggatatata gaattcaggc 471
agctgttttcg ttgtagcaca ttaaaaaatat tttcccactt caaaaaaaaaa aaacc 526

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<210> 320
 <211> 989
 <212> DNA
 <213> Homo sapiens

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<221> sig_peptide
 <222> 44..112
 <223> Von Heijne matrix
 score 8.30000019073486
 seq VRLLLXLLLLLLIA/LE

<221> polyA_site
 <222> 978..989

<400> 320

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                                         Met Arg Arg Ile
                                         -20
tcc ctg act tct agc cct gtg cgc ctt ctt ttg tdt ctg ctg ttg cta      103
Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Xaa Leu Leu Leu Leu
          -15                      -10                      -5
cta ata gcc ttg gag atc atg gtt ggt ggt cac tct ctt tgc ttc aac      151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn
          1                      5                      10
ttc act ata aaa tca ttg tcc aga cct gga cag ccc tgg tgt gaa gcg      199
Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala
          15                      20                      25
cat gtc ttc ttg aat aaa aat ctt ttc ctt cag tac aac agt gac aac      247
His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn
          30                      35                      40                      45
aac atg gtc aaa cct ctg ggc ctc ctg ggg aag aag gta tat gcc acc      295
Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr
          50                      55                      60
agc act tgg gga gaa ttg acc caa acg ctg gga gaa gtg ggg cga gac      343
Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu Val Gly Arg Asp
          65                      70                      75
ctc agg atg ctc ctt tgt gac atc aaa ccc car ata aag acc agt gat      391
Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile Lys Thr Ser Asp
          80                      85                      90
cct tcc act ctg caa gtc kar atk ttt tgt caa cgt gaa gca gaa cgg      439
Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg Glu Ala Glu Arg
          95                      100                      105
tgc act ggt gca tcc tgg cag ttc gcc acc aat gga gag aaa tcc ctc      487
Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly Glu Lys Ser Leu
          110                      115                      120                      125
ctc ttt gac gca atg aac atg acc tgg aca gta att aat cat gaa gcc      535
Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile Asn His Glu Ala
          130                      135                      140
agt wag atc aag gag aca tgg aag aaa gac aga ngg ctg gaa aak tat      583
Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa Leu Glu Xaa Tyr
          145                      150                      155
ttc agg aag ctc tca aar gga gac tgc gat cac tgg ctc agg gaa ttc      631
Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp Leu Arg Glu Phe
          160                      165                      170
tta ggg cac tgg gaa gca atg cca raa ccg ama gtg tcm cca rta aat      679

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Leu	Gly	His	Trp	Glu	Ala	Met	Pro	Xaa	Pro	Xaa	Val	Ser	Pro	Xaa	Asn		
175						180					185						
gct	tca	raw	atc	cac	tgg	tct	tct	tct	art	cta	cca	raw	ara	tgg	atc	727	
Ala	Ser	Xaa	Ile	His	Trp	Ser	Ser	Ser	Xaa	Leu	Pro	Xaa	Xaa	Trp	Ile		
190					195				200					205			
atc	ctg	ggg	gca	ttc	atc	ctg	tta	vtt	tta	atg	gga	att	gtt	ctc	atc	775	
Ile	Leu	Gly	Ala	Phe	Ile	Leu	Leu	Xaa	Leu	Met	Gly	Ile	Val	Leu	Ile		
				210					215					220			
tgt	gtc	tgg	tgg	caa	aat	ggc	ara	ara	tcc	acc	tad	arg	tgata	accacg		824	
Cys	Val	Trp	Trp	Gln	Asn	Gly	Xaa	Xaa	Ser	Thr	Xaa	Xaa					
				225					230								
gcggcgcaaaa	attgttcacc	tgtggtcctc	gatcgctgac	agccttggct	cccactgctg											884	
tgtgttcct	gagtcagt	gagggcgagc	ctgcaatgag	cggaratcgc	gcctctgcat											944	
tccagtcttg	gcaacagarc	aagactccgt	ctcaaaaaaa	aaaaa												989	

<210> 321
 <211> 1017
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..581

<221> sig_peptide
 <222> 3..182
 <223> Von Heijne matrix
 score 6.69999980926514
 seq LWPFLTWINPALS/IC

<221> polyA_site
 <222> 1006..1016

<400>	321																
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	Met	Cys	Pro	Ser	Leu	Glu	Glu	Ala	Pro	Ser	Val	Lys	Gly	Thr	Leu		
	-60				-55				-50								
ccc	tgc	tca	gga	caa	cag	cag	cct	ttc	ccg	ttt	gga	gcc	tca	aac	atc	95	
Pro	Cys	Ser	Gly	Gln	Gln	Gln	Pro	Phe	Pro	Phe	Gly	Ala	Ser	Asn	Ile		
-45				-40				-35				-30					
cca	cta	ctc	ctg	ggc	agg	agc	aga	aag	gtg	gct	cga	ggt	gca	ccg	gtc	143	
Pro	Leu	Leu	Leu	Gly	Arg	Ser	Arg	Lys	Val	Ala	Arg	Gly	Ala	Pro	Val		
				-25				-20				-15					
ctg	tgg	cca	ttt	ctc	act	tgg	ata	aac	cct	gca	ctg	tcc	atc	tgt	gac	191	
Leu	Trp	Pro	Phe	Leu	Thr	Trp	Ile	Asn	Pro	Ala	Leu	Ser	Ile	Cys	Asp		
			-10				-5					1					
ccc	tta	gga	tcc	tgc	gga	tgg	cyw	tgc	cac	acg	gcc	car	gtc	cct	gcg	239	
Pro	Leu	Gly	Ser	Cys	Gly	Trp	Xaa	Cys	His	Thr	Ala	Gln	Val	Pro	Ala		
5				10				15									
ccc	ctg	car	ttg	cct	act	gcc	tgt	cct	ccc	ctc	cca	cat	ggc	acc	cgg	287	
Pro	Leu	Gln	Leu	Pro	Thr	Ala	Cys	Pro	Pro	Leu	Pro	His	Gly	Thr	Arg		
20				25				30				35					
gct	gta	ggc	ccc	acg	cca	ggc	ctc	ctc	cct	gag	gct	gca	gcc	cca	sgc	335	
Ala	Val	Gly	Pro	Thr	Pro	Gly	Leu	Leu	Pro	Glu	Ala	Ala	Ala	Pro	Xaa		
				40				45				50					
acg	tgk	ggg	gca	ctg	tcc	tca	cgc	agc	agg	cac	tgg	tca	tgt	tcc	att	383	
Thr	Xaa	Gly	Ala	Leu	Ser	Ser	Arg	Ser	Arg	His	Trp	Ser	Cys	Ser	Ile		
			55				60					65					
gtc	arc	tgc	ctc	cac	ctg	cac	ara	ctc	ctg	tct	gtg	gag	acc	aga	arc	431	
Val	Xaa	Cys	Leu	His	Leu	His	Xaa	Leu	Leu	Ser	Val	Glu	Thr	Arg	Xaa		

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      70      75      80
ttc cas aaa cat ctg ttg gtg ctg ctg gtg gct gtg gcc cat agt gtt 479
Phe Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val
      85      90      95
ctg gaa cca cct gcc ctg gtc cca aat gtg cag tgt gag atg tgc aca 527
Leu Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr
100      105      110      115
cac tca ggg ccc cgt gac ctg gaa gcc gca gtc gtg tcc cca gca cct 575
His Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro
      120      125      130
tgg gaa tgagcctgtc ctctgtgtga aggaggggggt ggttctcaaa ccactgactc 631
Trp Glu
ttggtgctca ggaggggacct gctgctgtcc tgggcatggg gtgggtcattg ttcaagactg 691
aggcagactc agtctttgaa aggggtgcaga ggccaggcgc ggtgggtcac gcctgtaatt 751
ccagcacttt gggaggccaa ggtggacaga tcatgagggtc aggagttcga gaccagcctg 811
gccaatatcgg tgaaaccgca tctctactaa rraatawcaaw aaattagtcg ggcattgggtg 871
atgtgtgctt gtagtcccag ctactcatga ggyctgaggc agaagaatca cctgaatctg 931
ggaggcagag gttgcagtga accaagatcg cactgactgta caccagcctg ggcgacagag 991
tgagactccg tctcaaaaaa aaaaam 1017

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<210> 322
 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..427

<221> sig_peptide
 <222> 107..190
 <223> Von Heijne matrix
 score 3.79999995231628
 seq RFLSLSAADGSDG/SH

<221> polyA_signal
 <222> 499..504

<221> polyA_site
 <222> 516..529

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                                     Met Val Leu
acg ctc gga gaa agt tgg ccg gta ttg gtg ggg agg agg ttt ctc agt 163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
-25      -20      -15      -10
ctg tcc gca gcc gac ggc agc gat ggc agc cac gac agc tgg gac gtg 211
Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser Trp Asp Val
      -5      1      5
gag cgc gtc gcc gag tgg ccc tgg ctc tcc ggg acc att cga gct gtt 259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
      10      15      20
tcc cac acc gac gtt acc aag aag gat ctg aag gtg tgt gtg gaa ttt 307
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys Val Glu Phe
      25      30      35
gak ggg gaa tct tgg agg aaa aga aga tgg ata gaa gtc tac agc ctt 355
Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val Tyr Ser Leu
40      45      50      55

```

```

cta agg aaa gca ttt tta gta aaa cat aat ttg gtt tta gct gaa cga      403
Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu Ala Glu Arg
      60                      65                      70
aag tca cct gaa att tct tgg ggt taaccatctt tagttaaatg gaattttaat      457
Lys Ser Pro Glu Ile Ser Trp Gly
      75
ttaaatgacg ctttgctaatt tttaagtgtt aagcattttg cattaataaata ttcataataat      517
aaaaaaaaaa aa                                                              529

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<210> 323
 <211> 1046
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..407

<221> sig_peptide
 <222> 45..83
 <223> Von Heijne matrix
 score 5.69999980926514
 seq MLVLRALTRALA/SR

<221> polyA_signal
 <222> 1008..1013

<221> polyA_site
 <222> 1032..1042

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<400> 323
aaaaggacac ggctggctgc ttttctcagc gccgaagccg cgcc atg ctc gtc ctc      56
                                         Met Leu Val Leu
                                         -10
aga agc gcc ctg act cgg gcg ctg gcc tca cgg acg ctg gcg cct cag      104
Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr Leu Ala Pro Gln
      -5                      1                      5
atg tgc tca tct ttt gct acg gga ccc aga caa tac gat gga ata ttc      152
Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr Asp Gly Ile Phe
      10                      15                      20
tat gaa ttt cgt tct tat tac ctt aag ccc tca aag atg aat gag ttc      200
Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys Met Asn Glu Phe
      25                      30                      35
ctg gaa aat ttt gag aaa aac gct caa ctt cgg aca gct cac tct gaa      248
Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr Ala His Ser Glu
      40                      45                      50                      55
ttg gtt gga tac tgg agt gta kaa ttt gga ggc aga atg awt aca gtg      296
Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg Met Xaa Thr Val
      60                      65                      70
ttt cat att tgg aag tat gat aat ttt gct cat cga act gaa ttt cag      344
Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Glu Phe Gln
      75                      80                      85
aaa gcc ttg gcc aaa gat aag gaa tgg caa gaa caa ttc ctc att cca      392
Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Pro
      90                      95                      100
aat ttg gct ctc aat tgataaaca gatagtgaga ttacttatct ggtaccatgg      447
Asn Leu Ala Leu Asn
      105
tgcaaattag aaaaacctcc aaaagaagga gtctatgaac tggccacttt tcagatgaaa      507
cctggtgggc cagctctgtg gggatgatgca tttaaaaggg cagttcatgc tcatgtcaat      567

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ctaggctaca caaaactagt tggagtgttc cacacagagt acggagcact caacagagtt 627
catgttcttt ggtggaatga gagtgcagat agtcgtgcag ctgggagaca taagtcccat 687
gaggatccca gagggtgtgc agctgttcgg gaaagtgtca actacctagt atctcagcag 747
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aacatttcat taactgctat aggatctgtc tgctaattgg gcttaaattc tcccaagagg 867
ttctcacttt tatttgaagg aggtggtaag ttaatttgc atgtttcttg cattatgaag 927
gctacatctg tgctttgtaa gtaccacttc aaaaaatakt tctgtttact ttctgcatgg 987
tatttcagtg tctgtcatat attaaaaata cttgtcactg tttyaaaaaa aaaaammcc 1046

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<210> 324
 <211> 880
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 201..332

<221> sig_peptide
 <222> 201..251
 <223> Von Heijne matrix
 score 7.80000019073486
 seq VLWLISFFTFDTG/HG

<221> polyA_site
 <222> 869..880

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yhccwsvar tyctggwgtg amgagataaa tcaccagtca cagactatgc acccgactgc 180
tgctgttcag tccagggaaa atg aaa gtt gga gtg ctg tgg ctc att tct ttc 233
                               Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe
                               -15                               -10
ttc acc ttc act gac ggc cac ggt ggc ttc ctg ggg gtg agt tgg tgc 281
Phe Thr Phe Thr Asp Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys
-5                               1                               5                               10
tat gtc tca tat ctc ttc tca act aac tct cct ctc tgg ttc cgg cgc 329
Tyr Val Ser Tyr Leu Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg
                               15                               20                               25
att tagaaccct cactctctag gggactgcaa ctgcataatt taatgtactt 382
Ile
gagatcagaa gtcctgagtt ctggtttcaa cattaccaac attcactgtg tggccttgga 442
taagtragtc atttcatctc ttcggagctt agatgatcma actgcaarag gaggatcttt 502
gattamacta tcttagagat cttttccagt tcaacacatg ctgtactatg gcttctcgga 562
tgcagaaaaa tcacatggat ggacattagc aatccttara cactgtcttt cctgtctaca 622
ctcgcttgag tgatgckttc atctaggatc atgggtttta tattctctac atgctgatga 682
ctcccagctg tatagctcca tctcagaacc tctcccctgt ccacactcac atatccatta 742
cctacgtggt atttccagct gggaaatcca gcggaacctc ggnaacttca tttgnttcaa 802
aatcgnaacc caatccttct tgcttatctc agcaagtggg atcactatct ttccagctac 862
ttaggcaaaa aaaaaaaaaa
880

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<210> 325
 <211> 1217
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 217..543

<221> sig_peptide
<222> 217..255
<223> Von Heijne matrix
score 6.40000009536743
seq MCLLTALVTQVIS/LR

<221> polyA_site
<222> 1206..1217

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gaacactcga gctgagaaac atttttaggat ctttgtgtct tttgtgatga tttgttttct      120
graagrwgga aasctgtcta aaaatattca agtgtgcaac caaggattta gatgaagcca      180
gcaaacaaag gaatcatgta atcaggacct gagcga atg tgc tta ctc acg gcg      234
                               Met Cys Leu Leu Thr Ala
                               -10
tta gtt aca cag gtg att tcc tta aga aaa aat gca gag aga act tgt      282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
                               -5                               1                               5
tta tgc aag agg aga tgg ccc tgg ngc ccc tcg ccc cgg atc tac tgc      330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
10                               15                               20                               25
tca tcc acc cca tgc gat tcc aaa ttc ccc acc gtc tac tcc agt gcc      378
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser Ala
                               30                               35                               40
cca ttc cat gcc ccc ctc ccc gtc cag aat tcc tta tgg ggg cac ccg      426
Pro Phe His Ala Pro Leu Pro Val Gln Asn Ser Leu Trp Gly His Pro
                               45                               50                               55
ctc cat ggt tgt tcc tgg caa tgc cac cat ccc cag gga car aat ctc      474
Leu His Gly Cys Ser Trp Gln Cys His His Pro Gln Gly Gln Asn Leu
60                               65                               70
cag cct gcc agt ctc cad acc cat ctc tcc aag ccc aag cgc cat ttt      522
Gln Pro Ala Ser Leu Xaa Thr His Leu Ser Lys Pro Lys Arg His Phe
75                               80                               85
ara aar aar rra tgt caa gcc tgatgaarac atgagtggca aaaacattgc      573
Xaa Lys Lys Xaa Cys Gln Ala
90                               95
aatgtacara aatgagggtt tctatgctga tccttacctt tatcacgagg gacggatgag      633
catascctca tcccatggtg gacacccact ggatgtcccc gaccacatca ttgcatatca      693
ccgcaccgcc atccggtcag cgagtgttta ttgtaacccc tcaatgcaag cggaaatgca      753
tatggaacaa tcaactgtaca gacagaaatc aaggaaatat ccggatagcc atttgcctac      813
actgggctcc aaaacacccc ctgcctctcc tcacagaktc agtgacctga ggatgataga      873
catgcacgct cactataatg cccacggccc ccctcacacc atgcagccag accgggcctc      933
tccgagccgc caggccttta aaaaggagcc aggcaccttg gtgtatatag aaaagccacg      993
gagcgctgca ggattatcca gccttgtaga cctcggccct cctctaattg agaagcaagt      1053
ttttgcctac agcacggcga caatacccaa agacagagag accagagaga ggatgcaagc      1113
catggagaaa cagattgccg gtttaactgg ccttggttcag tctgcgcttt ttaaaggggc      1173
cattacaagt tatagcaaar atgcgtctag ctaaaaaaaaaa aaaa      1217

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 score 4.09999990463257
 seq GILILWIIRLLFS/KT

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 <222> 930..935

<221> polyA_site
 <222> 948..959

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 gag atg gta cag gcg ctt tac gag gct cct gct tac cat ctt att ttg 98
 Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu
 -30 -25 -20 -15
 gaa ggg att ctg atc ctc tgg ata atc aga ctt ctt ttc tct aag act 146
 Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr
 -10 -5 1
 tac aaa tta caa gaa cga tct gat ctt aca gtc aag gaa aaa gaa gaa 194
 Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu
 5 10 15
 ctg att gaa gag tgg caa cca gaa cct ctt gtt cct cct gtc cca aaa 242
 Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys
 20 25 30
 gac cat cct gct ctc aac tac aac atc gtt tca ggc cct cca agc cac 290
 Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His
 35 40 45 50
 aaa act gtg gtg aat gga aaa gaa tgt ata aac ttc gcc tca ttt aat 338
 Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn
 55 60 65
 ttt ctt gga ttg ttg gat aac cct agg gtt aag gca gca gct tta gca 386
 Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala
 70 75 80
 tct cta aag aag tat ggc gtg ggg act tgt gga ccc tgt gga ttt tat 434
 Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr
 85 90 95
 ggc aca ttt gaa tgaaratgaa ggatcattga tttccttgtg tatggataat 486
 Gly Thr Phe Glu
 100
 ccgggaacag gccaaactaaa tatttgatga atgtatgatt tcaaatacag tgaattccct 546
 gggagtcac aaaraagacg gcattttatg gttgttttta ttaagtgtat attcctttgct 606
 cctgaaaatg ttattaaata attgtttagg ccgggcatgg tggctcatgc ctgtaatccc 666
 agcactttca aaggctgagg caggcagatc acctgaggtc aggagttcaa aaccagcctg 726
 gccaacatgc tgaaacctcg tctctactaa aaatacaaaa attagctggg cgtgggtggg 786
 grtgccctgtg gtcccagctr cgtgggaggg tgaggtggga gaattgcttc aacctgggag 846
 gcggaggttg cagtgaagcc agatcatgcc actgcactcc agcctgggca acagagcaag 906
 actgtctcaa aaataaataa ataaataaaa ttgttttaaat gaaaaaaaaa aaa 959

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<222> 29..724

<221> sig_peptide

<222> 29..118

<223> Von Heijne matrix

score 3.90000009536743

seq VAHALSLPAESYG/NX

<221> polyA_signal

<222> 886..891

<221> polyA_site

<222> 910..920

<400> 327

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                               -30                               -25

gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg ctt tct ctg      100
Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala Leu Ser Leu
                               -20                               -15                               -10

cca gca gag tcg tat ggy aac grt yct gac att gag atg gct tgg gcc      148
Pro Ala Glu Ser Tyr Gly Asn Xaa Xaa Asp Ile Glu Met Ala Trp Ala
                               -5                               1                               5                               10

atg aga gca atg cag cat gct gaa gtc tat tac aag ctg att tca tca      196
Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu Ile Ser Ser
                               15                               20                               25

gtt gac cca cag ttc ctg aaa ctc acc aaa gta gat gac caa att tac      244
Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp Gln Ile Tyr
                               30                               35                               40

tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat gtg ttg grc      292
Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp Val Leu Xaa
                               45                               50                               55

cca gaa gan ctc aag tca gaa tca gcn aaa gag ccc cca gga tac aat      340
Pro Glu Xaa Leu Lys Ser Glu Ser Ala Lys Glu Pro Pro Gly Tyr Asn
                               60                               65                               70

tct ttg cca ttg aaa ttg ctc gga acc ggg aag gct ata aca aag ctg      388
Ser Leu Pro Leu Lys Leu Leu Gly Thr Gly Lys Ala Ile Thr Lys Leu
75                               80                               85                               90

ttt ata tca gtg ttc agg aca aag aag gag aga aag gag tca aca atg      436
Phe Ile Ser Val Phe Arg Thr Lys Lys Glu Arg Lys Glu Ser Thr Met
                               95                               100                               105

gag gag aaa aaa gag ctg aca gtg gag aag aag aga aca cca aga atg      484
Glu Glu Lys Lys Glu Leu Thr Val Glu Lys Lys Arg Thr Pro Arg Met
                               110                               115                               120

gag gag aga aag gag ctg ata gtg gag aag aaa aag agg aag gaa tca      532
Glu Glu Arg Lys Glu Leu Ile Val Glu Lys Lys Lys Arg Lys Glu Ser
                               125                               130                               135

aca gag aag aca aaa ctg aca aag gag gag aaa aag gga aag aag ctg      580
Thr Glu Lys Thr Lys Leu Thr Lys Glu Glu Lys Lys Gly Lys Lys Leu
                               140                               145                               150

aca aag aaa tca aca aaa gtg gtg aaa aag cta tgt aag gta tac agg      628
Thr Lys Lys Ser Thr Lys Val Val Lys Lys Leu Cys Lys Val Tyr Arg
155                               160                               165                               170

gaa cag cac tct aga agc tat gac tca att gag act aca agt acc acg      676
Glu Gln His Ser Arg Ser Tyr Asp Ser Ile Glu Thr Thr Ser Thr Thr
                               175                               180                               185

gtg cta ctt gca cag acc cct ttg gtt aaa tgt aaa ttc ttg tac aat      724
Val Leu Leu Ala Gln Thr Pro Leu Val Lys Cys Lys Phe Leu Tyr Asn
                               190                               195                               200

tgaaggatac gcagaaggac atctttctag tctaacagtc aggagctgct ctgggtcattc      784
ccttgatatga actggtctaa agactggttag tgggggtgta gttgattttt cctgggtatac      844

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tgtttcttgg ctgacactac tgggtcaagta agaaatttgt aaataaaattt cttttgggttc 904
 ttattaamaa aaaaaas 921

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 <222> 404..586

<221> sig_peptide
 <222> 404..466
 <223> Von Heijne matrix
 score 4.09999990463257
 seq SLMFFSMMATCTS/NV

<221> polyA_signal
 <222> 1304..1309

<221> polyA_site
 <222> 1334..1344

<400> 328
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 agacaatttt aaaatcctgg gamccawatt tatttagaag tagctgttag taaaacatta 180
 gaaaaggagt caggccatba gggtatttat nbnaatctct aagcaattag gntgaagtta 240
 ttaagtcaag cctagaaaaag ctgcctcctt gtaaggcttt catgacaatg tatagtaatc 300
 brcagtgtcc aattcttcgc actcctcagg aatatcacta cctcagggtta cggtaacacag 360
 gctataattg atgatgatgt tcagataact gaagacacaa taa atg aca ttc aga 415
 Met Thr Phe Arg
 -20
 cat cag gac aat tcc ctc atg ttc ttt tct atg atg gcc acc tgt acc 463
 His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met Ala Thr Cys Thr
 -15 -10 -5
 agc aac gtg ggt ttc acc cac aca acg atg aac tgt tct ctt act tct 511
 Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys Ser Leu Thr Ser
 1 5 10 15
 cca gtt gat ttt aaa gac ttg tta aga gtc tta cta ata aaa ttt ggg 559
 Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu Ile Lys Phe Gly
 20 25 30
 tat gat aga aaa tcc aca atc aaa tct tgaaccaa aacatattaa 606
 Tyr Asp Arg Lys Ser Thr Ile Lys Ser
 35 40
 attactaata ttttaagtgt ggaagacaca caaaaaactt aaaagcacga acaacctaac 666
 ttgaaaaara attttaaaat atgattaacc tgaaraaaaa araatcctaa ragccaaaagc 726
 tcctttttat ttagcttgga attttcctat tgggttcctaa caaactgtcc caatgtcata 786
 taaggaaaca tgatctatta cattccttta taacaacgtg gararactat aaacctatgt 846
 aagtagtaaa actatatcag adactcagga ractgactww aaggcctgga tctgcagtgt 906
 attatctgta taaaaattgg cagggggaag ctaaaaggaa aggagattgg agatctcaat 966
 tctatcatgg tgtatttcat acgcaaatca ragcatgcatt tgttttttgt ttttggaar 1026
 avaarggaag tgtgttctgc cccatgtttc cttccgtgtt tatagttcaa actctatata 1086
 tacttcaggt atttttttgt tagcccttca ttataaatgg gcaggaaatt gtttatcaac 1146
 ctageccagtt tattactagt gaccttgact tcagtatcct gagcattcct ttatatTTTT 1206
 cttttattat cctgagtctg taactaaaca attttgcctt caaattttta tccaatatcc 1266
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 aacttgtaaa aaaaaaaa 1344

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 <222> 331..432

<221> sig_peptide
 <222> 331..387
 <223> Von Heijne matrix
 score 7
 seq AGLSSCLLPLCWL/ER

<221> polyA_signal
 <222> 548..553

<221> polyA_site
 <222> 573..585

<400> 329
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 gcgcgggass ggtgccagtc tttaaacaac ctctcgatgg gtcccacgaa gatgtttcca 120
 gacccttgga atgccaagtt caagttagc tatgtctcgc ggagaggccg gtggaagaag 180
 caacgagaat gaagcacccc agttctctgc tgagcacatg ggcattctgca ataaagattt 240
 aatttcccag cttctcctga agctcggtat ggccacaaca ctaaattctg cccgaggaga 300
 ttgagcaaaa tagtatggga cttccaagaa atg ttt tta aag tca ggg gca ggc 354
 Met Phe Leu Lys Ser Gly Ala Gly
 -15
 ctt tct tca tgc ctt ctt cct ctt tgc tgg ctg gaa cgc aaa gac cat 402
 Leu Ser Ser Cys Leu Leu Pro Leu Cys Trp Leu Glu Arg Lys Asp His
 -10 -5 1 5
 ggc agg agg cca agc asc cat cct gga agg tgaaagcctc atactaagga 452
 Gly Arg Arg Pro Ser Xaa His Pro Gly Arg
 10 15
 cgtcaracag cgaaataara rcctgggtcc ttgacctgt aaasatctcc ctcccatcc 512
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 aaaaaaaaaa aaa 585

<210> 330
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<220>
 <221> CDS
 <222> 59..703

<221> sig_peptide
 <222> 59..220
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 score 5.09999990463257
 seq FLLSQMSQHQVHA/VQ

<221> polyA_signal
 <222> 886..891

<221> polyA_site

<222> 903..914

<400> 330

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atg aac rra tat gca agt cca ttc aac tgw caa ttg ard tat ttg gak      106
Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
      -50                      -45                      -40
ttg agc agr ttc gag tgt gtr cat aga gat gga aga gta att aca ctg      154
Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
      -35                      -30                      -25
tct tat cag gag cag gag cta cag gat ttt ctt ctg tct cag atg tca      202
Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
      -20                      -15                      -10
cag cac cag gta cat gca gtt cag caa ctc gcc aag gtt atg ggc tgg      250
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
      -5                      1                      5                      10
caa gta ctg agc ttc agt aat cat gtg gga ctt gga cct ata gag agc      298
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
      15                      20                      25
abt ggt aat gca tct gcc atc acg gtg gcc ccc caa gtg gtg act atg      346
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
      30                      35                      40
cta ttt cag ttc gta atg gac ctg aaa gtg gca gca aga tta tgg ttc      394
Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
      45                      50                      55
agt ttc ctc gta acc aat gta aar acc ttc caa aaa gtg atg ttt tac      442
Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
      60                      65                      70
aar ata aca aat gga gtc atc ttc gtg ggc cat tca aar aag ttc agt      490
Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
      75                      80                      85                      90
gga ata aaa tgg aag gtc kaa att ttg ttt ata aaa tgg arm tgc tta      538
Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
      95                      100                      105
tgt ctg cac tta gcc ctt gtc tac tat gat ttt ttc car atg ttt cct      586
Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
      110                      115                      120
aaa raa gtt tcc ara aac ttt gac ttg aaa tgt ttg car atc aac tat      634
Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
      125                      130                      135
aag cac aaa gaa gar ata act tcc aaa aga gtg ctg ttt tta aaa ata      682
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
      140                      145                      150
ata att agg aaa tgt ttt att tagcactttc aaacttttca ctttataaat      733
Ile Ile Arg Lys Cys Phe Ile
      155                      160
gacaagtgct ttgaaatgca gaagtttatg tacagttgta tatacagtat gacaagatgt      793
aaaataatat gtttttcatg cagtttaaaa tattactaac ttaagggttt ctatgtgctt      853
tttaaaatat tccttctttg atgttgacat caaataaagt atgtgggttta aaaaaaaaaa      913
a                                                                                   914
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<211> 1161

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 672..752

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 <222> 672..722
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LLYAHLSTSKRA/VV

<221> polyA_site
 <222> 1150..1161

<400> 331
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 ataaagcctt ccttttaaagc tttataataa tcatatttat taataatgct gttgtgcata 120
 cttatagtat gcatatatc agcatatggt gcatgtsttc agaattacat aagatgaaat 180
 ccctttcatt gcaacttgca agtgagaaaa gatccttagt ggctctgggtg gaagaaatag 240
 tatttcttct tctcaggggtg tctccctgcc ttggcccttc ccagaagccc cggctttaaa 300
 agtgaaaatg tttgaaacat gaaacatgct tgtaggaagc atcagcatgg ccataagtgc 360
 artgattttc atatatgcct ctgcccattt caaatatatt tttgacatga ataaatctaa 420
 cagtatacar aataattcat gtaaraccct aacgtgtaca tgtgaaaaag catttctata 480
 taatgtgagg agcactggcc atcaattagg gaaataaagg tcatgtaata ttgcaaattt 540
 tcaaaataga gcsstgcaag ataactgcaa tcataccaaa aactatttga gtaaatggat 600
 ttttaaagta atttttggtt aaaaaaattt atatttcaga agsagaaaat gtcaaattgat 660
 agtctttgta a atg gtg gtg cac ctt ctc tat gca cat ctg tct ttt aca 710
 Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr
 -15 -10 -5
 tca aaa aga gct gtg gtc atg cta aaa tta gag ata act ttt 752
 Ser Lys Arg Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
 1 5 10
 tgaatgactt ggtcaagctg tgtgtaaaaat atttaaccat aagtcaagta cagtgtacta 812
 tgtttaataa agttacattt aatgcattta ttgcatatat gaatatatac atgaagaggc 872
 tttatgtctt ctgggtatttg attttgaatg ttttttaagt cagtgggtgcc tttaggcaag 932
 aactttcgaa attaatcatt ctttgtgttt tctgattttt caggtaacat gtacactatt 992
 tagaaacat catagtttat tcaccttaaa aaattgattg tattatttaa atatatcact 1052
 tagatgggca tttcctataa ttaggatatt ccaaatagtt gctgaaatca attgtgccat 1112
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 57..311

<221> sig_peptide
 <222> 57..128
 <223> Von Heijne matrix
 score 5.30000019073486
 seq LFHLLFLPHYIET/FK

<221> polyA_signal
 <222> 332..337

<221> polyA_site
 <222> 351..363

<400> 332
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 Met

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tgt tct cat gcc tcc atg tct ttt cac aca ctg ttc cat ttg ctc ttc      107
Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu Phe
                -20                      -15                      -10
ctc cca cat tac att gaa act ttc aag cct cag tcg aaa cat tgc ttc      155
Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys Phe
                -5                      1                      5
ttc tgg ata gca gcc ttc ttg aca tcc ctc ctc act ccc cag tcc cta      203
Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser Leu
10                      15                      20                      25
cag ggc ttc cat agc tct tta tgt gca ctt cga tcc cag cat ttt cca      251
Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe Pro
                30                      35                      40
tcg act tgt aat tgt ttc tgc tac ctg aca atc atc gcc ttg drd tac      299
Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa Tyr
                45                      50                      55
tgg gac aac ctt tgattactca ttatatcctc aataaatatt tgttgaacca      351
Trp Asp Asn Leu
                60
aaaaaaaaaa aa      363

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<210> 333

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 80..232

<221> sig_peptide

<222> 80..127

<223> Von Heijne matrix

score 3.70000004768372

seq IALTLIPSMLSRA/AG

<221> polyA_signal

<222> 617..622

<221> polyA_site

<222> 634..645

<400> 333

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ttataaccgt ctttccctt atg cta agg ata gcc ctt aca ctc atc cca tct      112
                Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser
                -15                      -10
atg ctg tca agg gct gct ggt tgg tgc tgg tac aag gag ccc act cag      160
Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln
-5                      1                      5                      10
cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg aat aar aaa ggc      208
Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly
                15                      20                      25
aac gtt ttg cag ctt cca aat ttc tgaaraaact aatctcarat tggcagttaa      262
Asn Val Leu Gln Leu Pro Asn Phe
                30                      35
agtcaaaatg ttgccaaata tttattcctt ttgcctaakt ttggctaccc ggttcaattg      322
ctttttatatt ttaatgtctt gactcttcar agttctgtacc tcaaaaraac aatgaraaca      382
tttgctttgc tttctgctga atccctaata tcaacaatct atacctggac tgtccagttc      442
tcctcctgtg ctatcttctc ttctatccaa gtaraatgta ygccaggarc tccttccctc      502
tarcaatttc tactaaaatg tccaagtara atgtttcctt ttacaatcaa attactgtat      562

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ttattaattt gctaraatcc aktaaactcat ttggttagct ctggctgtgc tatcaataaa 622
aagatgaaag caaaaaaaaaaaa aaa 645

<210> 334
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..291

<221> sig_peptide
<222> 91..219
<223> Von Heijne matrix
score 3.79999995231628
seq LISVLYLIPKTLT/TN

<221> polyA_signal
<222> 367..372

<221> polyA_site
<222> 389..400

<400> 334
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taaaatattt tgttcttcaa ttacagagcg atg acc cca cag tat ctg cct cac 114
Met Thr Pro Gln Tyr Leu Pro His
-40
ggt gga aaa tac caa gtt ctt gga gat tac tct ttg gca gtg gtc ttc 162
Gly Gly Lys Tyr Gln Val Leu Gly Asp Tyr Ser Leu Ala Val Val Phe
-35 -30 -25 -20
ccc ctg cac ttt tct gat cta att tct gtt tta tac ctt ata ccc aaa 210
Pro Leu His Phe Ser Asp Leu Ile Ser Val Leu Tyr Leu Ile Pro Lys
-15 -10 -5
aca ctt act acc aac aca gct gtt aaa cat tct ata caa aaa aat tgt 258
Thr Leu Thr Thr Asn Thr Ala Val Lys His Ser Ile Gln Lys Asn Cys
1 5 10
atg mat ctg gta tta gga aaa tta ctt tca cag taaatatcaa agaaaaaaga 311
Met Xaa Leu Val Leu Gly Lys Leu Leu Ser Gln
15 20
ttaagggtct ctttgccatg cttttcatca tatgcaccaa atgtaaattt tgtacaataa 371
aattttattt cctaagyaaa aaaaaaaaaa 400

<210> 335
<211> 496
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 196..384

<221> sig_peptide
<222> 196..240
<223> Von Heijne matrix
score 6.69999980926514
seq ILSTVTALTFARA/LD


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      -5              1              5
tcc att tct gag ctc tgc aag gga caa gaa cta gag cca tca ggg gct      296
Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala
      10              15              20
ggg ctc act gtg gcc cca ccc caa gcc gtc agc ctc cag ggw atc tac      344
Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile Tyr
      25              30              35
acc ctg cct tgg ctg cta cag ctt ttt cac tcc act gcc cta rgg gna      392
Thr Leu Pro Trp Leu Gln Leu Phe His Ser Thr Ala Leu Xaa Xaa
      40              45              50              55
dtt cag caa cct aat gga tct cta tct ctg aac atc tct tca tcc cat      440
Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser His
      60              65              70
gct ccr rgt cca rca acc tgc acc ctg gaa cca gga gtg gac cct acc      488
Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro Thr
      75              80              85
cga sct gtc tgt att aat ccc cat ccc cca cca cca atc tta aaa abc      536
Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys Xaa
      90              95              100
cct ctg tcc ccc tac cct aaa ccc cag tta ggt acc cat gct ggg caa      584
Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly Gln
      105              110              115
gtc aat taacaattta tgcacaggta ctagttttat tgtattaccg ttccagggta      640
Val Asn
120
gctttgaaaa aagtatctca aaaaggcaac atgggcccag cgcagtggct cagcctgta      700
atcccagcac tttgggaggc caaggtgggc agatcgccct aggtctggag ttcaagacca      760
gcttgcccaa cagggtgaaa ccccgctctct acaaaaatar gaaaatttrgc caggtgtggt      820
ggcagacgtc tgrgtccca gctattcagg agactgaggc acgagaattc catgaaccca      880
ggatgcggag ttgcagtga gccgagattg tgccactgcg ctccagcctg ggcgacagag      940
tggtattctg tttcaaaaaa aaaaaamcm      968

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<210> 337
 <211> 901
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..846

<221> sig_peptide
 <222> 133..345
 <223> Von Heijne matrix
 score 9.39999961853027
 seq VVSFLLLLAGLIA/TY

<221> polyA_site
 <222> 890..901

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<400> 337
aagcagcttc caggatcctg agatccggag cagccgggggt cggagcggct cctcaagagt      60
tactgatcta tnnatggcag agaaaaaaaa attgtgacca gagacgtgta gcaatgaaca      120
aggaacrtca ta atg rwn nnk ttc aca gac ccc tct tca gtg aat gaa aag      171
      Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
      -70              -65              -60
aag agg agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag      219
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
      -55              -50              -45
ccg ctc att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg      267

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Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu
-40 -35 -30
aag gaa tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct 315
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser
-25 -20 -15
ttt tta ctg ctg ctt gct ggg ctt ata gct acg tat tat gtt gaa gga 363
Phe Leu Leu Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly
-10 -5 1 5
gtg cat caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat 411
Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr
10 15 20
gcc tac tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca 459
Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr
25 30 35
ggg ctg cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt 507
Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val
40 45 50
aca tta gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc 555
Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro
55 60 65 70
tat cct gat cag att att tgt cca gat gaa gag ggc act gaa gga acc 603
Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr
75 80 85
att tct ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg 651
Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met
90 95 100
tgg ggt atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc 699
Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala
105 110 115
aga gca gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag 747
Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln
120 125 130
gaa ttt gaa gag atg ctg gaa cat gca gag tct gca caa gta aga aca 795
Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr
135 140 145 150
gtg ggg ata gaa aat aga aca ctt tac ttc ttc cta aag agg cta tta 843
Val Gly Ile Glu Asn Arg Thr Leu Tyr Phe Phe Leu Lys Arg Leu Leu
155 160 165
agg taaaattggt agtagttact ctgaagaaga aaactgctaa agtaaaaaaa aaaaa 901
Arg

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<210> 338

<211> 1347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 138..671

<221> sig_peptide

<222> 138..248

<223> Von Heijne matrix

score 3.5

seq LVFNFLILTILT/IW

<221> polyA_signal

<222> 1319..1324

<221> polyA_site

<222> 1338..1347

<400> 338

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aagaatgctt gtgaagtagc aactaaagtg gcagtgtttc ttctgaaatt ctcaggcagt      60
cagactgtct taggcaaato ttgataaaat agcccttatac caggttttta tctaaggaat      120
cccaagaaga ctgggga atg gag aga cag tca agg gtt atg tca gaa aag      170
                Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys
                -35                                -30

gat gag tat cag ttt caa cat cag gga gcg gtg gag ctg ctt gtc ttc      218
Asp Glu Tyr Gln Phe Gln His Gln Gly Ala Val Glu Leu Leu Val Phe
-25                                -20                                -15

aat ttt ttg ctc atc ctt acc att ttg aca atc tgg tta ttt aaa aat      266
Asn Phe Leu Leu Ile Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn
-10                                -5                                1                                5

cat cga ttc cgc ttc ttg cat gaa act gga gga gca atg gtg tat ggc      314
His Arg Phe Arg Phe Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly
-10                                10                                15                                20

ctt aya atg gga cta att tta csa tat gct aca gca cca act gat att      362
Leu Xaa Met Gly Leu Ile Leu Xaa Tyr Ala Thr Ala Pro Thr Asp Ile
25                                30                                35

gaa agt ggr rct gtc tat gac tgt gta aaa cta act ttc agt cca tca      410
Glu Ser Gly Xaa Val Tyr Asp Cys Val Lys Leu Thr Phe Ser Pro Ser
40                                45                                50

act ctg ctg gtt aat atc act gac caa gtt tat gar tat aaa tac aar      458
Thr Leu Leu Val Asn Ile Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys
55                                60                                65                                70

aga gaa ata agt cag cac amc atc aat cct cat cam gga aat gct ata      506
Arg Glu Ile Ser Gln His Xaa Ile Asn Pro His Xaa Gly Asn Ala Ile
75                                80                                85

ctt gaa aag atg aca ttt gat cca raa atc ttc ttc aat gtt tta ctg      554
Leu Glu Lys Met Thr Phe Asp Pro Xaa Ile Phe Phe Asn Val Leu Leu
90                                95                                100

cca cca att ata ttt cat gca gga tat agt cta aag aag aga cac ttt      602
Pro Pro Ile Ile Phe His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe
105                                110                                115

ttt caa aac tta gga tct att tta acg tat gcc ttc ttg gga act gcc      650
Phe Gln Asn Leu Gly Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala
120                                125                                130

atc tcc tgc atc gtc ata ggg taagtacat tcggagctca agttgcaggt      701
Ile Ser Cys Ile Val Ile Gly
135                                140

ggctgtgggg tcygtgatct gtgtgagggga tctaactactt ccaggattct tgctggckgg      761
gaaaattgtc ttttttttar tawatcacaw atttgtatgt tttttcwgac ttaattccac      821
ggcttckgam aaatacaagg cttcaaataca aagcaaacta waggattgct ggactttctc      881
tgtgagttct ggacttctga cttagggaat gtggatcact tgccttgagt tatgtgaagc      941
gcattgcatt cttcttttag tttagtaaat sccgatatgc tcaactgcatt cttttttgtc      1001
ttgtattgag agaccttacc tgtatttgcc aggagtgcaa aagtaactat atgccaagag      1061
ttttctttct aaaggaaagt ttacaagaca gcagtctgaa acagatatgt ccaaataatca      1121
acagagttgc ttaatacagg gatagctttt cagttaatac cctgtagaat gcagactctt      1181
tttttcattg tattttcttg attatgctac tgagccctaa gtcacacgtt atatactctg      1241
gcttgcagct catcataaag taaaatgtgg taccaaatgg tgaaggcaat ccagcctctg      1301
ataatcccgt ccaatacatt aaagctccac tgcaggaaaa aaaaaa      1347

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<210> 339

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 124..411

<221> sig_peptide

<222> 124..186

<223> Von Heijne matrix

score 6.30000019073486

seq MVALCCCLWKISG/CE

<221> polyA_signal

<222> 948..953

<221> polyA_site

<222> 971..983

<400> 339

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aagacgctgc ctttagggag agataaaaag cataatgaca ttagctagga aagttaattt      60
tcagttctta ctgaagtgtc gtatgaaact gaaatttcca aggaactgaa tttgtgagc      120
caa atg agc atg caa ttc ttg ttt aag atg gtg gcc tta tgc tgt tgt      168
  Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys
    -20                -15                -10
ctc tgg aag atc tcc ggc tgt gag gaa gtc cct cta act tac aac ctg      216
Leu Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu
   -5                1                5                10
ctc aag tgc ctc cta gat aaa gcg cac tgt gta ctc ctg aca cct tgt      264
Leu Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys
           15                20                25
ggg tac atc ttt tcc ttg atc agt cca gaa att ctc aaa ctc act tta      312
Gly Tyr Ile Phe Ser Leu Ile Ser Pro Glu Ile Leu Lys Leu Thr Leu
           30                35                40
atc act ttg cav atc ctc tta ata ctc aaa aat cta cac tta ctg tgg      360
Ile Thr Leu Xaa Ile Leu Leu Ile Leu Lys Asn Leu His Leu Leu Trp
           45                50                55
ctg aca gtt tca agc awa tgt gtt cat cgc agt agt gca aga aaa gaa      408
Leu Thr Val Ser Ser Xaa Cys Val His Arg Ser Ser Ala Arg Lys Glu
           60                65                70
aag tagaagaacc ctgcagagat ttgatggaac ccagcttcta ttcattaaaa      461
Lys
75
ccaatggcaa aatataaaagc aaataggagg tgacgaaggt tacaaaaata cgtattgttt      521
atgtttttccc tgggggtgtgc tgattgtcag gcatcagttc cctgtgccat tcattcccca      581
acacagcatg catcagaaat tttatcaata aatgctttct ctctcaatgt tcaacctatg      641
ctgatagacc attaaataca gtttttgggt tcacagcttg tcatcatcat ttgtctatac      701
ctgtgggcaaa gaatatctaa taagatactc tcagcatttt gcacacttaa actaagatgc      761
tgaatgctgt attttacgga ataatcagcc acattaaatt tggagactca acaagcatgc      821
tgtgaacatt caacattagg tttaaatttt atttttaaaa gttaataata aaaggatata      881
tgtaagtat tatgaaaccc tgcataact gtaataaaat ggtggatgtg aatggacaat      941
atatgcaata aaatttataa tttgattcya aaaaaaaaaa aamccv      987

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<210> 340

<211> 748

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 372..494

<221> sig_peptide

<222> 372..443

<223> Von Heijne matrix

score 5.30000019073486
seq RILLLHFYCLLRS/SE

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..745

<400> 340
 acatgaaatg tgcttggtct gtgatctctt ggtcagatat ctgccttcca ggcgatacctt 60
 tgaggttgtg taattcagct ggccctggct cctggtcctt gttactgagc tgggcagtcg 120
 aaccgaaggc agatgagctc aagatcatgc cttgggaagc atgggtgctct aggggtgcct 180
 ttttattcct ttcattgtat tatagactgt ttccaagttt atggttagaa atggtaaagt 240
 ggggtctggtg ttttgaggta gaaccagacc tagggcaaga tatgaactgt tcttgaggta 300
 gaaatgtcta cagtcagttg tttcatctag cttgcatctt aaaacacaaa cccttcagtt 360
 gctttcactt a atg cac aca ttt gcc aat gac aga ggg tta tac agg atc 410
 Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile
 -20 -15
 ctt ctt tta cat ttc tat tgt ctg cta cgc tca tca gag tat att ttg 458
 Leu Leu Leu His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu
 -10 -5 1 5
 ggg tac aag gtt ttg ggg gtt ttt tty ccc att ttg taactgcctt 504
 Gly Tyr Lys Val Leu Gly Val Phe Phe Pro Ile Leu
 10 15
 attgaaaadt aaktgccctt ccattccagg cctcctcata ttgtacttgt ttcctgccaa 564
 atctggggga tcatttgtat ttttaactttg taatctatgg ctctgtactg ttgaaagstc 624
 tcaattctgt ggggtctcct tagtatgtat gtgacttttc atgttgcaat atcacacgat 684
 gggatggccc gacttttgct ctttaataaat aatctgaatg agtaagaraa aaaaaaaaaa 744
 accc 748

<210> 341
 <211> 1106
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..450

<221> sig_peptide
 <222> 112..192
 <223> Von Heijne matrix
 score 7.19999980926514
 seq SLLFFLLLEGGXT/EQ

<221> polyA_signal
 <222> 1053..1058

<221> polyA_site
 <222> 1095..1106

<400> 341
 aagacctcgg aacgagagcg ccccggggag ctcgagagcgc gtgcacgcgt ggcavacgga 60
 gaaggcvakk rcnnnnrctt gaaggttctg tcaccttttg cagtgggtcca a atg aga 117
 Met Arg
 raa aag tgg aaa atg gga ggc atg aaa tac atc ttt tcg ttg ttg ttc 165
 Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
 -25 -20 -15 -10
 ttt ctt ttg cta gaa gga ggc kaa aca gag caa gtr amn cat tca gag 213

Phe	Leu	Leu	Leu	Glu	Gly	Gly	Xaa	Thr	Glu	Gln	Val	Xaa	His	Ser	Glu		
				-5					1				5				
aca	tat	tgc	atg	ttt	caa	gac	aag	aag	tac	aga	gtg	ggt	gag	aga	tgg	261	
Thr	Tyr	Cys	Met	Phe	Gln	Asp	Lys	Lys	Tyr	Arg	Val	Gly	Glu	Arg	Trp		
	10						15					20					
cat	cct	tac	ctg	gaa	cct	tat	ggg	ttg	gtt	tac	tgc	gtg	aac	tgc	atc	309	
His	Pro	Tyr	Leu	Glu	Pro	Tyr	Gly	Leu	Val	Tyr	Cys	Val	Asn	Cys	Ile		
	25						30					35					
tgc	tca	gag	aat	ggg	aat	gtg	ctt	tgc	agc	cga	gtc	aga	tgt	cca	aat	357	
Cys	Ser	Glu	Asn	Gly	Asn	Val	Leu	Cys	Ser	Arg	Val	Arg	Cys	Pro	Asn		
	40					45				50				55			
gtt	cat	tgc	ctt	tct	cct	gtg	cat	att	cct	cat	ctg	tgc	tgc	cct	cgc	405	
Val	His	Cys	Leu	Ser	Pro	Val	His	Ile	Pro	His	Leu	Cys	Cys	Pro	Arg		
				60					65					70			
tgc	cca	gaa	gac	tcc	tta	ccc	cca	gtg	aac	aat	rwg	gtg	acc	agc		450	
Cys	Pro	Glu	Asp	Ser	Leu	Pro	Pro	Val	Asn	Asn	Xaa	Val	Thr	Ser			
				75				80						85			
tagtcttgck	agtacaatgg	gacaacttac	caacatggas	agctgttcgt	agctgrrggg											510	
ctctttcaga	atcggcaacc	cmatcaatgc	acccagtgca	gctgttcgga	rggaaacktg											570	
tattgtggtc	tcaagacttg	cccaaatta	acctgtgcct	tcccagtcctc	tggtccarat											630	
tcctgtctgcc	gggtwtgcag	argagatgga	caactgtcat	gggaacmttc	tgatgggtgat											690	
atcttccggc	aacctgccaa	cagagaagca	agacattctt	accaccgctc	tcactatgat											750	
cctccaccaa	gccgacaggc	tggaggtctg	tcccgcttct	ctggggccag	aagtcaccgg											810	
ggagctctta	tggattccca	gcaagcatca	ggaaccattg	tgcaaattgt	catcaataac											870	
aaacacaagc	atggacaagt	gtgtgtttcc	aatggaaaga	cctattctca	tgccgagtc											930	
tggcacccaa	acctccgggc	atttggcatt	gtggagtgtg	tgctatgtac	ttgtaatgtc											990	
accaagcaag	agtgtaaaga	aatccactgc	cccaatcgat	acccctgcaa	gtatcctcaa											1050	
aaaatagacg	gaaaatgctg	caaggtgtgt	ccaggtaaaa	aagcaaaaaa	aaaaaa											1106	

<210> 342

<211> 1191

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 117..866

<221> sig_peptide

<222> 117..170

<223> Von Heijne matrix

score 10.6999998092651

seq LILLALATGLVGG/ET

<221> polyA_signal

<222> 1159..1164

<221> polyA_site

<222> 1178..1190

<400> 342

aaaacccagc	ctacctgctg	tagctgccgc	cactgccgctc	tccgccgcca	ctggwccccc	60	
agagcbtnmag	ccccagagcc	taggaacctg	gggcccgcctc	ctccccctc	caggcc atg	119	
					Met		
agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg						167	
Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly							
	-15		-10		-5		
gga gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag						215	
Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln							
1		5		10		15	


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ccc tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg      263
Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
                20                      25                      30
acg ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag      311
Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
                35                      40                      45
ccc cgc tac ata ktt cac ctg ggg cag cac aac ctc cag aag gag gag      359
Pro Arg Tyr Ile Xaa His Leu Gln His Asn Leu Gln Lys Glu Glu
                50                      55                      60
ggc tgt gag car acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc      407
Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly
                65                      70                      75
ttc aac aac agc ctc ccc aac aaa gac cam mgc aat gac atc atg ctg      455
Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met Leu
                80                      85                      90                      95
gtg aak atg gma tgc cca gtc tcc atc acc tgg gct gtg cga ccc ctc      503
Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu
                100                      105                      110
acc ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc      551
Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser
                115                      120                      125
ggc tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg      599
Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu
                130                      135                      140
cga tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc      647
Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala
                145                      150                      155
tac ccc ggc aac atc aca gac acc atg gtg tgt gcc agc gtg cag gaa      695
Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu
                160                      165                      170                      175
ggg ggc aag gac tcc tgc cag ggt gac tcc ggg ggc cct ctg gtc tgt      743
Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
                180                      185                      190
aac cag tct ctt caa ggc att atc tcc tgg ggc cag gat ccg tgt gcg      791
Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
                195                      200                      205
atc acc cga aag cct ggt gtc tac acg aaa gtc tgc aaa tat gtg gac      839
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val Asp
                210                      215                      220
tgg atc cag gag acg atg aag aac aat tagactggac ccacccacca      886
Trp Ile Gln Glu Thr Met Lys Asn Asn
                225                      230
cagcccatca ccctccattt ccacttggtg tttgggttcct gttcactctg ttaataagaa      946
accctaagcc aagaccctct acgaacattc tttgggcctc ctggactaca ggagatgctg      1006
tcaacttaata atcaacctgg ggttcgaaat cagtgagacc tggattcaaa ttctgccttg      1066
aaatattgtg actctgggaa tgacaacacc tggtttgttc tctgttgat ccccgagcccc      1126
aaakwcagct cctggccata tatcaaggtt tcaataaata tttgctaaat gaawaaaaaa      1186
aaaac                                           1191

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<210> 343

<211> 1070

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 13..465

<221> sig_peptide

<222> 13..75

<223> Von Heijne matrix
score 3.90000009536743
seq PVAVTAAPVLS/IN

<221> polyA_signal
<222> 1035..1040

<221> polyA_site
<222> 1060..1070

<400> 343

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agagtcggga aa atg gct gcg agt acc tcc atg gtc ccg gtg gct gtg acg      51
          Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr
          -20                      -15                      -10

gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg      99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
          -5                      1                      5
cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag      147
Arg Glu Ile Lys Lys Gln Leu Leu Ile Ala Gly Leu Thr Arg Glu
          10                      15                      20
cgg ggc cta cta cac agt agc aaa tgg tgg gcg gag ttg gct ttc tct      195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
          25                      30                      35                      40
ctc cct gca ttg cct ctg gcc gag ctg caa ccg cct ccg cct att aca      243
Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr
          45                      50                      55
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac      291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
          60                      65                      70
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc      339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
          75                      80                      85
aat gca aga aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg      387
Asn Ala Arg Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
          90                      95                      100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
          105                      110                      115                      120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
          125                      130
gaatgaatgt actttataca tagcaataat aaaaaaaga tatcataaat aaagttaaaa      545
aggatggttaa aaaaaaaaaat attccttagga atgactaaca ggataagtaa caacctgatt      605
atatttttac ttttaggttat ataaggttct tcatgcctgt gaattaatat tattgtgtaa      665
gaattaagtt aaaaagcctg ggctgacttt taaattttata aattcattta tcatgtttat      725
agtatattta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca      785
agtaaaccac cttaatactg tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tactttccta ctttttctta gttgttatct atataaattg attaaaaaaa      905
cattttatgt acttctcatt tcttagtaca gggttgagtat cccttatttg aagtgcttgg      965
gacaaaaagt gtttcagatt tcagattttt ttcagatttt ggtatatattg cattatactt      1025
actggttgaa ataaaaaatg ctgcagtgag tgtcaaaaaa aaaaaa      1070

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<210> 344
<211> 1213
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..718

<221> sig_peptide

<222> 2..76

<223> Von Heijne matrix

score 3.90000009536743

seq RVGLLLGGGGVYG/SR

<221> polyA_signal

<222> 1170..1175

<221> polyA_site

<222> 1203..1213

<400> 344

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a atg ccc cgg aag cgg aag tgc gat ctt cgg gct gtc aga gtt ggt ctg      49
Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
-25 -20 -15 -10
tta ctc ggt ggt ggc gga gtc tac gga agc cgt ttt cgc ttc act ttt      97
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
-5 1 5
cct ggc tgt aga gcg ctt tcc ccc tgg cgg gtg aga vtg cag aga cga      145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
10 15 20
agg tgc gag atg agc act atg ttc gcg gac act ctc ctc atc gtt ttt      193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
25 30 35
atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg gtc ctg      241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
40 45 50 55
gtt tac agg aca gac aag tac aag aga ctg aag gca gaa gtg gaa aaa      289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
60 65 70
cag agt aaa aaa ttg gaa aag aag aag gaa aca ata aca gag tca gct      337
Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
75 80 85
ggg cga caa cag aaa aar aaa ata gag aga cdd kaa kas amc ctg arg      385
Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
90 95 100
aat aac aac aga gat cta tca atg gtt cga atg aaa tcc atg ttt gct      433
Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
105 110 115
att ggc ttt tgt ttt act gcc cta atg gga atg ttc aat tcc ata ttt      481
Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
120 125 130 135
gat ggt aga gtg gtg gca aag ctt cct ttt acc cct ctt tct tas rtc      529
Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
140 145 150
sra gga ctg tct cat cga aat ctg ctg gga gat gac acc aca gac tgt      577
Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
155 160 165
tcc ttc att ttc ctg taw att ctc tgt act atg tgc att cga cag aac      625
Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
170 175 180
att cag aag att ctc ggc ctt gcc cct tca cga gcc gcc acc aag cag      673
Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln
185 190 195
gca ggt gga ttt ctt ggc cca cca cct cct tct ggg aag ttc tct      718
Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
200 205 210
tgaactcaag aactctttat tttctakcat tctttctaga cacacacaca tcagactggc      778
aactgttttg tascaagagc cataggtagc cttackactt gggcctcttt ctagtgttga      838
attattttcta agccttttgg gtatkattag agtgaaaatg gcagccagca aacttgatag      898

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tgcttttggt cctagatgat ttttatcaaa taagtggatt gattagttaa gttcaggtaa      958
tgtttatgta atgaaaaaca aatagcatcc ttcttgtttc atttacataa gtattttctg      1018
tgggaccgac tctcaaggca ctgtgtatgc cctgcaagtt ggctgtctat gagcatttag      1078
agatttagaa gaaaaattta gtttggttaa cccttgtaac tgtttgtttt gttggtgttt      1138
ttttttcaag ccaaatacat gacataarat caataaarag gccaaatttt tasctgtttt      1198
atgtaaaaaa aaaaaa                                     1213

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<210> 345

<211> 978

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 86..709

<221> sig_peptide

<222> 86..361

<223> Von Heijne matrix

score 6.30000019073486

seq LLMSILALIFIMG/NS

<221> polyA_signal

<222> 943..948

<221> polyA_site

<222> 963..973

<400> 345

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aaagcatcct tccctaggac tgctgtaagc tttgagcctc tagcaggaga catgcctcgg      60
ggacgaaaga gtcggcgccg ccgta atg cga gag ccg cag aag aga acc gca      112
                               Met Arg Glu Pro Gln Lys Arg Thr Ala
                               -90                               -85
aca atc gca aaa tyc rrg gcs tva gag ggc ctc cga gac ccc tat ggc      160
Thr Ile Ala Lys Xaa Xaa Ala Xaa Glu Gly Leu Arg Asp Pro Tyr Gly
                               -80                               -75                               -70
cgc ctc tgt ggt agc gag cac ccc cga aga cca cct gag cgg ccc gag      208
Arg Leu Cys Gly Ser Glu His Pro Arg Arg Pro Pro Glu Arg Pro Glu
                               -65                               -60                               -55
gaa gac ccg agc act cca gag gag gcc tct acc acc cct gaa gaa gcc      256
Glu Asp Pro Ser Thr Pro Glu Glu Ala Ser Thr Thr Pro Glu Glu Ala
                               -50                               -45                               -40
tcg agc act gcc caa gca caa aag cct tca gtg ccc cgg agc aat ttt      304
Ser Ser Thr Ala Gln Ala Gln Lys Pro Ser Val Pro Arg Ser Asn Phe
-35                               -30                               -25                               -20
cag ggc acc aag aaa agt ctc ctg atg tct ata tta gcg ctc atc ttc      352
Gln Gly Thr Lys Lys Ser Leu Leu Met Ser Ile Leu Ala Leu Ile Phe
                               -15                               -10                               -5
atc atg ggc aac agc gcc aag gaa gct ctg gtc tgg aaa gtg ctg ggg      400
Ile Met Gly Asn Ser Ala Lys Glu Ala Leu Val Trp Lys Val Leu Gly
                               1                               5                               10
aag tta gga atg cag cct gga cgt cas cac agc atc ttt gga gat ccg      448
Lys Leu Gly Met Gln Pro Gly Arg Xaa His Ser Ile Phe Gly Asp Pro
                               15                               20                               25
aag aar atc gtc aca gaa ran ttt gtg cgc aga ggg tac ctg att tat      496
Lys Lys Ile Val Thr Glu Xaa Phe Val Arg Arg Gly Tyr Leu Ile Tyr
30                               35                               40                               45
ara ccg gtg ccc cgt abc agt ccg gtg gag tat gas ttc ttc tgg ggg      544
Xaa Pro Val Pro Arg Xaa Ser Pro Val Glu Tyr Xaa Phe Phe Trp Gly
                               50                               55                               60

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ccc cga gca cac gtg gaa tcg agc ara ctg aaa stc wtg cat ttt gtg      592
Pro Arg Ala His Val Glu Ser Ser Xaa Leu Lys Xaa Xaa His Phe Val
           65                      70                      75
gca agg gtt cgt aac cga tgc tct aaa gac tgg cct tgt aat tat gac      640
Ala Arg Val Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp
           80                      85                      90
tgg gat tcg gac gat gat gca gag gtt gag gct atc ctc aat tca ggt      688
Trp Asp Ser Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly
           95                      100                     105
gct arg ggt tat tcc gcc cct taagtaratc tgaggcagac ccttgggggt      739
Ala Xaa Gly Tyr Ser Ala Pro
110                      115
gtaaaagaga gtcacaggta cccaaggag tagatgccag ggtcctaagt tgaaaatgmt      799
gtcgattggg ggcgggggac actgtatttg atatttgtga tcagtgatca ttgttcaact      859
gcgaaataga gtgtttgctt ttgataatgg aaaattgtat tcgttttaaa attccgtttg      919
ttgagaataa caatatgttt aaaaatataa ttgaacaaat tttaaaaaaa aaaamcccy      978

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<210> 346

<211> 810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 63..320

<221> sig_peptide

<222> 63..179

<223> Von Heijne matrix

score 3.90000009536743

seq VLAIGLLHIVLLS/IP

<221> polyA_signal

<222> 771..776

<221> polyA_site

<222> 799..810

<400> 346

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agggaaccga tcccggggccg ttgatcttcg gccccacacg aacagcagag aggggcatca      60
gg atg aat gtk ggc aca gcg cac ags dag gtg aac ccc aac acg cgg      107
Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg
           -35                      -30                      -25
gtk atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt      155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly
           -20                      -15                      -10
ctc ctc cac atc gtg ctg ctg agc atc ccg ttt gtk agt gtc cct gtc      203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val
           -5                      1                      5
gtc tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc      251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe
           10                      15                      20
ctg cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag      299
Leu His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
           25                      30                      35                      40
gcg agg ctg cta acc cac tgg tgagcagatg gattatgggg tccagttcac      350
Ala Arg Leu Leu Thr His Trp
           45
ggcctctcgg aaktctctga ccatcacacc catcgtgctg tacttccctca ccagcttcta      410
cactaaktac raccaaatac attttgtgct caacaccgtg tccctgatra gcgtgcttat      470

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ccccaaagctg cccagctcc acggaktccg gatttttggga atcaataakt actgaaaktg      530
cascccccttc ccctgcccag ggtggcaggg gaggggtagg gtaaaaggca tktgctgcaa      590
chctgaaaac  araaaraara rscctctgga cactgccara ratgggggtt gagcctctgg      650
cctaattttcc cccctcgctt cccccagtag ccaacttgga gtagcttgta ytggggttgg      710
ggtaggcccc  ctgggctctg accttttctg aattttttga tcttttcctt ttgctttttg      770
aatararact  ccatggagtt ggtcatggaa aaaaaaaaaa      810

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<210> 347
 <211> 771
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 299..418

<221> sig_peptide
 <222> 299..379
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LTLILLITPSPSPL/LF

<221> polyA_signal
 <222> 739..744

<221> polyA_site
 <222> 762..771

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<400> 347
accttgggct ccaaattcta gtcataaaag atgcaagtkt tgcaatttcc tataaatggt      60
taagaaaaga gcaagctgtc cagagagtga gaagtttgaa aagagaggtg cataagagag      120
aatgatgtc  catttgagcc ccaccacgga ggttatgtgg tcccaaaagg aatgatggcc      180
aagcaattaa tttttcctcc tagttcttag cttgcttctg cattgattgg ctttacacaa      240
ctggcattta gtctgcatta cacaaataga cactaattta tttggaacaa gcagcaaa      298
atg aga act tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act      346
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
      -25                      -20                      -15
ctg ctt cta atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt      394
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
      -10                      -5                      1                      5
ctg tcc ctc aga tca gca atg tct tagccctct cctctcttcc attccttct      448
Leu Ser Leu Arg Ser Ala Met Ser
      10
gttgggtactc atttcttcta actttttaata aacatttagg tataatacat tacagtaagt      508
gctattttaga tacaaactta aaacatacta tatatttttaa ggatctaaga atcctttara      568
rrrggcacat gactgaagta cctcagctgc gcagcctgta accagttttt ttaatgtaaa      628
agtaaraatg ccagccttaa cctabccctg carataaaaag ctaactttta ttaataccag      688
ccctgaataa tggcactaat ccacactctt ccttaragtg atgctggaaa aataaaatca      748
ggggcttcag attaaaaaaaa aaa      771

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<210> 348
 <211> 409
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 186..380

<221> sig_peptide
 <222> 186..233
 <223> Von Heijne matrix
 score 4
 seq FFLFLSFVLMYDG/LR

<221> polyA_signal
 <222> 383..388

<221> polyA_site
 <222> 396..409

<400> 348
 ataaaagaag cagcaaataag aatttccac aaagtaagtt gactctaaat cttaagtatt 60
 acctagtttt ttaaagggtt gaatataata atgcagtatt tgcagtataa aaaggaagga 120
 atttgtagag aatcattttg gtgctcaagt ctcttagcag tgccttattg cctcatagca 180
 agaag atg ctg ggg ttt ttt ttg ttt ttg tcc ttt gta tta atg tat gat 230
 Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
 -15 -10 -5
 ggt ttg cgc ctt ttt ggc att ctt tca aca tgt cgt gta cat cac acc 278
 Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
 1 5 10 15
 atg aat cag ttc cta att gat ata tct agc ttt acc tcc cga gtt aaa 326
 Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Lys
 20 25 30
 aaa aaa atc ttt tta ttt tat gcc ttc awa ggt tgc ycg ttt car agt 374
 Lys Lys Ile Phe Leu Phe Tyr Ala Phe Xaa Gly Cys Xaa Phe Gln Ser
 35 40 45
 gcc aca taaataaaat gtttaacaaa aaaaaaaaaa 409
 Ala Thr

<210> 349
 <211> 613
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..458

<221> sig_peptide
 <222> 69..233
 <223> Von Heijne matrix
 score 4
 seq AALCGISLSQLFP/EP

<221> polyA_signal
 <222> 564..569

<221> polyA_site
 <222> 602..613

<400> 349
 aagaacctga gcagcctgtc ttcagacaga gagaggccca cggtctgttc ttgaaaytgg 60
 cgctggga atg gcc atg tgg aac agg cca tgb bag ang ctg cct cag cag 110
 Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln
 -55 -50 -45
 cct cts sta gct gag ccc act gca gag ggg gag cca cac ctg ccc acg 158
 Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr

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-40          -35          -30
ggc cgg gas byg act gag gcc aac cgc ttc gcc tat gct gcc ctc tgt      206
Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
-25          -20          -15          -10
ggc atc tcc ctg tcc cag tta ttt cct gaa ccc gaa cac agc tcc ttc      254
Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
          -5          1          5
tgc aca gag ttc atg gca ggc ctg gtg ckm tgg ctg gag ttg tct gaa      302
Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
          10          15          20
gct gtc ttg cca acc atg act gct ttt gcg agc ggc ctg gga ggt gaa      350
Ala Val Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu
          25          30          35
gga sca vma tgt gtt tgt tca aat ttt act gaa gga ccc cat ctt gaa      398
Gly Xaa Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu
40          45          50          55
gga cga ccc gac ggt gat cac tca gga cct tct gag ctt ctc act caa      446
Gly Arg Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln
          60          65          70
gga tgg gca cta tgacccccgg gccagagtcc tcgtttgccca catgacctcc      498
Gly Trp Ala Leu
          75
ctgctccaag tgcccttggga ggagctggat gtccttgaaa agatgttcct ggagagcctg      558
aaggaaatca aagaagagga atctgaaatg gccgagggcat cccraaaaaa aaaaa      613

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<210> 350
 <211> 986
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..638

<221> sig_peptide
 <222> 12..263
 <223> Von Heijne matrix
 score 4.19999980926514
 seq ITMLQMLALLGYG/LF

<221> polyA_signal
 <222> 951..956

<221> polyA_site
 <222> 975..985

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<400> 350
accctatcaa g atg gtc aac ttc ccc cag aaa att gca ggt gaa ctc tat      50
          Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr
          -80          -75
gga cct ctc atg ctg gtc ttc act ctg gtt gct atc cta ctc cat ggg      98
Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly
-70          -65          -60
atg aag acg tct gac act att atc cgg gag ggc acc ctg atg ggc aca      146
Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr
-55          -50          -45          -40
gcc att ggc acc tgc ttc ggc tac tgg ctg gga gtc tca tcc ttc att      194
Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile
          -35          -30          -25
tac ttc ctt gcc tac ctg tgc aac gcc cag atc acc atg ctg cag atg      242

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Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met
      -20      -15      -10
ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat tgc att gtc ctg ttc      290
Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe
      -5      1      5
atc acc tat aat atc cac ctc cgc gcc ctc ttc tac ctc ttc tgg ctg      338
Ile Thr Tyr Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu
10      15      20      25
ttg gtg ggt gga ctg tcc aca ctg cgc atg gta gca gtg ttg gtg tct      386
Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser
      30      35      40
cgg acc gtg ggc ccc aca cad cgg mtg ctc ctc tgt ggc acc ctg gct      434
Arg Thr Val Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala
      45      50      55
gcc cta cac atg ctc ttc ctg ctc tat ctg cat ttt gcc tac cac aaa      482
Ala Leu His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys
60      65      70
dtg gta dag ggg atc ctg gac aca ctg gag ggc ccc aac atc ccg ccc      530
Xaa Val Xaa Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro
75      80      85
atc cag agg gtc ccc aga gac atc cct gcc atg ctc cct gct gct cgg      578
Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg
90      95      100      105
ctt ccc acc acc gtc ctc aac gcc aca gcc aaa gct gtt gcg gtg acc      626
Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr
110      115      120
ctg cag tca cac tgacccacc tgaaattctt ggccagtcct ctttcccgca      678
Leu Gln Ser His
125
gctgcagaga ggargaasac tattaaagga cagtcctgat gacatgtttc gtagatgggg      738
tttgcagctg ccaactgagct gtagctgcgt aagtaacctcc ttgatgcctg tcggcacttc      798
tgaaaggcac aaggccaaga actcctggcc aggactgcaa ggctctgcag ccaatgcaga      858
aaatgggtca gctcctttga gaacccctcc ccacctaccc cttccttcct ctttatctct      918
cccacattgt cttgctaaat atagacttgg taattaaaat gttgattgaa gtctggaaaa      978
aaaaaaaaat                                     986

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<210> 351
 <211> 1447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 282..389

<221> sig_peptide
 <222> 282..332
 <223> Von Heijne matrix
 score 3.5
 seq RWWCFHLQAEASA/HP

<221> polyA_signal
 <222> 1413..1418

<221> polyA_site
 <222> 1437..1447

<400> 351
 ataataatat ctaaaaagct aaattttaaa taccagcttt acataaatga ttgtkgactc 60
 tgggtctgtkt ctgacacctt tccagaaaaa agtcaattgt tcagggtacac caaagaggaa 120

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gaagagctgt ggaggccacc ctctacaaag ctttatagaa cttctggatc taactcaciaa 180
acaagcttcc agaagagact agagacctta ggccaggaga tgaaggagtt cagtagcaaa 240
gtcacacctg tccaattccc tgagctttgc tcaactcagct a atg gga tgg caa agg 296
                                         Met Gly Trp Gln Arg
                                         -15
tgg tgg tgc ttt cat ctt cag gca gaa gcc tct gcc cat ccc cct caa 344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
-10 -5 1
ggg ctg cag gcc caa ttc tca tgc tgc cct tgg gtg ggc atc tgt 389
Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp Val Gly Ile Cys
5 10 15
taacaaadga aaacgtcttg gtggcggcag casctttgct ctgagtgcct acaaagctaa 449
tgcttggtgc tagaaacatc atcattatta aacttcagaa aagcagcagc catgttcagt 509
caggctcatg ctgcctcact gcttaagtgc ctgcaggagc cgcttgccaa rctcccccttc 569
ctacacctgg cacactgggg tctgcacaag gctttgtcaa ccaaaracag cttccccccww 629
ttgattgcct gtagactttg gagccaaraa acactctgtg tgactctaca cacacttcag 689
gtggtttgtg cttcaaagtc attgatgcaa cttgaaagga aacagtttaa tgggtggaaat 749
gaactaccat ttataacttc tgttttttta ttgagaaaat gattcacgaa kkccaaatca 809
gattgccagg aagaaatagg acgtgacggt actgggccct gtgattctcc cagcccttgc 869
agtccgctag gtgagaggaa aagctcttta cttccgcccc tggcagggac ttctgggtta 929
tgggagaaac cagagatggg aatgaggaaa atatgaacta cagcagaagc ccctgggcag 989
ctgtgatgga gcccctgaca ttactcttct tgcactctgc ctgccttctt tccctctgcg 1049
aggcagtggg gtgggattca gagtgccttag tctgctcact gggagaagaa gagttcctgc 1109
gcatgcaagc cctgctgtgt ggctgtcgtt tacatttggg aggtgtcctg tatgtctgta 1169
cgttggggag tgcctgtatt tggaaagatt aaaaacctag catcctgttc tcaccctcta 1229
agctgcattg agaaatgact cgtctctgta ttgtattaa gccttaacac ttttcttaag 1289
tgcattcggt gccaacattt tttagagctg taccaaaaca aaaagcctgt actcacatca 1349
camtgtcatt ttgataggag cgttttgtaa tttttacaag gcagaatggg gtgtaacagt 1409
tgaattaaac ttagcaatca cgtgctcaaa aaaaaaaaa 1447

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<210> 352

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 208..339

<221> sig_peptide

<222> 208..294

<223> Von Heijne matrix

score 5.59999990463257

seq LFLQLLVSHIVC/AT

<221> polyA_site

<222> 1631..1641

<400> 352

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agaaccgtga tgggaagatg gacaaggaag agaccaaaga ctggatcctt ccctcagact 60
atgatcatgc agaggcagaa gccaggcacc tgggtctatga atcagaccaa aacaaggatg 120
gcaagcttac caaggaggag atcgttgaca agtatgactt atttggtggc agccaggcca 180
cagatttttg ggaggcctta gtacggc atg atg agt tct gag cta cgg agg aac 234
                                         Met Met Ser Ser Glu Leu Arg Arg Asn
                                         -25
cct cat ttc ctc aaa agt aat tta ttt tta cag ctt ctg gtt tca cat 282
Pro His Phe Leu Lys Ser Asn Leu Phe Leu Gln Leu Leu Val Ser His
-20 -15 -10 -5
gaa att gtt tgc gct act gag act gtt act aca aac ttt tta aga cat 330
Glu Ile Val Cys Ala Thr Glu Thr Val Thr Thr Asn Phe Leu Arg His

```

	1	5	10	
gaa aag gcg taatgaaaac catcccgctcc ccattcctcc tcctctctga				379
Glu Lys Ala				
15				
gggactggag ggaagccgtg cttctgagga acaactctaa ttagtacact tgtgtttgta				439
ratattacacw wtgtattatg tattaacatg gcgtgtttat ttttgatatt ttctctgggt				499
gggagtatka tatgaaggat caaratcctc aactcacaca tgtaracaaa cattasctct				559
ttactctttc tcaaccctt wtatgatttt aataattctc acttaactaa ttttgtaagc				619
ctgagatcaa taagaaatgt tcaggagaga ggaaagaaaa aaaatatatg ctccacaatt				679
tatattttaga gagagaacac ttagtccttg ctgtcaaaaa gtccaacatt tcataggtag				739
tagggggccac atattacatt cagttgctat aggtccagca actgaacctg ccattacctg				799
ggcaaggaaa gatccctttg ctctaggaaa gcttggtcca aattgatttt cttctttttc				859
cccctgtagg actgactgtt ggctaatttt gtcaagcaca gctgtggtgg gaagagttag				919
ggccagtgtc ttgaaaatca atcaagtagt gaatgtgatc tctttgcara gctatagata				979
gaaacagctg gaaaactaaa ggaaaaatc aagtgttttc ggggcataca ttttttttct				1039
gggtgtgcat ctgttgaaat gctcaagact taattatttg ccttttgaaa tctactgtaa				1099
tgcccccatc cggttcctct tcttcccarg tgtgccagg aattaatctt ggtttacta				1159
caattaaaat tcaactcctt ccaatcatgt cattgaaagt gcctttaacg aaagaaatgg				1219
tactgaatg ggaattctct taagaaaccc tgagattaaa aaaagactat ttggataact				1279
tataggaaaag cctagaacct ccagtagag tggggatttt tttcttcttc cctttctctt				1339
ttggacaata gttaaattag cagtattagt tatgagtttg gttgcagtgt tcttatcttg				1399
tgggctgatt tccaaaaacc acatgctgct gaatttacca gggatcctca tacctcacia				1459
tgcaaaccac ttactaccag gcctttttct gtgtccactg gagagcttga gctcacactc				1519
aaagatcaga ggacctacag agagggtctc ttggtttgag gaccatggct tacctttcct				1579
gcctttgacc catcacaccc catttcctcc tctttcctc tcccgtctg caaaaaaaaa				1639
aa				1641

<210> 353

<211> 884

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..557

<221> sig_peptide

<222> 69..224

<223> Von Heijne matrix

score 4.69999980926514

seq LGLALGRLEGGSA/RH

<221> polyA_signal

<222> 849..854

<221> polyA_site

<222> 870..883

<400> 353

attggctccg gatcgtgcgt gaggcggcctt cgtgggcagc gagagtcaca gacaagacag	60
caagcagg atg gag cac tac cgg aaa gct ggc tct gta gag ctc cca gcg	110
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala	
-50 -45 -40	
cct tcc cca atg ccc cag cta cct cct gat acc ctt gag atg cgg gtc	158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val	
-35 -30 -25	
cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct ctg ggt cgg	206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg	
-20 -15 -10	
ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt tct ggc agg	254

```

Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
-5          1          5          10
gct gca gga aag gct gtc agc tgc gct gag att gtc aag cgg cgg gtc 302
Ala Ala Gly Lys 15 Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
cgc ggc ctg cac cag ctc acc aag cta ckt ttc ctt caa act gag gac 350
Pro Gly Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp
agc tgg gtc cca scc tca cct gac aca ggg cta rac ccc ctc aca gtg 398
Ser Trp Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val
cgc cgc cat gtg cct gca ktg tgg gtg ctg ctc asc cgg gac ccc ctg 446
Arg Arg His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu
gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc cct ggc ctg 494
Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu
ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cra aaa agg gct 542
Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala
cra rac acc cga tgc tgaaaacctg ctgasccagc ctgttctcgc ggcctraatg 597
Xaa Xaa Thr Arg Ser
tctgggggtgc ttgtgccttt tctranaagc gttgtgaskg ctcaacatcc ccatcaaggt 657
ttgagtgccac aaaagtggac ctccctatca tgcttcccct tccctctagc atgtgggaag 717
ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt gctaaataag 777
ggcttccctc gccttctacc tacagtgcac ttgaactgcc ttctgaaaga ggtccakgga 837
gggatttagg aaataaagtt tctacctatt tgaaaaaaaa aaaacac 884

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<210> 354

<211> 729

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 134..325

<221> sig_peptide

<222> 134..274

<223> Von Heijne matrix

score 5.90000009536743

seq TWLGLLSFQNLHC/FP

<221> polyA_site

<222> 718..729

<400> 354

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atcattttct tatccctgct gattttcaaac cttcccatgg tttagaagca taacctgtaa 60
tgtaatgcaa gtcccctaac tccctggttg ctaacattaa cttccttaag taataatcaa 120
tgaaagavat tct atg cat ggt ttt gaa ata ata tcc ttg aaa gag gaa 169
Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu
-45          -40
tca cca tta gga aag gtg agt cag ggt cct ttg ttt aat gtg act agt 217
Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser
-35          -30          -25          -20
ggc tca tca tca cca gtg acc tgg ttg ggc cta ctc tcc ttc cag aac 265
Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn
-15          -10          -5
ctg cat tgc ttc cca gac ctc ccc act gag atg cct cta ara gcc aaa 313

```

Leu His Cys Phe Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys
 1 5 10
 gga ktc aac act tgagcctagg gtgggctaca acaaaaaratt ctaatttacc 365
 Gly Xaa Asn Thr
 15
 ttgcttcac taggtccagg cccaaktag cttgctgaag gaacttaaaa agtagctgtt 425
 atttattgta ttgtataasc taaaaacatt tatttttggt gaatcraaac aattccatgt 485
 ascaatcttt tttctgttca cggtgtttgt gataaaacct taaattccgc aagcatcagt 545
 tttttgaaaa aatgggaatt gaccggatag wwacaggcaa agwtataaat agctacaaca 605
 tcatttaact tttataaaca tgccttctct ctattgaara catctgatat ttttgctgga 665
 aagttggatc tatectcagt aactctgcc tgaattcctg tttckkggtt ccaaaaaaaaa 725
 aaaa 729

<210> 355

<211> 1013

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 78..731

<221> sig_peptide

<222> 78..227

<223> Von Heijne matrix

score 5.09999990463257

seq RTALILAVCCGSA/SI

<221> polyA_site

<222> 1002..1013

<400> 355

agtttccaag ggaaggagca gcgtgtggga aagcacagaa gagtgagaag gaagcgacta 60
 aattttattt actttct atg cat cat ggc ctc aca cca ctg tta ctt ggt 110
 Met His His Gly Leu Thr Pro Leu Leu Leu Gly
 -50 -45 -40
 gta cat gag caa aaa cag caa gtg gtg aaa ttt tta atc aag aaa aaa 158
 Val His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys
 -35 -30 -25
 gca aat tta aat gca ctg gat aga tat gga aga act gct ctc ata ctt 206
 Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu
 -20 -15 -10
 gct gta tgt tgt gga tcg gca agt ata gtc agc ctt cta ctt gag caa 254
 Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Glu Gln
 -5 1 5
 aac att gat gta tct tct caa gat cta tct gga cag acg gcc aaa aag 302
 Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys
 10 15 20 25
 tat gct gtt tct agt cgt cat aat gta att tgc cag tta ctt tct gac 350
 Tyr Ala Val Ser Ser Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp
 30 35 40
 tac aaa raa aaa cag atr cta aaa gtc tct tct gaa aac agc aat cca 398
 Tyr Lys Xaa Lys Gln Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro
 45 50 55
 raa caa gac tta aag ctg aca tca gag gaa gag tca caa agg ctt aaa 446
 Xaa Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys
 60 65 70
 gga agt gaa aat agc cag cca gag gaa atg tct caa gaa cca gaa ata 494
 Gly Ser Glu Asn Ser Gln Pro Glu Glu Met Ser Gln Glu Pro Glu Ile
 75 80 85

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aat arg ggt ggt gat aga aag gtt gaa raa raa atg aar aag cac gga      542
Asn Xaa Gly Gly Asp Arg Lys Val Glu Xaa Xaa Met Lys Lys His Gly
90                      95                      100                      105
agt wct cat atg gga ttc cca raa aac ctg mct aac ggt gcc act gct      590
Ser Xaa His Met Gly Phe Pro Xaa Asn Leu Xaa Asn Gly Ala Thr Ala
                      110                      115                      120
gac aat ggt gat gat gga tta att ccm cca rgg aaa asc ara aca cct      638
Asp Asn Gly Asp Asp Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro
                      125                      130                      135
gaa agc cas caa ttt cct gac act gag aat gaa cag tat cac agg gac      686
Glu Ser Xaa Gln Phe Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp
                      140                      145                      150
ttt tct ggc cat ccc mac ttt ccc acd acc ctt ccc atc aaa cag      731
Phe Ser Gly His Pro Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln
                      155                      160                      165
tgatgaacaa aatgatactc hsaagcmmct ttctgaagam caraacactg gaatattaca      791
agatgagatt ctgattcatg aagaaaagca gatagaagtg gctgaaaatg aattctgagc      851
tttctcttag ttataaraaa gaaaaagacc tcttgcatga aaatagtacg ttgcaggaag      911
aaattgtcat gctaaractg gaactagack taatgaaaca tcagagccag ctaararaaa      971
araaatattht ggaggaaatt gaaagtgtgg aaaaaaaaaa aa      1013

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<210> 356
 <211> 973
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..693

<221> sig_peptide
 <222> 46..90
 <223> Von Heijne matrix
 score 7.59999990463257
 seq CVLVLAAAAGAVA/VF

<221> polyA_signal
 <222> 937..942

<221> polyA_site
 <222> 962..973

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<400> 356
aagcggctgg tccccggaag ttggacgcat gcgccgtttc tctgc atg gtg tgc gtt      57
                                   Met Val Cys Val
                                   -15
ctc gtt cta gct gcg gcc gca gga gct gtg gcg gtt ttc cta atc ctg      105
Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu
-10                      -5                      1                      5
cga ata tgg gta gtg ctt cgt tcc atg gac gtt acg ccc cgg gag tct      153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser
                      10                      15                      20
ctc agt atc ttg gta gtg gct ggg tcc ggt ggg cat acc act gag atc      201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile
                      25                      30                      35
ctg agg ctg ctt ggg agc ttg tcc aat gcc tac tca cct aga cat tat      249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr
                      40                      45                      50
gtc att gct gac act gat gaa atg agt gcc aat aaa ata aat tct ttt      297
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys Ile Asn Ser Phe

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      55              60              65
gaa cta rat cga gsk gat aga rac cct agt aac atg twt acc aaa tac      345
Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met Xaa Thr Lys Tyr
70              75              80              85
tac att cac cga att cca ara agc cgg gag gtt cag cag tcc tgg ccc      393
Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln Gln Ser Trp Pro
90              95              100
tcc acc gtt tyc acc acc ttg cac tcc atg tgg ctc tcc ttk ccc cta      441
Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu Ser Xaa Pro Leu
105              110              115
att cac agg gtg aag cca rat ttg gtg ttg tgt aac gga cca gga aca      489
Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn Gly Pro Gly Thr
120              125              130
tgt gty cct atc tgt gta tct gcc ctt ctc ctt ggg ata cta gga ata      537
Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly Ile Leu Gly Ile
135              140              145
aag aaa gtg atc att gtc tac gtt gaa agc atc tgc cgt gta aaa acs      585
Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys Arg Val Lys Thr
150              155              160              165
tta tcc atg tcc gga aag att ctg ttt cat ctc tca aat tac ttc att      633
Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser Asn Tyr Phe Ile
170              175              180
gtt cag tgg ccg gct ctg aaa gaa aag tat ccc aaa tcg gtg tac ctt      681
Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys Ser Val Tyr Leu
185              190              195
ggg cga att gtt tgacaaatgg caactgactt ctttagaatt ttgcasttaa      733
Gly Arg Ile Val
200
cagtartatg tactcaaatt ggggggaaaa aaaccctaca tgtttcttgt aaaggcgtct      793
gacagtccctg araattattg atggtaagga ataaaaaatg twcagatrac tcagtgaara      853
aactgaggct tctcttatga aacaaacatt gataaacgta actacyaaat gtttatgcct      913
ctgtaaacca aatttctttt ctarataaaa atatgtatta ctacctgcaa aaaaaaaaaa      973

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<210> 357
 <211> 868
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..527

<221> sig_peptide
 <222> 126..182
 <223> Von Heijne matrix
 score 3.90000009536743
 seq ILFHGVFYAGGFA/IV

<221> polyA_signal
 <222> 834..839

<221> polyA_site
 <222> 856..867

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<400> 357
actggaagaa ctcgtcatgc tctttgtagc gtggtgcttc tgttgctcac aggacaactt      60
gcctttgatg attttcaaga gagttgtgct atgatgtggc aaagtatgca ggaagcaggc      120
gggtca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc      170
Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala

```

-15

-10

-5

```

ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg      218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
               1               5               10
act tta tat tac aag ttg gca gtg gar cag ctg car arc cat ccc gag      266
Thr Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu
               15               20               25
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc      314
Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
               30               35               40
atc gac agg gaa aac ttc gtg gac att gtt rat gcc aag ttg aaa att      362
Ile Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile
               45               50               55               60
cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc      410
Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
               65               70               75
aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag      458
Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
               80               85               90
ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac      506
Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
               95               100               105
ggt gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt      557
Gly Asp Glu Val Lys Lys Glu
               110               115
ctagtccatc cttccctcat ctctaccata tggccactgg ggtggtggcc catctcagtg      617
acagacactc ctgcaaccca gktttccagc caccagtggg atgatggtat gtgccagcac      677
atggtaattt tgggtgtaatt ctaacttggg cacaacgaat gctatttgtc atttttaaac      737
tgaatccgaa agaaaactcct attataaatt taagataatg taatgtattt gaaagtgtt      797
tgtataaaaa agcacatgat aaaaggaatc agaattaata aaatgtttgt tgatctttaa      857
aaaaaaaaaa h                                                                868

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<210> 358
 <211> 519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..320

 <221> sig_peptide
 <222> 66..113
 <223> Von Heijne matrix
 score 3.5
 seq TALAAXTWLGVWG/VR

<221> polyA_signal
 <222> 490..495

<221> polyA_site
 <222> 508..519

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<400> 358
aattagcgcg taacgcasag actgcttgct gcggcagaga cgccagakgt gcagctccag      60
cagca atg gca gtg acg gcg ttg gcg gcg mrg acg tgg ctt ggc gtg tgg      110
      Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
            -15            -10            -5
ggc gtg agg acc atg caa gcc cga ggc ttc ggc tcg gat cag tcc gag      158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
      1              5              10              15

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aat gtc gac cgg ggc gcg ggc tcc atc cgg gaa gcc ggt ggg gcc ttc      206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
                20                      25                      30
gga aag aga gag cag gct gaa gag gaa cga tat ttc cga gca cag agt      254
Gly Lys Arg Gly Gln Ala Glu Glu Arg Tyr Phe Arg Ala Gln Ser
                35                      40                      45
aca gaa caa ctg gca rct ttg aaa aaa crc cat gaa gaa gar atc gtt      302
Thr Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val
                50                      55                      60
cat cat aga gaa gga gat tgagcgtctg cagaaagaaa ttgagcgcca      350
His His Arg Glu Gly Asp
        65
taagcagaag atcaaaatgc tagaacatga tgattaagtg cacaccgtgt gccatagaat      410
ggcacatgtc attgccact tctgtgtaaa catggttctg gtttaactaa tatttgtctg      470
tgtgtacta acagattata ataaattgtc atcagtgaaa aaaaaaaaaa      519

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<210> 359
<211> 1028
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 73..948

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<221> sig_peptide
<222> 73..159
<223> Von Heijne matrix
      score 4.40000009536743
      seq IVLHLVLQGMVYT/EY

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<221> polyA_site
<222> 1016..1028

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<400> 359
agcttttaaag gcctggccag gggaggagca cagatatattt cctgtataat tccagaatgt      60
cttcagagag cc atg cat gga ttg ctt cat tac ctt ttc cat acg aga aac      111
      Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn
                        -25                      -20
cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act      159
His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr
      -15                      -10                      -5
gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc      207
Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser
      1                      5                      10                      15
ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt      255
Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe
                20                      25                      30
ttt ttc acc ctg act tgt gga acc aat cct ggc att ata aca aaa gca      303
Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala
                35                      40                      45
aat gaa tta tta ttt ctt cat gtt tat gaa ttt gat gaa ktg atg ttt      351
Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe
                50                      55                      60
cca aaa aac gtg agg tgc tct act tgt gat tta agg aaa cca gct cga      399
Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg
      65                      70                      75                      80
tcc aas cac tgc akt gtg tgt aac tgg tgt gtg cac cgt ttc rac cat      447
Ser Xaa His Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His
                85                      90                      95

```

```

cac tgt gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc agg tmc      495
His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa
      100                      105                      110
ttc ctc atc tac gtc ttg acc ttg acg gcc tcg gct gcc acc gtc gcc      543
Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala
      115                      120                      125
att gtg agc acc act ttt ctg gtc cac ttg gtg gtg atg tca gat tta      591
Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu
      130                      135                      140
tac cag gag act tac atc gat gac ctt gga cac ctc cat gtt atg gac      639
Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp
      145                      150                      155                      160
acg gtc ttt ctt att cag tac ctg ttc ctg act ttt cca cgg att gtc      687
Thr Val Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val
      165                      170                      175
ttc atg ctg ggc ttt gtc gtg gtt ctg arc ttc ctc ctg ggt ggc tac      735
Phe Met Leu Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Tyr
      180                      185                      190
ctg ttg ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac gag      783
Leu Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu
      195                      200                      205
tgg tac aga rgt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg gcc      831
Trp Tyr Arg Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala
      210                      215                      220
tgg cct ccg tca gca gar ccc caa gtc cac cgg aac att cac tcc cat      879
Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His
      225                      230                      235                      240
ggg ctt cgg arc aac ctt caa gar atc ttt cta cct gcc ttt cca tgt      927
Gly Leu Arg Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys
      245                      250                      255
cat gag agg aag aaa caa gaa tgacmagtgt atgactgcct ttgagctgta      978
His Glu Arg Lys Lys Gln Glu
      260
gttccccgttt atttacacat gtggatectc gttttccaaa aaaaaaaaaa      1028

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<210> 360

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..434

<221> sig_peptide

<222> 69..236

<223> Von Heijne matrix

score 4.90000009536743

seq FACVPGASPTTLA/FP

<221> polyA_signal

<222> 419..424

<221> polyA_site

<222> 441..452

<400> 360

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acagcgtgas tcgccgccca gaagaatatg aaaaagcaga gcganctcgg ttaagggaaa      60
gcgccgag atg acg ggc ttt ctg ctg ccg ccc gca agc aga ggg act cgg      110
      Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg

```

```

          -55          -50          -45
aga tca tgc agc aga agc aga aaa agg caa acg aga aga agg agg aac      158
Arg Ser Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Arg Asn
          -40          -35          -30
cca agt agc ttt gtg gct tcg tgt cca acc ctc ttg ccc ttc gcc tgt      206
Pro Ser Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys
          -25          -20          -15
gtg cct gga gcc agt ccc acc acg ctc gcg ttt cct cct gta ktg ctc      254
Val Pro Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu
          -10          -5          1          5
aca ggt ccc avc acc gat ggc att ccc ttt gcc ctr nak tct gca gcg      302
Thr Gly Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala
          10          15          20
ggg ccc ttt tgt gct tcc ttc ccc tca ggt avc ctc tct ccc cct ggg      350
Gly Pro Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly
          25          30          35
cca ctc ccg ggg gtg agg ggg tta ccc ctt ccc agt gtt ttt tat tcc      398
Pro Leu Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser
          40          45          50
tgt ggg gct cac ccc aaa gta tta aaa gta gct ttg taattcaaaa      444
Cys Gly Ala His Pro Lys Val Leu Lys Val Ala Leu
55          60          65
aaaaaaaaa

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<210> 361
 <211> 875
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 628..804

<221> sig_peptide
 <222> 628..711
 <223> Von Heijne matrix
 score 4.19999980926514
 seq LMPVIPALQEAXA/GG

<221> polyA_site
 <222> 864..875

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<400> 361
aaagatggac accgcggagg aagacatatg tagagtgtgt cggtcagaag gaacacctga      60
gaaaccgctt tatcatcctt gtgtatgtac tggcagtatt aagttngtcc atcaagaatg      120
cttagttcaa tggctgaaac acagtcgaaa agaatactgt gaattatgca agcacagatt      180
tgcttttaca ccaatttatt ctccagatat gccttcacgg cttccaattc aagacatatt      240
tgctggactg gttacaagta ttggcactgc aatacgatat tggtttcatt atacacttgt      300
ggcctttgca tggttgggag ttgttcctct tacagcatgt gagtattcat gcctctgatt      360
ggagttattt aaacattgca taactactta atattataaa gcaatattgc atcatattat      420
tatttgactg atgttttagtt atttgatgtc agagtgtcat gtattaggaa agccttactt      480
araaratgtt catcggaact aaraatgakt ttaacagggtc agttttttga gtgaatgtgg      540
gaaaraacac agcatacaga atggctaacc atgaaagttc atgaaagcgt kgaaaaaatc      600
aaatcaaadc ataattagat atgaagt atg cta rag ctt tca agg gct aca aaa      654
                                Met Leu Xaa Leu Ser Arg Ala Thr Lys
                                -25          -20
rac ggc cgg gcg cgg tgg ctt atg cct gta atc cca gca ctt cag gag      702
Xaa Gly Arg Ala Arg Trp Leu Met Pro Val Ile Pro Ala Leu Gln Glu
                                -15          -10          -5
gcc gan gca ggc gga tca cga ggt cag gag ttt gaa act agc ctg gcc      750

```

```

Ala Xaa Ala Gly Gly Ser Arg Gly Gln Glu Phe Glu Thr Ser Leu Ala
      1           5           10
aac atg gag act gag gca gga gaa ttg ctt aaa ccc agg agg cgg agg      798
Asn Met Glu Thr Glu Ala Gly Glu Leu Leu Lys Pro Arg Arg Arg Arg
      15           20           25
ttg car tgaactgaga tcgcaccact gcactccagc ttgggcaaca gagcaagact      854
Leu Gln
30
ttgtctcgca aaaaaaaaaa a      875

```

```

<210> 362
<211> 531
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 70..366

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<221> sig_peptide
<222> 70..108
<223> Von Heijne matrix
      score 3.5
      seq MHLLSNWANPASS/RR

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<221> polyA_signal
<222> 496..501

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<221> polyA_site
<222> 521..531

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<400> 362
aagtggccat ggcggatata ggcactacag catcgggcggc ggcggctagt gccgctagcg      60
cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga      111
      Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
              -10           -5           1
cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc      159
Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
              5           10           15
gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc      207
Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
      20           25           30
tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac      255
Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
      35           40           45
agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca      303
Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
      50           55           60           65
cca atg aga aga tct tca tgc cat tta gaa tgt crg gtt ata ttc ctt      351
Pro Met Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu
              70           75           80
ttg gga cgc caa ttg taaktgttac cttcaaagga tttccttttc taaaaatta      406
Leu Gly Arg Gln Leu
      85
ttttaratgt ctaactttat gttattgctc acgggtatct gactgaattg ttgatttagg      466
ataagtcaat tcctggaggg aaattaccaa ataaatgat atgtatttct taccacaaaa      526
aaaaa      531

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<210> 363
 <211> 1244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..366

<221> sig_peptide
 <222> 70..108
 <223> Von Heijne matrix
 score 3.5
 seq MHLISNWNANPASS/RR

<221> polyA_site
 <222> 1233..1244

<400> 363
 aagtggccat ggcggataca gcgactacag catcggcggc ggcggctagt gccgctagcg 60
 cctcgagcg atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga 111
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
 -10 -5 1
 cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc 159
 Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
 5 10 15
 gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc 207
 Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
 20 25 30
 tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac 255
 Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
 35 40 45
 agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca 303
 Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
 50 55 60 65
 cca atg aga aga tct tca tgc cat tta raa tgt cag gtt ata ttc ctt 351
 Pro Met Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu
 70 75 80
 ttg gga cgc caa ttg tagtcggtct tctcttgccc aaccagacac tggcatccac 406
 Leu Gly Arg Gln Leu
 85
 tgtcttcttg cagtggctga accagagcca caatgcctgt gtcaactatg caaaccgcaa 466
 tgraccaag ccttcacctg catccaagtt catccaggga tacctgggag ctgtcatcag 526
 cgccgtctcc attgctgttg gccttatktc ctgggttcaga aagccaacaa gttcacccca 586
 gccaccgcgc ttctcatcca gaggtttgtg ccgttccctg ctgtagccag tgccaatatc 646
 tgcaatgttg tcctgatgcg gtacggggag ctggaggaag ggattgatgt cctggacagc 706
 gatggcaacc tcgtgggctc ctccaagatc gcagcccgac acgccttctg ggagacggcg 766
 ctgacgcgag tggctctgcc catgcccac cttggtgtac ccccgatcgt catgtccatg 826
 ctggagaaga cggctctcct gcaggcacgc ccccggtctg tcctccctgt gcaaagcctc 886
 gtgtgccttg cagccttcgg cctggccctg ccgctggcca tcagcctctt cccgcaaagt 946
 tcagagattg aaacatccca attagagccg gagatagccc aggccacgag cagccggaca 1006
 gtggtgtaca acaaggggtt gtgagtgttg tcagcggcct ggggacggag cactgtgcag 1066
 ccggggagct gaggggcarg gccgtagact cacgggtgca cctgcaggga gcagcacgcc 1126
 aacccagca gtcttgggcc ccctgggaga gtgctcaacc tacagtggag ggagactgac 1186
 ccattcacat tttaacatag gcaagaggag ttctaacaca tttcgtacaa aaaaaaaaa 1244

<210> 364
 <211> 631
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 111..434

<221> sig_peptide

<222> 111..185

<223> Von Heijne matrix

score 3.90000009536743

seq WIAAVTIAAGTAA/IG

<221> polyA_site

<222> 618..631

<400> 364

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aatcgcgagg tcggtgcttt agtacgccgc tggcaccttt actctcgccg gccgcgcgaa      60
cccgtttgag ctcggtatcc tagtgcacac gccttgcaag cgacggcgcc atg agt      116
                                   Met Ser
                                   -25
ctg act tcc agt tcc agc gta cga gtt gaa tgg atc gca gca gtt acc      164
Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
                                   -20                                   -15                                   -10
att gct gct ggg aca gct gca att ggt tat cta gct tac aaa aga ttt      212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
                                   -5                                   1                                   5
tat gtt aaa gat cat cga aat aaa gct atg ata aac ctt cac atc cag      260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
10                                   15                                   20                                   25
aaa gac aac ccc aag ata gta cat gct ttt gac atg gag gat ttg gga      308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly
                                   30                                   35                                   40
gat aaa gct gtg tac tgc cgt tgt tgg agg tcc aaa aag ttc cca ttc      356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
                                   45                                   50                                   55
tgt gat ggg gct cac aca aaa cat aac gaa gag act gga gac aat gtg      404
Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val
60                                   65                                   70
ggc cct ctg atc atc aag aaa aaa gaa act taaatggaca cttttgatgc      454
Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
75                                   80
tgcaaatacag cttgtcgtga agttacctga ttgtttaatt araatgacta ccacctctgt      514
ctgattcacc ttcgctggat tctaaatgtg gtatattgcm aactgcagct ttcacattta      574
tggcatttgt cttgttgaaa catcgtggtg cacatttgtt taaacaaaaa aaaaaaa      631

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<210> 365

<211> 781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 19..567

<221> sig_peptide

<222> 19..63

<223> Von Heijne matrix

score 8.39999961853027

seq AMWLLCVALAVLA/WG

<221> polyA_signal

<222> 749..754

<221> polyA_site

<222> 771..781

<400> 365

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aagtgtgtgct tacccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      51
                      Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                      -15                      -10                      -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
                      1                      5                      10
atg aag agt cgg gag cag gga aga cgg ctg gga gcc gaa agc cgg acc      147
Met Lys Ser Arg Glu Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr
                      15                      20                      25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc      195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
                      30                      35                      40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
45                      50                      55                      60
ttc tct gca gga aat tac tac aat caa gga gag act cgt aag aaa gaa      291
Phe Ser Ala Gly Asn Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu
                      65                      70                      75
ctt ttg car agc tgt gat gtt ttg ggg att cca ctc tcc agt gta atg      339
Leu Leu Gln Ser Cys Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met
                      80                      85                      90
att att gac aac agg gat ttc cca rat gac cca ggc atg cag tgg gac      387
Ile Ile Asp Asn Arg Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp
                      95                      100                      105
aca rag cac gtg gcc ara gtc ctc ctt cag cac ata gaa gtg aat ggc      435
Thr Xaa His Val Ala Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly
110                      115                      120
atc aat ctg gtg gtg act ttc gat gca ggg gga rta agt ggc cac agc      483
Ile Asn Leu Val Val Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser
125                      130                      135                      140
aat cac att gct ctg tat gca gct gtg agg aag ctt gag ggc caa att      531
Asn His Ile Ala Leu Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile
                      145                      150                      155
tgc aag ccc tgt ggc act gga caa gac ttt aag gaa tgagtgtgt      577
Cys Lys Pro Cys Gly Thr Gly Gln Asp Phe Lys Glu
                      160                      165
caatcagtgt gcctccacct tcaccatctt cttccctta ctctcacttc cgtcatgtgt      637
tttataacaac tctcaaatct ttcttggaga aggaggatat acatacataa tatgaaatgt      697
gtttgttctt cacagtcacc cgattttact gatatttatt tgcattttac caataaaaag      757
aaaatgcaag ctcaaaaaaa aaaa      781

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<210> 366

<211> 931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 19..312

<221> sig_peptide

<222> 19..63

<223> Von Heijne matrix

score 8.39999961853027

seq AMWLLCVALAVLA/WG

<221> polyA_signal

<222> 896..901

<221> polyA_site

<222> 921..931

<400> 366

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aagtgtgtgt tacccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      51
                        Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                        -15                      -10                      -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
                        1                      5                      10
atg aag agt cgg gag cag gga rga cgg ctg gga gcc gaa agc cgg acc      147
Met Lys Ser Arg Glu Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr
                        15                      20                      25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc      195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
                        30                      35                      40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
                        45                      50                      55                      60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa rgt ctt      291
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu
                        65                      70                      75
acc tct gaa ccc ctc ama gcc tagggacagg arcggccggc ttacctggtg      342
Thr Ser Glu Pro Leu Xaa Ala
                        80
ggttggggga cgtcggcagc tcregtacta cgccagcagg attganganc acagaaacag      402
ttgchsttgg ttgtattcag tacctkcatt tccgttggga actccaccwg tacttggttat      462
kctgtggaac ttttttttat ttgtagaagg agcaagaata ttgaccttac tatatagcac      522
acgaaacaat ctatgctgta tcgtgcctgc tcaatcctta aagttaactt ctaatgatag      582
taaaaracct tcctgctgcc tttaaaatgc agcttgtgct aktaacatgc atgtgtcaaa      642
ttgaaraatt agacatagat gactaratar aaagtaattt tgtaggtaat tttaragttc      702
aactccaccc agctttcakt gaaggaacct ttcaaataat aratttttgc ttaccatara      762
raaaaratca aatgacaaag caaatattga ccattaagct ggaatatggg gataattgaa      822
cagttgtata aatgaaktaa ttgaattgta cacatacaat ggggtgaattt tatggcatgt      882
caaagtatac ctcaataaag ctattttttt aaattgcmaa aaaaaaaaaa      931

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<210> 367

<211> 849

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 64..612

<221> sig_peptide

<222> 64..234

<223> Von Heijne matrix

score 3.79999995231628

seq QLWLVMEFCGAGS/VT

<221> polyA_site

<222> 839..849

<400> 367


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acatacggggc aagttttataa gggtcgtcat gtcaaaacgg gccagcttgc agccatcaag      60
ggt atg gat gtc aca ggg gat gaa gag gaa gaa atc aaa caa gaa att      108
Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile
-55 -50 -45
aac atg ttg aag aaa tat tct cat cac cgg aat att gct aca tac tat      156
Asn Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr
-40 -35 -30
ggg gct ttt atc aaa aag aac cca cca ggc atg gat gac caa ctt tgg      204
Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp
-25 -20 -15
ttg gtg atg gag ttt tgt ggt gct ggc tct gtc acc gac ctg atc aag      252
Leu Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys
-10 -5 1 5
aac aca aaa ggt aac acg ttg aaa gag gag tgg att gca tac atc tgc      300
Asn Thr Lys Gly Asn Thr Leu Lys Glu Glu Trp Ile Ala Tyr Ile Cys
10 15 20
msg gaa atc tta cgg ggg ctg art cac ctg cac cag cat aaa gtg att      348
Xaa Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile
25 30 35
cat cga rat att aaa ggg caa aat gtc ttg ctg act gaa aat gca gaa      396
His Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu
40 45 50
gtt aaa cta gtg gac ttt gga rtc akt gct cag ctt gat cga aca gtg      444
Val Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val
55 60 65 70
ggc agg arg aat act ttc att gga act ccc tac tgg atg gca cca raa      492
Gly Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa
75 80 85
gtt att gcc tgt gat gaa aac cca sat gcc aca tat gat ttc aar art      540
Val Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa
90 95 100
gac ttg tgg tct ttg ggt atc acc gcc att gaa atg gca gaa ggg ctc      588
Asp Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu
105 110 115
ccc ctc tct gtg aca tgc acc cca tgagagctct cttcctcatc ccccggaatc      642
Pro Leu Ser Val Thr Cys Thr Pro
120 125
cagcgctctg gctgaagtct aagaagtggc caaaaaaatt ccagtcattt attgagagct      702
gcttggtaaa aaatcacagc cagcgaccag caacagaaca attgatgaag catccattta      762
tacgagacca acctaattgag cgacaggtcc gcattcaact caaggaccat attgatagaa      822
caaagaagaa gcgaggaaaa aaaaaaaa      849

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<210> 368

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..458

<221> sig_peptide

<222> 39..80

<223> Von Heijne matrix

score 4.40000009536743

seq FLTALLWRGRIPG/RQ

<221> polyA_signal

<222> 613..618

<221> polyA_site

<222> 633..644

<400> 368

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agcggagacg cagagtcttg agcagcgcgn caggcacc atg ttc ctg act gcg ctc      56
                                     Met Phe Leu Thr Ala Leu
                                     -10
ctc tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg      104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg
          -5              1              5
cgg ccg cgg ttc gtg tcg ttg cgc gcc aag cag aac atg atc cgc cgc      152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg
          10              15              20
ctg gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg      200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met
          25              30              35              40
acc cgg gag cag gag cgc ggc cac gcc gcg ttg cgc agg agg gag gcc      248
Thr Arg Glu Gln Glu Arg Gly His Ala Ala Leu Arg Arg Arg Glu Ala
          45              50              55
ttc gag gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga      296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg
          60              65              70
ttc att gcg gac cag ctc gac cat ctc aat vgt cac caa gaa atg gtc      344
Phe Ile Ala Asp Gln Leu Asp His Leu Asn Xaa His Gln Glu Met Val
          75              80              85
cta atc ctg agt cgt cac cct tgg att tta tgg atc acg gag ctg acc      392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr
          90              95              100
atc ttt acc tgg tct gga ctg aaa aac tgt agc ttg tgt gaa aat gag      440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu
          105              110              115              120
ctt tgg acc agt ctt tat taaaacaaac aaacatgagt agtctgcata      488
Leu Trp Thr Ser Leu Tyr
          125
tcgaatatct agagctctaa acccccctaat acttaaaagt ctaattgctg tctgtggtt      548
tcattagtct gataggaaga tagggatttc ctcagtcaca gatgatattt tgaaggaaag      608
ctgcaataaa gccacaatga tttgaaaaaa aaaaaa      644

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<210> 369

<211> 918

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 9..185

<221> sig_peptide

<222> 9..50

<223> Von Heijne matrix

score 3.70000004768372

seq AALVTVLFTGVRR/LH

<221> polyA_site

<222> 906..918

<400> 369

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agctcagc atg gct gct tta gtg act gtt ctc ttc aca ggt gtc cgg agg      50
          Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg
          -10              -5

```

```

ctg cac tgc agc gcr scg ctt ggg cgg gcg gcc agt ggc grc tac agc      98
Leu His Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser
1          5          10          15
agg aac tgg ctg cca acc cct ccg gct acg ggc ccc tta ccg agc tcc      146
Arg Asn Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser
          20          25          30
cag act ggt cat atg cgg atg gcc gcc ctg ctc ccc caa tgaaaggcca      195
Gln Thr Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
          35          40          45
gcttcgaaaa aaagctgaaa gggagacktt tgcaaracra kttgtactgc tgtcacagga      255
aatggacgct ggattacaas catggcasct caggcagcar aakttgcagg aaraacaaaag      315
gaagcaggaa aatgctctta aaccctaaagg ggcttcactg aaaascccac ttccaaktca      375
ataaaaagca actcctgcct cccttctctca ccctgtctct ggatttcttt tctatcacct      435
aratgcttca tccagccara aaatagcctt cackktcccc atctgtcttc aragcaaaar      495
agctgggacm ccaaraacaa gctgttarat cactgcctgg gaggcttggc ttartactct      555
catctctggt tccattccag ttcagctaag tcttgcttta aaatttttac ctctagctg      615
ggtgcggtg ctcacgcctg taatcccagc actttgggag gctgaggcgg gcagatcaca      675
agatcaggag ttcgagacca gcctggccaa cccagcctgg tcaacatggt gaaacctgt      735
ccctactaaa gatacaaca attagccggg cgtgggtggg tgcgcttgta atcccagcta      795
ctcaggaggc tgaggcagga gaatcgctta aactcgggag gtagagggtg cagtgcagca      855
aggtcacacc attgcactcc aacctgggag acagggcgag actctgtctc aaaaaaaaaa      915
aaa

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<210> 370
 <211> 472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..316

 <221> sig_peptide
 <222> 14..121
 <223> Von Heijne matrix
 score 5.19999980926514
 seq PLRLNLLILIEG/SV

<221> polyA_signal
 <222> 442..447

<221> polyA_site
 <222> 458..471

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<400> 370
attatataga gcc atg ggg cct tac aac gtg gca gtg cct tca gat gta      49
          Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val
          -35          -30          -25
tct cat gcc cgc ttt tat ttc tta ttt cat cga cca tta agg ctg tta      97
Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu
          -20          -15          -10
aat ctg ctc atc ctt att gag ggc agt gtc gtc ttc tat cag ctc tat      145
Asn Leu Leu Ile Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr
          -5          1          5
tcc ttg ctg cgg tgg gag aag tgg aac cac aca ctt tcc atg gct ctc      193
Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu
          10          15          20
atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt ctc cgg gac aga      241
Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg
          25          30          35          40

```

```

wta kta tta ggc agg gca tac tcc tac cca ctc aac agt tat gaa ctc      289
Xaa Xaa Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu
      45                      50                      55
aag gca aac twa gct gcc tct caw caa tgagggagaaa ctcagataaa      336
Lys Ala Asn Xaa Ala Ala Ser Xaa Gln
      60                      65
aatatttttca tacgttctat ttttttcttg tgatttttat aaatatttaa gatattttat      396
attttgtata ctattatggt ttgaaagtcg ggaagagtaa gggatattaa atgtatccgt      456
aaacaaaaaa aaaaam      472

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<210> 371
 <211> 1504
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..1092

<221> sig_peptide
 <222> 70..234
 <223> Von Heijne matrix
 score 4.09999990463257
 seq AVCAALLASHPTA/EV

<221> polyA_signal
 <222> 1475..1480

<221> polyA_site
 <222> 1493..1504

```

<400> 371
agaaatcgta ggacttccga aagcagcggc ggcgtttgct tcaactgcttg gaagtgtgag      60
tgcgcgaag atg cga aag gtg gtt ttr att acc ggg gct agc agt ggc att      111
      Met Arg Lys Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile
      -55                      -50                      -45
ggc ctg gcc ctc tgc aag cgg ctg ctg gcg gaa gat gat gag ctt cat      159
Gly Leu Ala Leu Cys Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His
      -40                      -35                      -30
ctg tgt ttg gcg tgc agg aat atg agc aag gca gaa gct gtc tgt gct      207
Leu Cys Leu Ala Cys Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala
      -25                      -20                      -15                      -10
gct ctg ctg gcc tct cac ccc act gct gag gtc acc att gtc cag gtg      255
Ala Leu Leu Ala Ser His Pro Thr Ala Glu Val Thr Ile Val Gln Val
      -5                      1                      5
gat gtc agc aac ctg cag tca ttc ttc cgg gcc tcc aag gaa ctt aag      303
Asp Val Ser Asn Leu Gln Ser Phe Phe Arg Ala Ser Lys Glu Leu Lys
      10                      15                      20
caa agg ttt cag aga tta gac tgt ata tat cta aat gct ggg atc atg      351
Gln Arg Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met
      25                      30                      35
cct aat cca caa cta aat atc aaa gca ctt ttc ttt ggc ctc ttt tca      399
Pro Asn Pro Gln Leu Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser
      40                      45                      50                      55
aga aaa gtg att cat atg ttc tcc aca gct gaa ggc ctg ctg acc cag      447
Arg Lys Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln
      60                      65                      70
ggg gat aag atc act gct gat gga ctt cag gag gtg ttt gag acc aat      495
Gly Asp Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn
      75                      80                      85

```

```

gtc ttt ggc cat ttt atc ctg att cgg gaa ctg gag cct ctc ctc tgt      543
Val Phe Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys
      90                      95                      100
cac agt gac aat cca tct cag ctc atc tgg aca tca tct cgc agt gca      591
His Ser Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala
      105                      110                      115
agg aaa tct aat ttc agc ctc gag gac ttc cag cac agc aaa ggc aag      639
Arg Lys Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys
      120                      125                      130                      135
gaa ccc tac agc tct tcc aaa tat gcc act gac ctt ttg agt gtg gct      687
Glu Pro Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala
      140                      145                      150
ttg aac agg aac ttc aac cag cag ggt ctc tat tcc aat gtg gcc tgt      735
Leu Asn Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys
      155                      160                      165
cca ggt aca gca ttg acc aat ttg aca tat gga att ctg cct ccg ttt      783
Pro Gly Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe
      170                      175                      180
ata tgg acg ctg ttg atg ccg gca ata ttg cta ctt cgc ttt ttt gca      831
Ile Trp Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala
      185                      190                      195
aat gca ttc act ttg aca cca tat aat gga aca gaa gct ctg gta tgg      879
Asn Ala Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp
      200                      205                      210                      215
ctt ttc cac caa aag cct gaa tct ctc aat cct ctg atc aaa tat ctg      927
Leu Phe His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu
      220                      225                      230
agt gcc acc act ggc ttt gga aga aat tac att atg acc cag aag atg      975
Ser Ala Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met
      235                      240                      245
gac cta gat gaa gac act gct gaa aaa ttt tat caa aag tta ctg gaa      1023
Asp Leu Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu
      250                      255                      260
ctg gaa aag cac att agg gtc act att caa aaa aca gat aat cag gcc      1071
Leu Glu Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala
      265                      270                      275
agg ctc agt ggc tca tgc cta taattccagc actttgggag gccaaaggcag      1122
Arg Leu Ser Gly Ser Cys Leu
      280                      285
aaggatcact tgagaccagg agttcaagac cagcctgaga aacatagtga gcccttgtct      1182
ctacaaaaag aaataaaaat aatagctggg tgtggtggca tgcgcatgta gtcccagcta      1242
ctcagaagga tgaggtggga ggatctcttg aggctgggag gcagagggtg cagtgaagctg      1302
agattgtgcc actgcactcc agcctgggtg acagcgagac cctgtctcaa aatatgtata      1362
tatttaatat atatataaaa ccagagctga caatgacact ctggaacatt gcataccttc      1422
tgtacattct ggggtacatg gatttctact gagttggata atatgcattt gtaataaaact      1482
atgaactatg aaaaaaaaaa aa                                          1504

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<210> 372
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 274..597

<221> sig_peptide
 <222> 274..399
 <223> Von Heijne matrix
 score 5.19999980926514

seq LLFDLVCHEFCQS/DD

<221> polyA_signal

<222> 731..736

<221> polyA_site

<222> 754..765

<400> 372

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accaggaaca tccagctatt tatgatagca tttgcttcat tatgtcaagt tcaacaaatg      60
ttgacttgct ggtgaagggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac      120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag      180
tctgaagagc agccagtgtt tcggcttggt ccctgtatac ttgaagctgc caaacaagta      240
cgttctgaaa atccagaatg gcttgatgtt tac atg cac att tta caa ctg ctt      294
Met His Ile Leu Gln Leu Leu

```

-40

```

act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act      342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35 -30 -25 -20

```

```

gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc      390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
-15 -10 -5

```

```

tgc cag tct gat gat cca gcc atc att ctt caa raa car aaa acr gtg      438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Xaa Gln Lys Thr Val
1 5 10

```

```

cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act      486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
15 20 25

```

```

gag caa gak tat cta aar ata raa aaa gga gac ggt ggc tca ggg agt      534
Glu Gln Xaa Tyr Leu Lys Ile Xaa Lys Gly Asp Gly Gly Ser Gly Ser
30 35 40 45

```

```

aaa gga agg cca ktt gan caa aca gaa ktg ttc ctc tgc att tca aaa      582
Lys Gly Arg Pro Xaa Xaa Gln Thr Glu Xaa Phe Leu Cys Ile Ser Lys
50 55 60

```

```

cct tct tcc ttt cta tagccctgtg gtggaagatt ttattaaaat cctacgtgaa      637
Pro Ser Ser Phe Leu

```

65

```

gttgataagg cgcttgctga tgacttgga aaaaacttcc caagtttgaa gggttcagact      697
taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcaactgacaa      757
aaaaaaaaa      765

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<210> 373

<211> 1041

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 230..469

<221> sig_peptide

<222> 230..307

<223> Von Heijne matrix

score 4.90000009536743

seq VLCTNQVLITARA/VP

<221> polyA_signal

<222> 1004..1009

<221> polyA_site

<222> 1027..1040

<400> 373

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aacttccaag ttgtagtggt gttgttttca gcctgctgct gctgctgcta ttgaggctag      60
gggaaccgtc gtggggaagg atgggtgtgcg aaaaatgtga aaagaaactt ggtactgtta      120
tcactccaga tacatggaaa gatgggtgcta ggaataccac agaaagtggg ggaagaaagc      180
tgaatgaaaa taaagctttg acttcaaaaa aagccagaat tgatccata atg gaa gaa      238
                                   Met Glu Glu
                                   -25
ata agt tct cca ctt gta gaa ttt gta aaa gtt ttg tgc acc aac cag      286
Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
                                   -20                -15                -10
gtt ctc att act gcc agg gct gtg cct aca aaa aag gca tct gtg cga      334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
                                   -5                1                5
tgt gtg gaa aaa agg ttt tgg ata cca aaa act aca agc aaa cat ctg      382
Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
10                15                20                25
tct aga tgt att gat gga att tct ggc ttt cta aat gat ttt act ttc      430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
                                   30                35                40
tgc ctt gaa ttt tca agg cat aga tgt caa ctt aca gaa taacatgkt      479
Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
                                   45                50
taagataatt aagtktaaac cagaraattt gattgttact cattttgctc tcatgktcta      539
aaacagcaac agtgtaacta gtcttttggt gtaaattggt attttcctta taaaaatttt      599
aaaaactaag tggcaaatc catgaaaata tttctcagtt ctgtatgcac ttttatttaa      659
cattattcat ataattctcc cccaccact ttatttataa atactgcaaa aktgaraagg      719
agataataaa tactttgctc tgaatttggc atccaaagtt aacatttctc cctcactcc      779
cttgctggtg tcatagttat tagaatcagc agcctcttaa ctaattgctg tttcatagga      839
tatataaatg tttcaagcca ttattgctga atgggttctt agttattaac ctagacccaa      899
atcaaagacc agttggattt atgatatttt ttatttggtc ttgcagccaa agtgccagtt      959
tctttaatat gtgaccaaga acacaaggag catccatagc gccaaataaa tacactgaat      1019
tttagaaaaa caaaaaaaaa ar                                          1041

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<210> 374

<211> 1164

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 72..545

<221> sig_peptide

<222> 72..203

<223> Von Heijne matrix

score 5.5

seq ILFFTGGWIMIDA/AV

<221> polyA_site

<222> 1151..1162

<400> 374

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aaagtcggcg tggacgtttg aggaagctgg gatacagcat ttaatgaaaa atttatgctt      60
aagaagtaaa a atg gca ggc ttc cta gat aat ttt cgt tgg cca gaa tgt      110
                                   Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys
                                   -40                -35
gaa tgt att gac tgg agt gag aga aga aat gct gtg gca tct gtt gtc      158
Glu Cys Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val

```

```

-30          -25          -20
gca ggt ata ttg ttt ttt aca ggc tgg tgg ata atg att gat gca gct      206
Ala Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
-15          -10          -5          1
gtg gtg tat cct aag cca gaa cag ttg aac cat gcc ttt cac aca tgt      254
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys
5          10          15
ggt gta ttt tcc aca ttg gct ttc ttc atg ata aat gct gta tcc aat      302
Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn
20          25          30
gct cag gtg aga ggt gat agc tat gaa agc ggc tgt tta gga aga aca      350
Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr
35          40          45
ggt gct cga gtt tgg ctt ttc att ggt ttc atg ttg atg ttt ggg tca      398
Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser
50          55          60          65
ctt att gct tcc atg tgg att ctt ttt ggt gca tat gtt acc caa aat      446
Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn
70          75          80
act gat gtt tat ccg gga cta gct gtg ttt ttt caa aat gca ctt ata      494
Thr Asp Val Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile
85          90          95
ttt ttt agc act ctg atc tac aaa ttt gga aga acc gaa gag cta tgg      542
Phe Phe Ser Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp
100          105          110
acc tgagatcact tcttaagtca cattttcctt ttgttatatt ctgtttgtag      595
Thr
atagggttttt tatctctcag tacacattgc caaatggagt agattgtaca ttaaagtgtt      655
tgtttctttta catttttatg ttctgagttt tgaaatagtt ttatgaaatt tctttatttt      715
tcattgcata gactgttaat atgtatataa tacaagacta tatgaattgg ataatgagta      775
tcagtttttt attcctgaga tttagaactt gatctactcc ctgagccagg gttacatcat      835
cttgatcattt tagaagtaac cactcttgct tctctggctg ggcacggtgg ctcatgcctg      895
taatcccagc actttgggag gccgaggcgg gccgattgct tgagggtcaag tgtttgagac      955
cagcctggcc aacatggcga aaccccatct actaaaaata caaaaattag ccaggcatgg      1015
tggtgggtgc ctgtaatccc aactacctag gaggctgagg caggagaatc gcttgaacct      1075
gggggggcaga ggttgyagtg agctgagttt gcgcactgc actctagcct gggggagaaa      1135
gtgaaactcc ctctcaaaaa aaaaaaamc      1164

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<210> 375

<211> 1250

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 36..425

<221> sig_peptide

<222> 36..119

<223> Von Heijne matrix

score 11.6000003814697

seq LLLLVQLLRFLRA/DG

<221> polyA_signal

<222> 1215..1220

<221> polyA_site

<222> 1240..1250

<400> 375


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atttcttccc cccgagctgg gcgtgcgcgg ccgca atg aac tgg gag ctg ctg      53
                               Met Asn Trp Glu Leu Leu
                               -25
ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc ttg gtg cag ctg      101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Val Gln Leu
-20 -15 -10
ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta cta tgg gcc gag      149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
-5 1 5 10
tgg cag gga cga cgc cca gaa tgg gag ctg act gat atg gtg gtg tgg      197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
15 20 25
gtg act gga gcc tcg agt gga att ggt gag gag ctg gct tac cag ttg      245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
30 35 40
tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga aga gtg cat gag      293
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg Arg Val His Glu
45 50 55
ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc aat tta aaa gaa      341
Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly Asn Leu Lys Glu
60 65 70
aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac act ggt tcc cat      389
Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp Thr Gly Ser His
75 80 85 90
gaa agc ggc tac caa agc tgt tct cca gga att tgg tagaatcgac      435
Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly Ile Trp
95 100
attctggtca acaatgtgga aatgtcccag cgttctctgt gcatggatac caacttggat      495
gtctacagaa agctaattgag agcttaacta cttaggggacg gtgtccttga caaaatgtgk      555
kctgcctcac atgatcgaga ngaarcaagg aaagattgtt actgtgaata gcatcctggg      615
tatcatatct gtacctcttt ccattggata ctgtgctagc aagcatgctc tccggggktk      675
ktttaatggc cttcraacag aacttgccac ataccargt ataatagttt ctaacatttg      735
cccaggacct gtgcaatcaa atattgtgga aaattcccta gctggagaag tcacaaagac      795
tataggcaat aatggagacc agtcccacaa gatgacaacc agtcgttgtg tgcggctgat      855
gttaatcagc atggccaatg atttgaaaga agtttggatc tcagaacaac ctttcttggt      915
agtaacatat ttgtggcaat acatgccaac ctgggcctgg tggataacca acaagatggg      975
gaagaaaagg attgagaact ttaagagtgg tgtggatgca gactcttctt attttaaaat      1035
ctttaagaca aaacatgact gaaaagagca cctgtacttt tcaagccact ggagggagaa      1095
atggaaaaca tgaaaacagc aatcttctta tgcttctgaa taatcaaaga ctaatttgtg      1155
attttacttt ttaatagata tgactttgct tccaacatgg aatgaaataa aaaataaata      1215
ataaaagatt gccatgaatc ttgcaaaaaa aaaaa      1250

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<210> 376

<211> 947

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 155..751

<221> sig_peptide

<222> 155..340

<223> Von Heijne matrix

score 3.70000004768372

seq SILGIISVPLSIG/YC

<221> polyA_signal

<222> 912..917

<221> polyA_site

<222> 937..947

<400> 376

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agtgaaaaga agatgcctag agaatggcaa tttaaaagaa aaagatatatac ttgttttgcc      60
ccttgacctg accgacctg gttcccatga agcggctacc aaagctgttc tccaggagtt      120
tggtagaatc gacattctgg tcaacaatgg tgga atg tcc cag cgt tct ctg tgc      175
                               Met Ser Gln Arg Ser Leu Cys
                               -60
atg gat acc agc ttg gat gtc tac aga rag cta ata gag ctt aac tac      223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
-55                               -50                               -45                               -40
tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc gag      271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
                               -35                               -30                               -25
agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc ata      319
Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
                               -20                               -15                               -10
tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc cgg      367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg
                               -5                               1                               5
ggg ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt ata      415
Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile
10                               15                               20                               25
ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg gaa      463
Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu
                               30                               35                               40
aat tcc cta gct gga gaa gtc aca aaa act ata ggc aat aat gga aac      511
Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asn
                               45                               50                               55
cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta atc      559
Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile
60                               65                               70
agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct ttc      607
Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro Phe
75                               80                               85
ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg tgg      655
Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp Trp
90                               95                               100                               105
ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt ggt      703
Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser Gly
110                               115                               120
gtg gat gcm rac tct tct tat ttt aaa atc ttt aag aca aaa cat gac      751
Val Asp Ala Xaa Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His Asp
125                               130                               135
tgaaaaganc acctgtactt ttcaagccac tggaggggaga aatggaaaac atgaaaacag      811
caatcttctt atgcttctga ataatacaag actaatttgt gattttactt tttaatagat      871
atgactttgc ttccaacatg grrtgaaata aaaaataaat aataaaaagat tgccatgrrt      931
cttgcaaaaa aaaaaa                                         947

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<210> 377

<211> 621

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..585

<221> sig_peptide

<222> 46..120

<223> Von Heijne matrix

score 6.30000019073486

seq AFSLSVMAALTFG/CF

<221> polyA_signal

<222> 584..589

<221> polyA_site

<222> 606..619

<400> 377

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aactgggtgt gcgtrtggag tccggactcg tgggagacga tcgcmg atg aac acg gtg      57
                                     Met Asn Thr Val
                                     -25
ctg tcg cgg gcg aac tca ctg ttc gcc ttc tcg ctg agc gtg atg gcs      105
Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu Ser Val Met Ala
-20                               -15                               -10
gcg ctc acc ttc ggc tgc ttc atc ayy acc gcc ttc aaa gac agg agc      153
Ala Leu Thr Phe Gly Cys Phe Ile Xaa Thr Ala Phe Lys Asp Arg Ser
-5                               1                               5                               10
gtc ccg gtg cgg ctg cac gtc tcg cga atc atg cta aaa aat gta gaa      201
Val Pro Val Arg Leu His Val Ser Arg Ile Met Leu Lys Asn Val Glu
15                               20                               25
gat ttc act gga cct aga gaa aga agt gat ctg gga ttt atc aca ttt      249
Asp Phe Thr Gly Pro Arg Glu Arg Ser Asp Leu Gly Phe Ile Thr Phe
30                               35                               40
gat ata act gct gat cta gag aat ata ttt gat tgg aat gtt aag cag      297
Asp Ile Thr Ala Asp Leu Glu Asn Ile Phe Asp Trp Asn Val Lys Gln
45                               50                               55
ttg ttt ctt tat tta tca gca gaa tat tca aca aaa aat aat gct ctg      345
Leu Phe Leu Tyr Leu Ser Ala Glu Tyr Ser Thr Lys Asn Asn Ala Leu
60                               65                               70                               75
aac caa ktt gtc cta tgg gac aag att gtt ttg aga ggt gat aat ccg      393
Asn Gln Xaa Val Leu Trp Asp Lys Ile Val Leu Arg Gly Asp Asn Pro
80                               85                               90
aag ctg ctg ctg aaa gat atg aaa aca aaa tat ttt ttc ttt gac gat      441
Lys Leu Leu Leu Lys Asp Met Lys Thr Lys Tyr Phe Phe Phe Asp Asp
95                               100                               105
gga aat ggt ctc wag gga aac agg aat gtc act ttg acc ctg tct tgg      489
Gly Asn Gly Leu Xaa Gly Asn Arg Asn Val Thr Leu Thr Leu Ser Trp
110                               115                               120
aac gtc gta cca aat gct gga att cta cct ctt gtg aca gga tca gga      537
Asn Val Val Pro Asn Ala Gly Ile Leu Pro Leu Val Thr Gly Ser Gly
125                               130                               135
cac gta tct gtc cca ttt cca gat aca tat gaa ata acg aag agt tat      585
His Val Ser Val Pro Phe Pro Asp Thr Tyr Glu Ile Thr Lys Ser Tyr
140                               145                               150                               155
taaattattc tgaatttgaa acaaaaaaaaaaaa aaahm      621

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<210> 378

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 378

Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val Leu Gln Leu Thr Thr
 -20 -15 -10 -5
 Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val Asn Pro Phe Glu Xaa
 1 5 10
 Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala His His Phe Ile His
 15 20 25
 Pro Cys Leu Asp
 30

<210> 379
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 379
 Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu Pro Pro Leu Xaa
 -20 -15 -10
 Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro Glu Arg Gly Ala
 -5 1 5
 Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg Phe Cys Pro Pro
 10 15 20 25
 Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp Lys Tyr Ser Asn
 30 35 40
 Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu Ser Pro Leu Glu
 45 50 55
 Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu Trp Asn Gln Gln
 60 65 70
 Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu Lys Glu Glu Phe
 75 80 85
 Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu Arg Thr Glu Ser
 90 95 100 105
 Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala Asp Phe Tyr Lys
 110 115 120
 Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr Tyr Asn Arg Asp
 125 130 135
 Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly Lys Val Ala
 140 145 150
 Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys Lys Arg Ser
 155 160 165
 Asn
 170

<210> 380
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 380
 Met Ala Phe Thr Leu Xaa Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
 -10 -5 1

Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
 5 10 15
 Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
 20 25 30
 Lys Ser Xaa Xaa Met Xaa Leu Ile Arg Ser Val Arg Thr Val Met Arg
 35 40 45 50
 Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
 55 60 65
 Phe Gly

<210> 381
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 381
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
 -20 -15 -10
 Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
 -5 1 5 10
 Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
 15 20 25
 Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu Thr Lys Ala Arg
 30 35 40
 Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
 45 50 55
 Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
 60 65 70 75
 Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu Gln Ala Xaa Ala Thr
 80 85 90
 Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
 95 100 105
 Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa Ala Trp Leu Gly Pro
 110 115 120
 Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro Pro Xaa Lys Gln Asn
 125 130 135
 His Ile Leu Trp Ala Leu Thr Gly His Val Xaa Arg Gln Xaa Arg Glu
 140 145 150 155
 Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile Gln Glu Lys Leu His
 160 165 170
 Thr Ala Ala Leu Pro Ala
 175

<210> 382
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 382
 Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg

-55 -50 -45 -40
 Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
 -35 -30 -25
 Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
 -20 -15 -10
 Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
 -5 1 5
 Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
 10 15 20 25
 Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
 30 35 40
 Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
 45 50 55
 Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
 60 65 70
 Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile
 75 80 85
 Pro Phe Ala Arg Asp Ala Val Lys Xaa Cys Phe Ala Val Cys Leu Ala
 90 95 100 105

<210> 383
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 383
 Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val
 -15 -10 -5
 Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile
 1 5 10
 Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly
 15 20 25 30
 Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro
 35 40 45
 Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser
 50 55 60
 Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met
 65 70 75
 Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
 80 85 90

<210> 384
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 384
 Met Ile Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu
 -20 -15 -10
 Phe Pro Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp

-5		1		5		10
Leu Tyr Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser						
	15		20		25	
Gln Lys Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val						
	30		35		40	

<210> 385
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 385														
Met Gly Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser														
-15		-10				-5							1	
Ala Lys Pro Asn Glu Gln Pro Trp Leu Leu Asn														
	5					10								

<210> 386
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 386														
Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile														
-20		-15				-10								
Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser														
-5		1				5						10		
Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp														
	15				20					25				
Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro														
	30				35					40				
Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Leu Glu Gly														
	45			50				55						
Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys														
60		65				70							75	
Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser														
	80					85							90	
Pro Ser Thr Xaa Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu														
	95					100							105	
Val Phe Met Arg Met Thr Pro Ser Met Met Asn Thr Pro Ser Gly														
	110				115					120				
Asn Xaa Gly Cys Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser														
	125				130					135				
Ser Ser Pro Val Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile														
140				145				150						155
Ile Ala Gly Glu Ser Ile Arg Asn Arg Ser														
	160							165						

<210> 387
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 387
 Met Glu Thr Gly Ala Leu Arg Arg Pro Gln Leu Leu Pro Leu Leu Leu
 -25 -20 -15
 Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys Arg Pro Val Leu Gln Asn
 -10 -5 1 5
 Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser Leu Glu Val Pro Thr Gly
 10 15 20
 Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly Pro Gly Leu Xaa Gly Ala
 25 30 35
 Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu Met Gly Arg Gln Arg Thr
 40 45 50
 Arg Lys Val Lys Gly Pro Ala Trp Xaa His Thr Ala Asn Gln Glu Leu
 55 60 65 70
 Asn Arg Met Arg Ser Leu Ser Ser Gly Ser Val Pro Val Gly His Leu
 75 80 85
 Glu Gly Gly Thr Val Lys Leu Gln Lys Asp Thr Gly Leu His Ser Cys
 90 95 100
 Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr Pro Ala Ser Val Leu Ala
 105 110 115
 Asp Ala Cys Pro Gly Phe His Asp Val Xaa Val Gln Xaa Ala Leu Phe
 120 125 130
 Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys Thr His Phe Cys Leu Ser
 135 140 145 150
 Ile Xaa Leu

<210> 388
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 388
 Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys
 -55 -50 -45 -40
 Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu
 -35 -30 -25
 Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr
 -20 -15 -10
 Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met
 -5 1 5
 Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly
 10 15 20 25
 Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr
 30 35 40
 Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu
 45 50 55
 Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala
 60 65 70

Pro Phe Pro Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser
 75 80 85
 Pro Gly Cys Tyr Arg Tyr
 90 95

<210> 389
 <211> 236
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 389
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
 -30 -25 -20
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala
 -15 -10 -5 1
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 5 10 15
 Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro Asp Leu
 20 25 30
 Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln Ala Ser
 35 40 45
 Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro Ala Ala
 50 55 60 65
 Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
 70 75 80
 Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
 85 90 95
 Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
 100 105 110
 Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu Gly Pro
 115 120 125
 Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe Glu Asp
 130 135 140 145
 Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
 150 155 160
 Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
 165 170 175
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly
 180 185 190
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
 195 200 205

<210> 390
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -100...-1

<400> 390
 Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
 -100 -95 -90 -85

[illegible]

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<210> 391
<211> 69
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -49..-1
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<400> 391
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
          -45                      -40                      -35
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
          -30                      -25                      -20
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
          -15                      -10                      -5
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
  1          5                      10                      15
Phe Phe Ile Pro Asp
          20

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<210> 392
<211> 241
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -30..-1
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<400> 392
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-30          -25          -20          -15
Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
          -10          -5          1
Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
      5          10          15
Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
      20          25          30

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Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
 35 40 45 50
 Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg Glu Ala Leu
 55 60 65
 Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp
 70 75 80
 Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala
 85 90 95
 Arg Ala Lys Gln Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile
 100 105 110
 Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser
 115 120 125 130
 Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu
 135 140 145
 Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile Lys Glu Asp
 150 155 160
 Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu Ile Ala Gln
 165 170 175
 Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln Ser Glu Lys
 180 185 190
 Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn Tyr Glu Arg
 195 200 205 210
 Pro

<210> 393
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 393
 Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys Trp Leu Glu Val Glu
 -30 -25 -20 -15
 Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn Ala Ser Ala Ile Ser
 -10 -5 1
 Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp Arg Arg Glu Ser
 5 10 15

<210> 394
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 394
 Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
 -25 -20 -15
 Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
 -10 -5 1
 Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
 5 10 15 20
 Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa

Ser 25 30 35

<210> 395
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 395
 Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe Leu Ser Tyr Leu Pro
 -20 -15 -10
 Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly Ser Thr Leu Gly Lys
 -5 1 5
 Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg Pro Trp Asp Ala Ala
 10 15 20
 Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa Asn Xaa Tyr Xaa Xaa
 25 30 35 40
 Trp Gly Gln Gly Thr His Ser Ser Leu
 45

<210> 396
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 396
 Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro Thr
 -15 -10 -5
 Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg Leu
 1 5 10
 Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala Leu
 15 20 25 30
 Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
 35 40

<210> 397
 <211> 192
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -93...-1

<400> 397
 Met Ala Glu Leu Gly Leu Asn Glu His His Gln Asn Glu Val Ile Asn
 -90 -85 -80
 Tyr Met Arg Phe Ala Arg Ser Lys Arg Gly Leu Arg Leu Lys Thr Val

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      -75      -70      -65
Asp Ser Cys Phe Gln Asp Leu Lys Glu Ser Arg Leu Val Glu Asp Thr
      -60      -55      -50
Phe Thr Ile Asp Glu Val Ser Glu Val Leu Asn Gly Leu Gln Ala Val
      -45      -40      -35      -30
Val His Ser Glu Val Glu Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn
      -25      -20      -15
Val Leu Leu Leu Arg Gln Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu
      -10      -5      1
Lys Leu Gln Thr Asp Ile Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu
      5      10      15
Gln Xaa Ala Glu Phe Glu Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys
      20      25      30      35
Pro Ile Leu Xaa Val Thr Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly
      40      45      50
Gly Thr Ala Lys Leu Leu Asn Lys Val Ile Cys Ile Ile Leu Arg Asn
      55      60      65
Gly Lys Ser Leu Ile Leu Ser Cys His Cys Leu Gly Trp Arg Asn Lys
      70      75      80
Ser Gly Arg Phe Val Ser Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
      85      90      95

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<210> 398
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -72...-1

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<400> 398
Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
      -70      -65      -60
Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
      -55      -50      -45
Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
      -40      -35      -30      -25
Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala
      -20      -15      -10
Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala
      -5      1      5
Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Ser Val
      10      15      20
Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala Pro Gly Pro Tyr
      25      30      35      40
Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro Val Ala Pro Gln
      45      50      55
His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn Gln Lys Thr Leu
      60      65      70
Phe Ser Met Val Gly
      75

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<210> 399
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 399
Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro
-20 -15 -10 -5
Leu Ala Gln Ala Leu Asp Cys His Val Cys Ala Tyr Asn Gly Asp Asn
1 5 10
Cys Phe Asn Pro Met Arg Cys Pro Ala Met Val Ala Tyr Cys Met Thr
15 20 25
Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met Lys Val Ser Lys Ser Cys
30 35 40
Val Pro Arg Cys Phe Glu Xaa Cys Val
45 50

<210> 400
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 400
Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
-20 -15 -10 -5
Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
1 5 10
Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
15 20 25
Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
30 35 40
Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
45 50 55 60
Pro Xaa Lys Leu Arg Gln
65

<210> 401
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21...-1

<400> 401
Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala Cys Gly Ser Leu Leu
-20 -15 -10
Pro Gly Leu Trp Gln His Leu Thr Ala Asn His Trp Pro Pro Phe Ser
-5 1 5 10
Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser Glu Gln Ile Ser Glu
15 20 25
Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg Ser Leu Asn Gln Glu
30 35 40
Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr Ser Ile Thr

45

50

55

<210> 402
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 402
 Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu Pro Leu Ser
 -25 -20 -15
 Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser
 -10 -5 1
 Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val Pro Glu Pro
 5 10 15 20
 Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg
 25 30 35
 Thr

<210> 403
 <211> 211
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 403
 Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu Glu Leu Thr
 -25 -20 -15
 Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr Asn Lys Phe
 -10 -5 1 5
 Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile Phe Ile Gly
 10 15 20
 Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu Ser Lys Asn
 25 30 35
 Asn Arg Phe Gly Arg Asn Pro Val Leu Leu Gly Ile Leu Val His
 40 45 50
 Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly Asp Ala Pro
 55 60 65
 Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile Lys Ser Ser
 70 75 80 85
 Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu Gly Asn Ser
 90 95 100
 Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu Tyr Ser Glu
 105 110 115
 Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln Ser Ile Cys
 120 125 130
 Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu His Trp Gln
 135 140 145
 Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile Ser Phe Phe
 150 155 160 165
 Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly Ser Asp Tyr
 170 175 180

Arg Ser Ile

<210> 404
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -80...-1

<400> 404
 Met Ser Thr Trp Tyr Leu Ala Leu Asn Lys Ser Tyr Lys Asn Lys Asp
 -80 -75 -70 -65
 Ser Val Arg Ile Tyr Leu Ser Leu Cys Thr Val Ser Ile Lys Phe Thr
 -60 -55 -50
 Tyr Phe His Asp Ile Gln Thr Asn Cys Leu Thr Thr Trp Lys His Ser
 -45 -40 -35
 Arg Cys Arg Phe Tyr Trp Ala Phe Gly Gly Ser Ile Leu Gln His Ser
 -30 -25 -20
 Val Asp Pro Leu Val Leu Phe Leu Ser Leu Ala Leu Leu Val Thr Pro
 -15 -10 -5
 Thr Ser Thr Pro Ser Ala Lys Ile Gln Ser Leu Gln Ile Asp Leu Pro
 1 5 10 15
 Gly Gly Trp Arg Leu Ala Thr Asp Arg Ile Phe Thr Leu Ser Pro Val
 20 25 30
 Pro Met Asp Xaa Pro Leu Ile Leu His Gln Leu
 35 40

<210> 405
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 405
 Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
 -25 -20 -15
 Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
 -10 -5 1 5
 Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu
 10 15 20
 Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp Val Leu
 25 30 35
 Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp Ser His
 40 45 50
 Ala His Trp Xaa Ser Xaa
 55 60

<210> 406
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 406

```

Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr
  -30          -25          -20
Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
  -15          -10          -5          1
Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
      5          10          15
Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
      20          25          30
Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
      35          40          45
Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn
      50          55          60          65
Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser
      70          75          80
Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser His Val Ser
      85          90          95
Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys
      100          105          110
Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp Asn Trp Glu
      115          120          125
Pro Asn
130
  
```

<210> 407
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 407

```

Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
  -35          -30          -25
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
  -20          -15          -10
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
  -5          1          5          10
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Xaa Gln
      15          20          25
Xaa Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
      30          35          40
Gly Phe Ser Phe Cys Gln Xaa Arg Leu Asn Lys Arg Lys Glu Tyr Met
      45          50          55
Val Arg
60
  
```

<210> 408
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 408
 Met Arg Phe Leu Pro Cys Cys Leu Leu Trp Ser Val Phe Asn Pro Glu
 -15 -10 -5 1
 Ser Leu Asn Cys His Tyr Phe Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser
 5 10 15
 Leu Gln Tyr Tyr Glu Ile Ser Leu Gln Glu Lys Leu Leu Gly Phe Leu
 20 25 30
 Trp Leu Cys Phe Leu Ser Tyr Phe Phe Arg Ala Val Tyr Phe Leu Ile
 35 40 45
 Asp Phe Ser Ser Phe Thr
 50 55

<210> 409
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45...-1

<400> 409
 Met His Ser Leu Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser
 -45 -40 -35 -30
 Phe Ser Phe Arg Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly
 -25 -20 -15
 Glu Asn Phe Leu Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser
 -10 -5 1
 Gly Ser Thr Phe Met Arg Asp Ile Glu Thr Asn Lys
 5 10 15

<210> 410
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 410
 Met Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser
 -20 -15 -10
 Ser Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys
 -5 1 5 10
 Asn Pro Phe Leu Trp Lys Leu
 15

<210> 411
 <211> 51
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 411

Met	Ala	Phe	Gln	Ser	Leu	Leu	Glu	Met	Lys	Phe	Phe	Leu	Cys	Ala	Ala
			-20					-15					-10		
Phe	Pro	Leu	Gly	Ala	Gly	Val	Lys	Met	Phe	His	Tyr	Leu	Gly	Pro	Gly
		-5				1					5				
Lys	Pro	Leu	Xaa	Gln	Ala	Ser	Pro	Ser	Pro	His	Pro	His	Arg	Xaa	Arg
10					15					20					25
Ile	Trp	Pro													

<210> 412

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 412

Met	Ala	Ser	Ser	His	Trp	Asn	Glu	Thr	Thr	Thr	Ser	Val	Tyr	Gln	Tyr
			-45					-40					-35		
Leu	Gly	Phe	Gln	Val	Gln	Lys	Ile	Tyr	Pro	Phe	His	Asp	Asn	Trp	Asn
		-30				-25						-20			
Thr	Ala	Cys	Phe	Val	Ile	Leu	Leu	Leu	Phe	Ile	Phe	Thr	Val	Val	Ser
	-15				-10						-5				
Leu	Val	Val	Leu	Ala	Phe	Leu	Tyr	Glu	Val	Leu	Xaa	Xaa	Cys	Cys	Cys
1				5				10					15		
Val	Lys	Asn	Lys	Thr	Val	Lys	Asp	Leu	Lys	Ser	Glu	Pro	Asn	Pro	Leu
		20					25						30		
Xaa	Xaa	Met	Met	Asp	Asn	Ile	Arg	Lys	Arg	Glu	Thr	Glu	Val	Val	
		35					40					45			

<210> 413

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32...-1

<400> 413

Met	Asp	Glu	Tyr	Ser	Trp	Trp	Cys	His	Val	Leu	Glu	Val	Val	Lys	Gly
		-30					-25					-20			
Gln	Met	Phe	Thr	Phe	Ile	Asn	Ile	Thr	Leu	Trp	Leu	Gly	Ser	Leu	Cys
	-15				-10						-5				
Gln	Arg	Phe	Phe	Tyr	Ala	Ser	Gly	Thr	Tyr	Phe	Leu	Ile	Tyr	Ile	Ser
1				5				10						15	
Thr	Val	Thr	Pro	Ser	Trp	Arg	Leu	Cys	Leu	Val	Ser				
			20					25							

<210> 414
 <211> 170
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -79...-1

<400> 414
 Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 -75 -70 -65
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 -60 -55 -50
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe
 -45 -40 -35
 Gln Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 -30 -25 -20
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 -15 -10 -5 1
 Pro Ser Ser Lys Ala Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa
 5 10 15
 Ala Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe
 20 25 30
 Pro Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa
 35 40 45
 Arg His Xaa Gln Xaa His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala
 50 55 60 65
 Cys Thr Xaa Cys Gly Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln
 70 75 80
 His Tyr Ile Arg His Ala Arg Gly Gly Leu
 85 90

<210> 415
 <211> 190
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -82...-1

<400> 415
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
 -15 -10 -5
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
 1 5 10
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp Ile
 15 20 25 30
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
 35 40 45

```

Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala Leu
      50                      55                      60
Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
      65                      70                      75
Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg His
      80                      85                      90
Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
      95                      100                      105

```

<210> 416
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

```

<400> 416
Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
-60                      -55                      -50                      -45
Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
      -40                      -35                      -30
Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
      -25                      -20                      -15
Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
      -10                      -5                      1
Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
5                      10                      15                      20
Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Lys
      25                      30                      35
Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser
      40                      45                      50
Ser Lys

```

<210> 417
 <211> 161
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -108...-1

```

<400> 417
Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln Ser Pro Gln Ala Leu
      -105                      -100                      -95
Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser Ile Thr Leu Thr Leu
      -90                      -85                      -80
Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg Asn Val Thr His Leu
      -75                      -70                      -65
Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu Ser Gly Arg Glu Ala
-60                      -55                      -50                      -45
His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro Thr Ala Trp Ser Ser
      -40                      -35                      -30
Asp Asp Cys Ala Leu His Gly His Cys Glu Gln Val Val Phe Thr Ala
      -25                      -20                      -15
Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe Pro Ser Leu Tyr Ser

```

-10 -5 1
 His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr Pro Arg Ser Gly Thr
 5 10 15 20
 Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln Asn Thr Pro Lys Ile
 25 30 35
 Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu Glu Lys Ser Ile Met
 40 45 50
 Leu

<210> 418
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 418
 Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
 -20 -15 -10
 Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
 -5 1 5 10
 Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
 15 20 25
 Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
 30 35 40
 Leu Arg Met
 45

<210> 419
 <211> 332
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 419
 Met Ile Xaa Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp
 -30 -25 -20
 Thr Arg Gln Leu Pro Leu Leu Thr Ser Ala Leu His Gly Leu Gln Gln
 -15 -10 -5
 Gln His Pro Ala Phe Ser Gly Val Ala Arg Leu Ala Lys Arg Trp Val
 1 5 10 15
 Arg Ala Gln Leu Leu Gly Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu
 20 25 30
 Val Ala Ala Ala Leu Phe Leu His Pro Glu Pro Phe Thr Pro Pro Ser
 35 40 45
 Ser Pro Gln Val Gly Phe Leu Arg Phe Leu Phe Leu Val Ser Thr Phe
 50 55 60
 Asp Trp Lys Asn Asn Pro Leu Phe Val Asn Leu Asn Asn Glu Leu Thr
 65 70 75 80
 Val Glu Glu Gln Val Glu Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala
 85 90 95
 Gln Leu Pro Val Met Val Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser
 100 105 110

```

Val Trp Thr Gln Asp Gly Pro Ser Ala Gln Ile Leu Gln Gln Leu Val
      115                      120                      125
Val Leu Ala Ala Glu Xaa Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp
      130                      135                      140
Pro Arg Gly Pro Gly Asp Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp
      145                      150                      155                      160
Ile Tyr Asp Val Leu Ile Arg Leu Ser Pro Arg His Ile Pro Arg His
      165                      170                      175
Arg Gln Ala Val Asp Ser Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu
      180                      185                      190
Ser Gln Pro Gly Pro Ser Ser Leu Met Pro Val Leu Gly Xaa Asp Pro
      195                      200                      205
Pro Gln Leu Tyr Leu Thr Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala
      210                      215                      220
Leu Phe Phe Tyr Asp Gln His Gly Gly Glu Val Ile Gly Val Leu Trp
      225                      230                      235                      240
Lys Pro Thr Ser Phe Gln Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys
      245                      250                      255
Gly Arg Met Val Met Ser Arg Gly Gly Glu Leu Val Met Val Pro Asn
      260                      265                      270
Val Glu Ala Ile Leu Glu Asp Phe Ala Val Leu Gly Glu Gly Leu Val
      275                      280                      285
Gln Thr Val Glu Ala Arg Ser Glu Arg Trp Thr Val
      290                      295                      300

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<210> 420
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

```

<400> 420
Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser Phe His
      -15                      -10                      -5
Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser Arg His
      1                      5                      10
His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu Glu Asn
      15                      20                      25
Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys Ile Val
      30                      35                      40                      45
Gly

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<210> 421
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

```

<400> 421
Met Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser
      -30                      -25                      -20                      -15
Thr Ser Met Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val

```


<220>
 <221> SIGNAL
 <222> -29...-1

<400> 424

Met	Thr	Cys	Arg	Gly	Ser	Cys	Ser	Tyr	Ala	Thr	Arg	Arg	Ser	Pro	Ser
				-25					-20					-15	
Glu	Leu	Ser	Leu	Leu	Pro	Ser	Ser	Leu	Trp	Val	Leu	Ala	Thr	Ser	Ser
			-10					-5					1		
Pro	Thr	Ile	Thr	Ile	Ala	Leu	Ala	Met	Ala	Ala	Gly	Asn	Leu	Cys	Pro
	5					10					15				
Leu	Pro	Ser	Ser	Xaa	Arg	Xaa	Lys	Arg	Arg	Trp	Cys	Gln	Ala	Xaa	Gln
20					25					30					35
Gln	Xaa	Ala	Leu	Leu											
					40										

<210> 425
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -56...-1

<400> 425

Met	Val	Pro	Trp	Pro	Arg	Gly	Lys	Val	Lys	Thr	Ala	Pro	Ile	Pro	Ile
	-55					-50					-45				
Ser	Arg	Phe	Pro	Phe	Leu	Pro	Thr	His	Asp	Pro	Pro	Thr	Pro	Ala	His
-40				-35					-30					-25	
Trp	Ser	Pro	Ala	Ser	His	Gln	Gln	Phe	Lys	His	Xaa	Ser	Pro	Leu	Leu
			-20					-15					-10		
Thr	Leu	Ala	Leu	Leu	Gly	Gln	Cys	Ser	Leu	Phe	Xaa	Asn	Leu	Arg	Lys
			-5				1				5				
Lys	Leu	Ala	Gly	Gln	Lys	Ala	Lys	Lys	Leu	Pro	Ser	Phe	Ser	Ser	Leu
10					15					20					
Pro	Leu	Thr	Leu	Trp	Pro	Leu	Thr	Pro	Gln	Phe	Ala	Glu	Leu	Thr	Thr
25				30					35					40	
Val	Ala	Gln	Lys	Lys	Leu	Arg	Trp	Ser	Gly	Thr	Leu	Gly	Trp	Gly	Pro
			45					50					55		
Val	Pro	Ser	Trp	Val	Gln	Phe	Phe	Leu	Gly						
			60					65							

<210> 426
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 426

Met	Ala	Cys	Glu	Thr	His	Gly	Val	Leu	Val	Pro	Ala	His	Leu	Ser	Gly
-30					-25					-20					-15
Leu	Ile	Thr	Cys	Leu	Leu	Ala	Phe	Trp	Val	Pro	Ala	Ser	Cys	Ile	Gln
			-10						-5					1	

Arg Cys Ser Gly Ser Pro Leu Pro Leu
5 10

<210> 427
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36...-1

<400> 427
Met Ala Pro His Thr Ala Ser Phe Gly Val Cys Pro Leu Leu Ser Val
-35 -30 -25
Thr Arg Val Val Ala Thr Glu His Trp Leu Phe Leu Ala Ser Leu Ser
-20 -15 -10 -5
Gly Ile Lys Thr Tyr Gln Ser Tyr Ile Ser Val Phe Cys Lys Val Thr
1 5 10
Leu Ile

<210> 428
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<400> 428
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
-15 -10 -5
Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
1 5 10
Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
15 20 25 30
Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
35 40 45
Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
50 55 60
Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
65 70 75
Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
80 85 90
Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg Xaa Glu Asn Xaa
95 100 105 110
Met Pro Gly Leu Ser Gly Val Leu
115

<210> 429
<211> 194
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -65...-1

<400> 429

Met	Gln	Asp	Ala	Pro	Leu	Ser	Cys	Leu	Ser	Pro	Thr	Lys	Trp	Ser	Ser
-65					-60					-55					-50
Val	Ser	Ser	Ala	Asp	Ser	Thr	Glu	Lys	Ser	Ala	Ser	Ala	Ala	Gly	Thr
				-45					-40					-35	
Arg	Asn	Leu	Pro	Phe	Gln	Phe	Cys	Leu	Arg	Gln	Ala	Leu	Arg	Met	Lys
			-30					-25					-20		
Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr	Gly	Val	Glu
		-15					-10					-5			
Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile	Phe	Ser	Arg	Ala
1				5						10				15	
Gly	Leu	Asp	Asn	Xaa	Arg	Gly	Phe	Ser	Leu	Gly	Asn	Trp	Ile	Cys	Met
			20						25					30	
Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr	Ala	Gln	Thr	Val	Leu	Asp
			35					40					45		
Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe	Gln	Ile	Asn	Ser	Phe	Ala	Trp
		50					55					60			
Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu	Asn	Asn	His	Cys	His	Val	Ala	Cys
	65					70				75					
Ser	Ala	Leu	Xaa	Thr	Asp	Asp	Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Xaa
80					85					90					95
Lys	Ile	Val	Lys	Glu	Thr	Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys
			100						105					110	
Lys	His	Cys	Glu	Gly	Arg	Asp	Leu	Ser	Xaa	Trp	Lys	Lys	Gly	Cys	Glu
			115					120					125		
Val	Ser														

<210> 430
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -69...-1

<400> 430

Met	Thr	Ser	Gln	Pro	Val	Pro	Asn	Glu	Thr	Ile	Ile	Val	Leu	Pro	Ser
				-65					-60					-55	
Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln
			-50					-45					-40		
Gly	Gln	Asp	Ser	Leu	Lys	Lys	His	Leu	His	Ala	Glu	Ile	Lys	Val	Ile
		-35					-30					-25			
Gly	Thr	Ile	Gln	Ile	Leu	Cys	Gly	Met	Met	Val	Leu	Ser	Leu	Gly	Ile
	-20					-15					-10				
Ile	Leu	Ala	Ser	Ala	Ser	Phe	Ser	Pro	Asn	Phe	Thr	Gln	Val	Thr	Ser
-5					1				5					10	
Thr	Leu	Leu	Asn	Ser	Ala	Tyr	Pro	Phe	Ile	Gly	Pro	Phe	Phe	Val	Xaa
			15				20						25		
Lys	Xaa	Ser	Glu	Glu	Gly	Arg	Met	Gly	Gln	Xaa	Gly	Glu	Glu	Xaa	Xaa
		30					35					40			
Asn	Ser	Leu	Asn	Phe	Pro	Xaa	Ala	Ser	Leu	Leu	Xaa	Leu	Ile	Cys	Gln
	45					50					55				
Xaa	Gln	Gly	Phe	Asn	Gly	Glu	Ser	Cys	Ser	Pro	Val	Gly			
60					65					70					

<210> 431
 <211> 248
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<400> 431
 Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
 -65 -60 -55
 Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
 -50 -45 -40
 Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Xaa Lys Val Ile
 -35 -30 -25
 Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
 -20 -15 -10
 Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
 15 20 25
 Ile Ser Gly Ser Leu Ser Ile Ala Thr Lys Lys Arg Leu Thr Asn Leu
 30 35 40
 Leu Val His Thr Thr Leu Val Gly Ser Ile Leu Ser Ala Leu Ser Ala
 45 50 55
 Leu Val Gly Phe Ile Xaa Leu Ser Val Lys Gln Ala Thr Leu Asn Pro
 60 65 70 75
 Ala Ser Leu Xaa Cys Glu Leu Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa
 80 85 90
 Tyr Val Xaa Tyr Phe Tyr His Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr
 95 100 105
 Thr Ala Lys Ala Xaa Leu Ala Gly Thr Leu Ser Leu Met Leu Ile Cys
 110 115 120
 Thr Leu Leu Glu Phe Cys Xaa Xaa Val Leu Thr Ala Val Leu Arg Trp
 125 130 135
 Lys Gln Ala Tyr Ser Asp Phe Pro Gly Ser Val Leu Phe Leu Pro Xaa
 140 145 150 155
 Ser Tyr Ile Gly Asn Ser Gly Met Ser Ser Lys Met Thr His Asp Cys
 160 165 170
 Gly Tyr Glu Glu Leu Leu Thr Ser
 175

<210> 432
 <211> 49
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 432
 Met Gln Val Pro His Leu Arg Val Trp Thr Gln Val Xaa Asp Thr Phe
 -35 -30 -25
 Ile Gly Tyr Arg Asn Leu Gly Phe Thr Ser Met Cys Ile Leu Phe His
 -20 -15 -10 -5
 Cys Leu Leu Ser Phe Gln Val Phe Lys Lys Lys Arg Lys Leu Xaa Leu
 1 5 10

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 435
Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
-15 -10 -5
Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
1 5 10 15
Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
20 25 30
Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser
35 40 45
Glu Ser Pro Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro
50 55 60
Val Pro Pro Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg
65 70 75 80
Ala Trp Gly Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala
85 90 95
Leu Gly Ser Gly Glu His Pro Xaa Xaa
100 105

<210> 436
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 436
Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
-15 -10 -5
Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
1 5 10 15
Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
20 25 30
Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys
35 40 45
Trp Ser Val Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro
50 55 60
Asn Asp Asn Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly
65 70 75 80
Val Ile Thr Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu
85 90 95
Thr Pro Gln Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln
100 105 110
Asp Pro Ser Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu
115 120 125
Pro Leu Cys Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln
130 135 140
Glu Gly
145

<210> 437
 <211> 110
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 437
 Met Xaa Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu Leu
 -20 -15 -10 -5
 Gly Xaa Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg Lys Ile
 1 5 10
 Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val Ala Asp Leu
 15 20 25
 Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp Asp Gly Lys Gly
 30 35 40
 Cys Glu Met Ile Cys Tyr Cys Asn Phe Lys Arg Ile Ala Leu Leu Pro
 45 50 55 60
 Lys Arg Arg Phe Leu Trp Thr Lys Asp Leu Phe Arg Asp Ser Leu Gln
 65 70 75
 Gln Ser Met Arg Ile Phe Met Tyr Ser Gly Glu His His Ser
 80 85 90

<210> 438
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 438
 Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val
 -15 -10 -5 1
 Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
 5 10 15
 Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys
 20 25 30
 Val Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile
 35 40 45
 Gln Val Pro Arg Arg Ala Gly
 50 55

<210> 439
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 439
 Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
 -20 -15 -10

Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
 -5 1 5
 Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
 10 15 20
 Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
 25 30 35 40
 Arg Cys Glu Thr Phe Val Phe Ser Ser Cys Asn Gly Asn Leu Asn Asn
 45 50 55
 Phe Lys Leu Lys Ile Glu Arg Glu Val Xaa Cys Val Ala Lys Tyr Lys
 60 65 70
 Pro Pro Arg
 75

<210> 440
 <211> 169
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 440
 Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
 -25 -20 -15 -10
 Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
 -5 1 5
 Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Gln Arg Phe Phe Ala
 10 15 20
 Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala
 25 30 35
 Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu
 40 45 50 55
 Asn His Gly Leu Val Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr
 60 65 70
 Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser
 75 80 85
 Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser
 90 95 100
 Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Xaa Ser Ala Glu Val
 105 110 115
 Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr Pro Leu His Ser Asp
 120 125 130 135
 Arg Thr Pro Asp Leu Pro Ala Leu Ala
 140

<210> 441
 <211> 167
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -76...-1

<400> 441
 Met Gly Asp Tyr Leu Leu Arg Gly Tyr Arg Met Leu Gly Glu Thr Cys
 -75 -65

Ala Asp Cys Gly Thr Ile Leu Leu Gln Asp Lys Gln Arg Lys Ile Tyr
 -60 -55 -50 -45
 Cys Val Ala Cys Gln Glu Leu Asp Ser Asp Val Asp Lys Asp Asn Pro
 -40 -35 -30
 Ala Leu Asn Ala Gln Ala Ala Leu Ser Gln Ala Arg Glu His Gln Leu
 -25 -20 -15
 Ala Ser Ala Ser Glu Leu Pro Leu Gly Ser Arg Pro Ala Pro Gln Pro
 -10 -5 1
 Pro Val Pro Arg Pro Glu His Cys Glu Gly Ala Ala Ala Gly Leu Lys
 5 10 15 20
 Ala Ala Gln Gly Pro Pro Ala Pro Ala Val Pro Pro Asn Thr Xaa Val
 25 30 35
 Met Ala Cys Thr Gln Thr Ala Leu Leu Gln Lys Leu Thr Trp Ala Ser
 40 45 50
 Ala Glu Leu Gly Ser Xaa Thr Ser Xaa Gly Lys Xaa Ala Ser Ser Cys
 55 60 65
 Val Ala Leu Ser Ala His Val Arg Arg Pro Cys Ala Ala Cys Ser Ser
 70 75 80
 Tyr Ser Thr Lys Arg Ser Pro
 85 90

<210> 442
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 442
 Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
 -15 -10 -5 1
 Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
 5 10 15
 Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Xaa Arg Thr Lys Tyr Glu
 20 25 30
 Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly Gly Asn Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Leu Ser Lys Arg Asp
 50 55

<210> 443
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 443
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15

Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys Gly Glu Thr Met
 65 70 75
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys
 80 85 90 95
 Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr
 100 105 110
 Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu Asn Leu Xaa Gln
 115 120 125
 Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr
 130 135 140
 Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu
 145 150 155
 Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile
 160 165 170 175
 Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg Phe Leu Ile Gly
 180 185 190
 Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly
 195 200 205
 Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala
 210 215 220
 Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp
 225 230 235
 Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr
 240 245 250 255
 Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser
 260 265 270
 Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His
 275 280 285
 Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile Xaa Glu Glu Val
 290 295 300
 Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu
 305 310 315
 Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser
 320 325 330 335
 Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu
 340 345

<210> 444

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 444

Met Tyr Tyr Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His
 -10 -5 1
 Leu Pro Ile Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr
 5 10 15
 Val Tyr Pro Thr Ser Ala Gly
 20 25

<210> 445
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 445
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 -35 -30 -25
 Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
 -20 -15 -10
 Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met Pro
 -5 1 5 10
 Asp Asn

<210> 446
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 446
 Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg Pro Leu Ala Ser
 -25 -20 -15
 Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser Gly Ser His Trp
 -10 -5 1 5
 Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser Leu Ser Ala Thr
 10 15 20
 Thr Arg Gly
 25

<210> 447
 <211> 242
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 447
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 -30 -25 -20 -15
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
 -10 -5 1
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 5 10 15
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 20 25 30
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly

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35          40          45          50
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
                    55          60          65
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
                    70          75          80
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
                    85          90          95
Pro Xaa Glu Gly Xaa Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
                    100          105          110
Glu Lys Glu Ala Leu Val Pro Xaa Gln Lys Ala Thr Asp Ser Phe His
115          120          125          130
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
                    135          140          145
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Xaa Glu
                    150          155          160
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
                    165          170          175
His Lys Asp Xaa Leu Xaa Xaa Gly Thr Glu Ser Ser Ser His Ser Arg
180          185          190
Leu Ser Pro Arg Lys Xaa His Leu Leu Tyr Ile Leu Xaa Pro Ser Arg
195          200          205          210
Gln Leu

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<210> 448

<211> 154

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -60...-1

<400> 448

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Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
-60          -55          -50          -45
Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
                    -40          -35          -30
Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
                    -25          -20          -15
Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
                    -10          -5          1
Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
5          10          15          20
Ala Leu Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu
                    25          30          35
Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met
                    40          45          50
Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe
                    55          60          65
Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln
70          75          80
Pro Glu Phe His Ile Glu Ile Leu Ser Ile
85          90

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<210> 449

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -61...-1

<400> 449

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Met Asn Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr
  -60                      -55                      -50
Glu Thr Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro
  -45                      -40                      -35                      -30
Glu Ala Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala
                      -25                      -20                      -15
Leu Leu Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg
                      -10                      -5                      1
Pro Asp Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro
  5                      10                      15
His Pro Cys Ala Thr Tyr Pro Pro Xaa
20                      25

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<210> 450

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 450

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Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr
  -25                      -20                      -15
Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro
  -10                      -5                      1                      5
Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile
                      10                      15                      20
Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly
                      25                      30                      35
Phe Asp Leu Asp Met Asp His Thr Ile
40                      45

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<210> 451

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34...-1

<400> 451

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Met Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser
                      -30                      -25                      -20
Trp Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser
                      -15                      -10                      -5
Ser Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys
                      1                      5                      10
Ala Ile Ile Leu Met Lys
15                      20

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<210> 452
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 452
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
 -35 -30 -25
 Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
 -20 -15 -10
 Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
 -5 1 5 10
 Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala Val Leu Trp
 15 20 25
 Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn Gln Trp Gln
 30 35 40
 His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser Ala Gln Ala
 45 50 55
 Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp Ile Pro Xaa
 60 65 70
 Leu Pro Gly Xaa Pro Gly Pro Pro Lys
 75 80

<210> 453
 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 453
 Met Ser Thr Val Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile
 -35 -30 -25
 Cys Pro Ala Pro Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu
 -20 -15 -10
 Ser Pro Gly Ile Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp
 -5 1 5 10
 Tyr Pro Ala Leu Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe
 15 20 25
 Val Lys Gly His Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn
 30 35 40
 Cys Val Val Leu Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His
 45 50 55
 Gln Thr Arg Ser Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu
 60 65 70 75
 Gln Glu Lys Val Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His
 80 85 90
 Lys Glu Lys Arg Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg
 95 100 105
 Ala Lys Glu Thr Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu
 110 115 120

Ser Ser Lys Lys Val His
125

<210> 454
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26...-1

<400> 454
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
40 45 50
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
55 60 65 70
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
75 80 85
Val Xaa Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
90 95 100
Gly Lys Met Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val
105 110 115
Glu Phe Xaa Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
120 125 130
Phe Asn Ile Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg
135 140 145 150
Arg Asn Trp Glu

<210> 455
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -64...-1

<400> 455
Met Thr Pro Arg Ile Leu Ser Glu Val Gln Phe Ser Ala Phe Cys Pro
-60 -55 -50
Tyr Trp Thr Ile Ala Arg Ile Leu Glu Arg Val Gly Ser Ala Cys Phe
-45 -40 -35
Arg Leu Glu Leu Cys Ala Ala Ile Val Gly Tyr Phe Val Leu Asp Val
-30 -25 -20
Arg Thr Phe Leu Phe Ile Val Val Cys Val Ile Cys Val Thr Leu Asn
-15 -10 -5
Phe Pro Arg Phe Tyr Phe Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly
1 5 10 15
Thr Pro Pro Ile Gly Val His Ile Pro Ser Pro

20

25

<210> 456
 <211> 257
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 456
 Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
 -20 -15 -10
 Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
 -5 1 5
 Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
 10 15 20 25
 Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
 30 35 40
 Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
 45 50 55
 Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
 60 65 70
 Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
 75 80 85
 Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg
 90 95 100 105
 Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly
 110 115 120
 Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
 125 130 135
 Asn His Glu Ala Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa
 140 145 150
 Leu Glu Xaa Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
 155 160 165
 Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val
 170 175 180 185
 Ser Pro Xaa Asn Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro
 190 195 200
 Xaa Xaa Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly
 205 210 215
 Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa
 220 225 230
 Xaa

<210> 457
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60...-1

<400> 457
 Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
 -60 -55 -50 -45

<400> 459

```

Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
      -10                      -5                      1
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
      5                      10                      15
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
20      25                      30                      35
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr
      40                      45                      50
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg
      55                      60                      65
Met Xaa Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
      70                      75                      80
Thr Glu Phe Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
      85                      90                      95
Phe Leu Ile Pro Asn Leu Ala Leu Asn
100                      105

```

<210> 460

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 460

```

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
      -15                      -10                      -5
Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
      1                      5                      10                      15
Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Ile
      20                      25

```

<210> 461

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 461

```

Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys
      -10                      -5                      1
Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro
      5                      10                      15
Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro
20      25                      30                      35
Thr Val Tyr Ser Ser Ala Pro Phe His Ala Pro Leu Pro Val Gln Asn
      40                      45                      50
Ser Leu Trp Gly His Pro Leu His Gly Cys Ser Trp Gln Cys His His
      55                      60                      65
Pro Gln Gly Gln Asn Leu Gln Pro Ala Ser Leu Xaa Thr His Leu Ser
      70                      75                      80
Lys Pro Lys Arg His Phe Xaa Lys Lys Xaa Cys Gln Ala

```

85

90

95

<210> 462
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 462
 Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala
 -40 -35 -30
 Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile
 -25 -20 -15 -10
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu
 -5 1 5
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp
 10 15 20
 Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu
 25 30 35
 Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His Lys Thr Val Val Asn
 40 45 50 55
 Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu
 60 65 70
 Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr
 75 80 85
 Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr Gly Thr Phe Glu
 90 95 100

<210> 463
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 463
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Xaa
 -10 -5 1
 Xaa Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Xaa Pro Glu Xaa Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Pro Pro Gly Tyr Asn Ser Leu Pro Leu Lys Leu Leu Gly
 70 75 80
 Thr Gly Lys Ala Ile Thr Lys Leu Phe Ile Ser Val Phe Arg Thr Lys
 85 90 95
 Lys Glu Arg Lys Glu Ser Thr Met Glu Glu Lys Lys Glu Leu Thr Val

100 105 110
 Glu Lys Lys Arg Thr Pro Arg Met Glu Glu Arg Lys Glu Leu Ile Val
 115 120 125 130
 Glu Lys Lys Lys Arg Lys Glu Ser Thr Glu Lys Thr Lys Leu Thr Lys
 135 140 145
 Glu Glu Lys Lys Gly Lys Lys Leu Thr Lys Lys Ser Thr Lys Val Val
 150 155 160
 Lys Lys Leu Cys Lys Val Tyr Arg Glu Gln His Ser Arg Ser Tyr Asp
 165 170 175
 Ser Ile Glu Thr Thr Ser Thr Thr Val Leu Leu Ala Gln Thr Pro Leu
 180 185 190
 Val Lys Cys Lys Phe Leu Tyr Asn
 195 200

<210> 464
 <211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 464
 Met Thr Phe Arg His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met
 -20 -15 -10
 Ala Thr Cys Thr Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys
 -5 1 5 10
 Ser Leu Thr Ser Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu
 15 20 25
 Ile Lys Phe Gly Tyr Asp Arg Lys Ser Thr Ile Lys Ser
 30 35 40

<210> 465
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 465
 Met Phe Leu Lys Ser Gly Ala Gly Leu Ser Ser Cys Leu Leu Pro Leu
 -15 -10 -5
 Cys Trp Leu Glu Arg Lys Asp His Gly Arg Arg Pro Ser Xaa His Pro
 1 5 10
 Gly Arg
 15

<210> 466
 <211> 215
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -54...-1

<400> 466

```

Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
      -50      -45      -40
Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
      -35      -30      -25
Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
      -20      -15      -10
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
      -5      1      5      10
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
      15      20      25
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
      30      35      40
Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
      45      50      55
Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
      60      65      70
Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
      75      80      85      90
Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
      95      100      105
Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
      110      115      120
Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
      125      130      135
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
      140      145      150
Ile Ile Arg Lys Cys Phe Ile
155      160

```

<210> 467

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 467

```

Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr Ser Lys Arg
      -15      -10      -5
Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
      1      5      10

```

<210> 468

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 468

Met Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu
 -20 -15 -10
 Phe Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys
 -5 1 5
 Phe Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser
 10 15 20
 Leu Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe
 25 30 35 40
 Pro Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa
 45 50 55
 Tyr Trp Asp Asn Leu
 60

<210> 469
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 469
 Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 470
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 470
 Met Thr Pro Gln Tyr Leu Pro His Gly Gly Lys Tyr Gln Val Leu Gly
 -40 -35 -30
 Asp Tyr Ser Leu Ala Val Val Phe Pro Leu His Phe Ser Asp Leu Ile
 -25 -20 -15
 Ser Val Leu Tyr Leu Ile Pro Lys Thr Leu Thr Thr Asn Thr Ala Val
 -10 -5 1 5
 Lys His Ser Ile Gln Lys Asn Cys Met Xaa Leu Val Leu Gly Lys Leu
 10 15 20
 Leu Ser Gln

<210> 471
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 471
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
 -15 -10 -5 1
 Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
 5 10 15
 Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
 20 25 30
 Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr Ser Ser Ala
 35 40 45

<210> 472
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -58...-1

<400> 472
 Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
 -55 -50 -45
 Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
 -40 -35 -30
 Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
 -25 -20 -15
 Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
 -10 -5 1 5
 Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
 10 15 20
 Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile
 25 30 35
 Tyr Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa
 40 45 50
 Xaa Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser
 55 60 65 70
 His Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro
 75 80 85
 Thr Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys
 90 95 100
 Xaa Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly
 105 110 115
 Gln Val Asn
 120

<210> 473
 <211> 238
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -71...-1

<400> 473

```

Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
  -70                      -65                      -60
Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55                      -50                      -45                      -40
Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
                      -35                      -30                      -25
Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu Leu
                      -20                      -15                      -10
Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His Gln
                      -5                      1                      5
Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr Trp
10                      15                      20                      25
Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu His
                      30                      35                      40
Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu Ala
                      45                      50                      55
Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro Asp
                      60                      65                      70
Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser Leu
                      75                      80                      85
Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly Ile
90                      95                      100                      105
Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala Ala
                      110                      115                      120
Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe Glu
                      125                      130                      135
Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr Val Gly Ile
                      140                      145                      150
Glu Asn Arg Thr Leu Tyr Phe Phe Leu Lys Arg Leu Leu Arg
155                      160                      165

```

<210> 474

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 474

```

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
  -35                      -30                      -25
Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
  -20                      -15                      -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
  -5                      1                      5                      10
Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Xaa Met Gly Leu
                      15                      20                      25
Ile Leu Xaa Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Xaa Val
                      30                      35                      40
Tyr Asp Cys Val Lys Leu Thr Phe Ser Pro Ser Thr Leu Leu Val Asn
                      45                      50                      55
Ile Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
60                      65                      70                      75
His Xaa Ile Asn Pro His Xaa Gly Asn Ala Ile Leu Glu Lys Met Thr
                      80                      85                      90
Phe Asp Pro Xaa Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe

```


	95		100		105										
His	Ala	Gly	Tyr	Ser	Leu	Lys	Lys	Arg	His	Phe	Phe	Gln	Asn	Leu	Gly
	110					115						120			
Ser	Ile	Leu	Thr	Tyr	Ala	Phe	Leu	Gly	Thr	Ala	Ile	Ser	Cys	Ile	Val
	125					130						135			
Ile	Gly														
140															

<210> 475
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400>	475														
Met	Ser	Met	Gln	Phe	Leu	Phe	Lys	Met	Val	Ala	Leu	Cys	Cys	Cys	Leu
	-20					-15					-10				
Trp	Lys	Ile	Ser	Gly	Cys	Glu	Glu	Val	Pro	Leu	Thr	Tyr	Asn	Leu	Leu
	-5			1				5					10		
Lys	Cys	Leu	Leu	Asp	Lys	Ala	His	Cys	Val	Leu	Leu	Thr	Pro	Cys	Gly
		15					20					25			
Tyr	Ile	Phe	Ser	Leu	Ile	Ser	Pro	Glu	Ile	Leu	Lys	Leu	Thr	Leu	Ile
	30					35					40				
Thr	Leu	Xaa	Ile	Leu	Leu	Ile	Leu	Lys	Asn	Leu	His	Leu	Leu	Trp	Leu
	45					50			55						
Thr	Val	Ser	Ser	Xaa	Cys	Val	His	Arg	Ser	Ser	Ala	Arg	Lys	Glu	Lys
60					65				70					75	

<210> 476
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400>	476														
Met	His	Thr	Phe	Ala	Asn	Asp	Arg	Gly	Leu	Tyr	Arg	Ile	Leu	Leu	Leu
				-20				-15					-10		
His	Phe	Tyr	Cys	Leu	Leu	Arg	Ser	Ser	Glu	Tyr	Ile	Leu	Gly	Tyr	Lys
			-5				1				5				
Val	Leu	Gly	Val	Phe	Phe	Pro	Ile	Leu							
	10					15									

<210> 477
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 477

```

Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
    -25                -20                -15
Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His
    -10                -5                1                5
Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
                10                15                20
Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
                25                30                35
Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys
                40                45                50
Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys
                55                60                65
Pro Arg Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr
                70                75                80                85
Ser

```

<210> 478

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18...-1

<400> 478

```

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
    -15                -10                -5
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
    1                5                10
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
    15                20                25                30
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
    35                40                45
Lys Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu
    50                55                60
Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
    65                70                75
Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met
    80                85                90
Leu Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
    95                100                105                110
Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
    115                120                125
Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
    130                135                140
Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
    145                150                155
Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
    160                165                170
Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
    175                180                185                190
Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
    195                200                205
Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
    210                215                220
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
    225                230

```

<210> 479
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 479
 Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
 -20 -15 -10
 Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
 -5 1 5 10
 Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
 15 20 25
 Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
 30 35 40
 Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
 45 50 55
 Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
 60 65 70 75
 Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
 80 85 90
 Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile
 95 100 105
 Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn
 110 115 120
 Gly Lys Val Lys Ser Phe Lys
 125 130

<210> 480
 <211> 239
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 480
 Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
 -25 -20 -15 -10
 Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
 -5 1 5
 Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
 10 15 20
 Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
 25 30 35
 Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
 40 45 50 55
 Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
 60 65 70
 Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala
 75 80 85
 Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa
 90 95 100

```

Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala
 105                      110                      115
Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe
120                      125                      130                      135
Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa
                      140                      145                      150
Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys
                      155                      160                      165
Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn
                      170                      175                      180
Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln
                      185                      190                      195
Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
200                      205                      210

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<210> 481
<211> 208
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -92...-1

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```

<400> 481
Met Arg Glu Pro Gln Lys Arg Thr Ala Thr Ile Ala Lys Xaa Xaa Ala
      -90                      -85                      -80
Xaa Glu Gly Leu Arg Asp Pro Tyr Gly Arg Leu Cys Gly Ser Glu His
      -75                      -70                      -65
Pro Arg Arg Pro Pro Glu Arg Pro Glu Glu Asp Pro Ser Thr Pro Glu
-60                      -55                      -50                      -45
Glu Ala Ser Thr Thr Pro Glu Glu Ala Ser Ser Thr Ala Gln Ala Gln
      -40                      -35                      -30
Lys Pro Ser Val Pro Arg Ser Asn Phe Gln Gly Thr Lys Lys Ser Leu
      -25                      -20                      -15
Leu Met Ser Ile Leu Ala Leu Ile Phe Ile Met Gly Asn Ser Ala Lys
      -10                      -5                      1
Glu Ala Leu Val Trp Lys Val Leu Gly Lys Leu Gly Met Gln Pro Gly
5                      10                      15                      20
Arg Xaa His Ser Ile Phe Gly Asp Pro Lys Lys Ile Val Thr Glu Xaa
      25                      30                      35
Phe Val Arg Arg Gly Tyr Leu Ile Tyr Xaa Pro Val Pro Arg Xaa Ser
      40                      45                      50
Pro Val Glu Tyr Xaa Phe Phe Trp Gly Pro Arg Ala His Val Glu Ser
      55                      60                      65
Ser Xaa Leu Lys Xaa Xaa His Phe Val Ala Arg Val Arg Asn Arg Cys
      70                      75                      80
Ser Lys Asp Trp Pro Cys Asn Tyr Asp Trp Asp Ser Asp Asp Ala
85                      90                      95                      100
Glu Val Glu Ala Ile Leu Asn Ser Gly Ala Xaa Gly Tyr Ser Ala Pro
      105                      110                      115

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<210> 482
<211> 86
<212> PRT
<213> Homo sapiens

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<220>

```

<221> SIGNAL
<222> -39...-1

<400> 482

Met	Asn	Val	Gly	Thr	Ala	His	Xaa	Xaa	Val	Asn	Pro	Asn	Thr	Arg	Val
				-35					-30					-25	
Met	Asn	Ser	Arg	Gly	Ile	Trp	Leu	Ser	Tyr	Val	Leu	Ala	Ile	Gly	Leu
			-20					-15					-10		
Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val
		-5					1				5				
Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu
10					15					20					25
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala
				30					35					40	
Arg	Leu	Leu	Thr	His	Trp										
				45											

<210> 483
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27...-1

<400> 483

Met	Arg	Thr	Leu	Phe	Gly	Ala	Val	Arg	Ala	Pro	Phe	Ser	Ser	Leu	Thr
		-25					-20				-15				
Leu	Leu	Leu	Ile	Thr	Pro	Ser	Pro	Ser	Pro	Leu	Leu	Phe	Asp	Arg	Gly
		-10				-5					1				5
Leu	Ser	Leu	Arg	Ser	Ala	Met	Ser								
				10											

<210> 484
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 484

Met	Leu	Gly	Phe	Phe	Leu	Phe	Leu	Ser	Phe	Val	Leu	Met	Tyr	Asp	Gly
	-15					-10					-5				
Leu	Arg	Leu	Phe	Gly	Ile	Leu	Ser	Thr	Cys	Arg	Val	His	His	Thr	Met
1			5					10					15		
Asn	Gln	Phe	Leu	Ile	Asp	Ile	Ser	Ser	Phe	Thr	Ser	Arg	Val	Lys	Lys
		20					25					30			
Lys	Ile	Phe	Leu	Phe	Tyr	Ala	Phe	Xaa	Gly	Cys	Xaa	Phe	Gln	Ser	Ala
		35					40					45			
Thr															

<210> 485
<211> 130

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -55...-1

<400> 485

Met	Ala	Met	Trp	Asn	Arg	Pro	Xaa	Xaa	Xaa	Leu	Pro	Gln	Gln	Pro	Leu
-55				-50						-45					-40
Xaa	Ala	Glu	Pro	Thr	Ala	Glu	Gly	Glu	Pro	His	Leu	Pro	Thr	Gly	Arg
				-35					-30					-25	
Xaa	Xaa	Thr	Glu	Ala	Asn	Arg	Phe	Ala	Tyr	Ala	Ala	Leu	Cys	Gly	Ile
		-20					-15					-10			
Ser	Leu	Ser	Gln	Leu	Phe	Pro	Glu	Pro	Glu	His	Ser	Ser	Phe	Cys	Thr
	-5					1				5					
Glu	Phe	Met	Ala	Gly	Leu	Val	Xaa	Trp	Leu	Glu	Leu	Ser	Glu	Ala	Val
10				15					20						25
Leu	Pro	Thr	Met	Thr	Ala	Phe	Ala	Ser	Gly	Leu	Gly	Gly	Glu	Gly	Xaa
				30					35					40	
Xaa	Cys	Val	Cys	Ser	Asn	Phe	Thr	Glu	Gly	Pro	His	Leu	Glu	Gly	Arg
		45						50				55			
Pro	Asp	Gly	Asp	His	Ser	Gly	Pro	Ser	Glu	Leu	Leu	Thr	Gln	Gly	Trp
	60						65					70			
Ala	Leu														
	75														

<210> 486
<211> 209
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -84...-1

<400> 486

Met	Val	Asn	Phe	Pro	Gln	Lys	Ile	Ala	Gly	Glu	Leu	Tyr	Gly	Pro	Leu
			-80					-75						-70	
Met	Leu	Val	Phe	Thr	Leu	Val	Ala	Ile	Leu	Leu	His	Gly	Met	Lys	Thr
		-65					-60					-55			
Ser	Asp	Thr	Ile	Ile	Arg	Glu	Gly	Thr	Leu	Met	Gly	Thr	Ala	Ile	Gly
	-50					-45						-40			
Thr	Cys	Phe	Gly	Tyr	Trp	Leu	Gly	Val	Ser	Ser	Phe	Ile	Tyr	Phe	Leu
	-35				-30						-25				
Ala	Tyr	Leu	Cys	Asn	Ala	Gln	Ile	Thr	Met	Leu	Gln	Met	Leu	Ala	Leu
-20				-15					-10						-5
Leu	Gly	Tyr	Gly	Leu	Phe	Gly	His	Cys	Ile	Val	Leu	Phe	Ile	Thr	Tyr
			1				5					10			
Asn	Ile	His	Leu	Arg	Ala	Leu	Phe	Tyr	Leu	Phe	Trp	Leu	Leu	Val	Gly
	15					20					25				
Gly	Leu	Ser	Thr	Leu	Arg	Met	Val	Ala	Val	Leu	Val	Ser	Arg	Thr	Val
	30				35					40					
Gly	Pro	Thr	Xaa	Arg	Xaa	Leu	Leu	Cys	Gly	Thr	Leu	Ala	Ala	Leu	His
45				50					55						60
Met	Leu	Phe	Leu	Leu	Tyr	Leu	His	Phe	Ala	Tyr	His	Lys	Xaa	Val	Xaa
		65						70					75		
Gly	Ile	Leu	Asp	Thr	Leu	Glu	Gly	Pro	Asn	Ile	Pro	Pro	Ile	Gln	Arg
		80					85				90				
Val	Pro	Arg	Asp	Ile	Pro	Ala	Met	Leu	Pro	Ala	Ala	Arg	Leu	Pro	Thr

95 100 105
 Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser
 110 115 120
 His
 125

<210> 487
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 487
 Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
 -15 -10 -5
 Ala His Pro Pro Gln Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp
 1 5 10 15
 Val Gly Ile Cys

<210> 488
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 488
 Met Met Ser Ser Glu Leu Arg Arg Asn Pro His Phe Leu Lys Ser Asn
 -25 -20 -15
 Leu Phe Leu Gln Leu Leu Val Ser His Glu Ile Val Cys Ala Thr Glu
 -10 -5 1
 Thr Val Thr Thr Asn Phe Leu Arg His Glu Lys Ala
 5 10 15

<210> 489
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -52...-1

<400> 489
 Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
 -50 -45 -40
 Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
 -35 -30 -25
 Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
 -20 -15 -10 -5
 Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala

```

      1           5           10
Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
      15           20           25
Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp Ser Trp
      30           35           40
Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val Arg Arg
      45           50           55           60
His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu Asp Pro
      65           70           75
Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
      80           85           90
Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala Xaa Xaa
      95           100           105
Thr Arg Ser
      110

```

<210> 490
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

```

<400> 490
Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
      -45           -40           -35
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
      -30           -25           -20
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
      -15           -10           -5           1
Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys Gly Xaa Asn Thr
      5           10           15

```

<210> 491
 <211> 218
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -50...-1

```

<400> 491
Met His His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
      -50           -45           -40           -35
Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
      -30           -25           -20
Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
      -15           -10           -5
Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
      1           5           10
Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys Tyr Ala Val Ser Ser
      15           20           25           30
Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Xaa Lys Gln
      35           40           45
Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro Xaa Gln Asp Leu Lys

```


BNSDOCID: <WO 9931236A2 I >

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 493

```

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly
      -15                      -10                      -5
Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr
      1                      5                      10
Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu Ala
      15                      20                      25
Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile
      30                      35                      40                      45
Asp Arg Glu Asn Phe Val Asp Ile Val Xaa Ala Lys Leu Lys Ile Pro
      50                      55                      60
Val Ser Gly Ser Lys Ser Glu Gly Leu Tyr Val His Ser Ser Arg
      65                      70                      75
Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu
      80                      85                      90
Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly
      95                      100                      105
Asp Glu Val Lys Lys Glu
110                      115

```

<210> 494

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 494

```

Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp Gly
      -15                      -10                      -5
Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu Asn
      1                      5                      10                      15
Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe Gly
      20                      25                      30
Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser Thr
      35                      40                      45
Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val His
      50                      55                      60
His Arg Glu Gly Asp
65

```

<210> 495

<211> 292

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29...-1

<400> 495

```

Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe
      -25                      -20                      -15
Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr
      -10                      -5                      1
Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr
      5                      10                      15
Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr
      20                      25                      30                      35
Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu
      40                      45                      50
Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe Pro Lys Asn
      55                      60                      65
Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Xaa His
      70                      75                      80
Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His His Cys Val
      85                      90                      95
Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa Phe Leu Ile
      100                      105                      110                      115
Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser
      120                      125                      130
Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu
      135                      140                      145
Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp Thr Val Phe
      150                      155                      160
Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu
      165                      170                      175
Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr Leu Leu Phe
      180                      185                      190                      195
Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg
      200                      205                      210
Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro
      215                      220                      225
Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His Gly Leu Arg
      230                      235                      240
Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg
      245                      250                      255
Lys Lys Gln Glu
260

```

<210> 496

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -56...-1

<400> 496

```

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
      -55                      -50                      -45
Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Asn Pro Ser
      -40                      -35                      -30                      -25
Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
      -20                      -15                      -10
Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu Thr Gly
      -5                      1                      5
Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala Gly Pro
      10                      15                      20

```

Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly Pro Leu
 25 30 35 40
 Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser Cys Gly
 45 50 55
 Ala His Pro Lys Val Leu Lys Val Ala Leu
 60 65

<210> 497
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 497
 Met Leu Xaa Leu Ser Arg Ala Thr Lys Xaa Gly Arg Ala Arg Trp Leu
 -25 -20 -15
 Met Pro Val Ile Pro Ala Leu Gln Glu Ala Xaa Ala Gly Gly Ser Arg
 -10 -5 1
 Gly Gln Glu Phe Glu Thr Ser Leu Ala Asn Met Glu Thr Glu Ala Gly
 5 10 15 20
 Glu Leu Leu Lys Pro Arg Arg Arg Arg Leu Gln
 25 30

<210> 498
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 498
 Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
 Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
 5 10 15
 Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
 20 25 30 35
 Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
 Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
 Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu Leu Gly
 70 75 80
 Arg Gln Leu
 85

<210> 499
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 499

```

Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
      -10      -5      1
Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
      5      10      15
Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
20      25      30      35
Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
      40      45      50
Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
      55      60      65
Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu Leu Gly
      70      75      80
Arg Gln Leu
      85

```

<210> 500

<211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 500

```

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
-25      -20      -15      -10
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
      -5      1      5
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
      10      15      20
Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
      25      30      35
Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
40      45      50      55
Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
      60      65      70
Asn Val Gly Pro Leu Ile Ile Lys Lys Glu Thr
      75      80

```

<210> 501

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 501

```

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15      -10      -5      1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu

```

```

      5              10              15
Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
      20              25              30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
      35              40              45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Gly Asn
      50              55              60              65
Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu Leu Leu Gln Ser Cys
      70              75              80
Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met Ile Ile Asp Asn Arg
      85              90              95
Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp Thr Xaa His Val Ala
      100             105             110
Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly Ile Asn Leu Val Val
      115             120             125
Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser Asn His Ile Ala Leu
      130             135             140             145
Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile Cys Lys Pro Cys Gly
      150             155             160
Thr Gly Gln Asp Phe Lys Glu
      165

```

<210> 502
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

```

<400> 502
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15              -10              -5              1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
      5              10              15
Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
      20              25              30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
      35              40              45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Val Phe
      50              55              60              65
Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu Thr Ser Glu Pro Leu
      70              75              80
Xaa Ala

```

<210> 503
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -57...-1

```

<400> 503
Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile Asn
      -55              -50              -45

```

```

Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr Gly
-40 -35 -30
Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp Leu
-25 -20 -15 -10
Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys Asn
-5 1 5
Thr Lys Gly Asn Thr Leu Lys Glu Glu Trp Ile Ala Tyr Ile Cys Xaa
10 15 20
Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile His
25 30 35
Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu Val
40 45 50 55
Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val Gly
60 65 70
Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa Val
75 80 85
Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa Asp
90 95 100
Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu Pro
105 110 115
Leu Ser Val Thr Cys Thr Pro
120 125

```

<210> 504
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

```

<400> 504
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
-10 -5 1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
5 10 15
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
20 25 30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
35 40 45 50
Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Thr Ser
55 60 65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
70 75 80
Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu
85 90 95
Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys
100 105 110
Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr
115 120 125

```

<210> 505
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -14...-1

<400> 505

Met	Ala	Ala	Leu	Val	Thr	Val	Leu	Phe	Thr	Gly	Val	Arg	Arg	Leu	His
				-10					-5					1	
Cys	Ser	Ala	Xaa	Leu	Gly	Arg	Ala	Ala	Ser	Gly	Xaa	Tyr	Ser	Arg	Asn
	5						10					15			
Trp	Leu	Pro	Thr	Pro	Pro	Ala	Thr	Gly	Pro	Leu	Pro	Ser	Ser	Gln	Thr
	20					25					30				
Gly	His	Met	Arg	Met	Ala	Ala	Leu	Leu	Pro	Gln					
35					40					45					

<210> 506

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36...-1

<400> 506

Met	Gly	Pro	Tyr	Asn	Val	Ala	Val	Pro	Ser	Asp	Val	Ser	His	Ala	Arg
	-35					-30					-25				
Phe	Tyr	Phe	Leu	Phe	His	Arg	Pro	Leu	Arg	Leu	Leu	Asn	Leu	Leu	Ile
-20					-15					-10					-5
Leu	Ile	Glu	Gly	Ser	Val	Val	Phe	Tyr	Gln	Leu	Tyr	Ser	Leu	Leu	Arg
				1				5				10			
Ser	Glu	Lys	Trp	Asn	His	Thr	Leu	Ser	Met	Ala	Leu	Ile	Leu	Phe	Cys
	15					20					25				
Asn	Tyr	Tyr	Val	Leu	Phe	Lys	Leu	Leu	Arg	Asp	Arg	Xaa	Xaa	Leu	Gly
30						35				40					
Arg	Ala	Tyr	Ser	Tyr	Pro	Leu	Asn	Ser	Tyr	Glu	Leu	Lys	Ala	Asn	Xaa
45					50					55					60
Ala	Ala	Ser	Xaa	Gln											
				65											

<210> 507

<211> 341

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -55...-1

<400> 507

Met	Arg	Lys	Val	Val	Leu	Ile	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Leu
-55					-50					-45					-40
Ala	Leu	Cys	Lys	Arg	Leu	Leu	Ala	Glu	Asp	Asp	Glu	Leu	His	Leu	Cys
				-35					-30					-25	
Leu	Ala	Cys	Arg	Asn	Met	Ser	Lys	Ala	Glu	Ala	Val	Cys	Ala	Ala	Leu
			-20					-15					-10		
Leu	Ala	Ser	His	Pro	Thr	Ala	Glu	Val	Thr	Ile	Val	Gln	Val	Asp	Val
		-5				1					5				
Ser	Asn	Leu	Gln	Ser	Phe	Phe	Arg	Ala	Ser	Lys	Glu	Leu	Lys	Gln	Arg
10					15					20					25

Phe Gln Arg Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met Pro Asn
 30 35 40
 Pro Gln Leu Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser Arg Lys
 45 50 55
 Val Ile His Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln Gly Asp
 60 65 70
 Lys Ile Thr Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn Val Phe
 75 80 85
 Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys His Ser
 90 95 100 105
 Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala Arg Lys
 110 115 120
 Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys Glu Pro
 125 130 135
 Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala Leu Asn
 140 145 150
 Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys Pro Gly
 155 160 165
 Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe Ile Trp
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 Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala Asn Ala
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 Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp Leu Phe
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 His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu Ser Ala
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 Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met Asp Leu
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 Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu Leu Glu
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 Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala Arg Leu
 270 275 280
 Ser Gly Ser Cys Leu
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<211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 508

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 -10 -5 1 5
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 10 15 20
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 <213> Homo sapiens

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 Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn Ala Gln Val
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 Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr Gly Ala Arg
 40 45 50
 Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser Leu Ile Ala
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 Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn Thr Asp Val
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Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
      25                      30                      35
Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
      40                      45                      50
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
      55                      60                      65
Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
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<400> 512

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Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val
-30                      -25                      -20                      -15
Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
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Val Gln Ser Asn Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys
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Cys Val Arg Leu Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val
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Met Pro Thr Trp Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg
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115                      120                      125                      130
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 Gly Asp Asn Pro Lys Leu Leu Leu Lys Asp Met Lys Thr Lys Tyr Phe
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 Thr Leu Ser Trp Asn Val Val Pro Asn Ala Gly Ile Leu Pro Leu Val
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 Thr Lys Ser Tyr
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 <212> PRT
 <213> Bos taurus

<400> 514
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 Arg Arg Arg Pro Val Leu Leu Ala Gly Leu His Arg Gln Leu Leu Tyr
 50 55 60
 Ile Thr Ser Phe Val Phe Val Gly Tyr Tyr Leu Leu Lys Arg Gln Asp
 65 70 75 80
 Tyr Met Tyr Ala Val Arg Asp His Asp Met Phe Ser Tyr Ile Lys Ser
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 <213> Homo sapiens

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 35 40 45

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 Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro
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<213> Mus musculus

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(21) International Application Number: PCT/IB98/02122 (22) International Filing Date: 17 December 1998 (17.12.98) (30) Priority Data: <table border="0" style="width: 100%;"><tr><td style="width: 30%;">60/069,957</td><td style="width: 40%;">17 December 1997 (17.12.97)</td><td style="width: 30%;">US</td></tr><tr><td>60/074,121</td><td>9 February 1998 (09.02.98)</td><td>US</td></tr><tr><td>60/081,563</td><td>13 April 1998 (13.04.98)</td><td>US</td></tr><tr><td>60/096,116</td><td>10 August 1998 (10.08.98)</td><td>US</td></tr></table> (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): BOUGUELERET, Lydie [FR/FR]; 108, avenue Victor Hugo, F-92170 Vanves (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire de Tours, F-75006 Paris (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		60/069,957	17 December 1997 (17.12.97)	US	60/074,121	9 February 1998 (09.02.98)	US	60/081,563	13 April 1998 (13.04.98)	US	60/096,116	10 August 1998 (10.08.98)	US	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 10 September 1999 (10.09.99)
60/069,957	17 December 1997 (17.12.97)	US												
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60/096,116	10 August 1998 (10.08.98)	US												
(54) Title: EXTENDED cDNAs FOR SECRETED PROTEINS (57) Abstract <p>The sequences of extended cDNAs encoding secreted proteins are disclosed. The extended cDNAs can be used to express secreted proteins or portions thereof or to obtain antibodies capable of specifically binding to the secreted proteins. The extended cDNAs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. The extended cDNAs may also be used to design expression vectors and secretion vectors.</p>														

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INTERNATIONAL SEARCH REPORT

International Application No

IB 98/02122

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47 C07K16/18 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E, L	WO 99 06549 A (GENSET (FR); DUMAS MILNE EDWARDS J.-B.; DUCLERT A.; LACROIX B.) 11 February 1999 (1999-02-11) L: Priority abstract page 6 - page 12 page 129 - page 133; claims Seq.ID:251 page 213 - page 214 Seq.ID:484 page 366 - page 367 ---	1-20
X	Database EMBL, entry HS695112 Accession number R50695 24 May 1995 95% identity with Seq.ID:40 nt.1-384 XP002097725 the whole document ---	2,5,8
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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& document member of the same patent family

Date of the actual completion of the international search

24 March 1999

Date of mailing of the international search report

27. 07. 99

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INTERNATIONAL SEARCH REPORT

International Application No

/IB 98/02122

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 34981 A (GENSET (FR); NICOLAEVNA MERENKOVA I.; DUMAS MILNE EDWARDS J.-B.G.) 7 November 1996 (1996-11-07) cited in the application abstract ---	
A	EP 0 625 572 A (KANAGAWA ACAD OF SCIENCE AND TECHNOL FOUNDATION (JP); KATO S; SEKINE S) 23 November 1994 (1994-11-23) cited in the application abstract ---	
A	CARNINCI P. ET AL.: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996 (1996-11-01), pages 327-336, XP002081729 cited in the application abstract ---	
A	KATO S. ET AL.: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1994, pages 243-250, XP002081364 cited in the application abstract ---	
A	WO 97 07198 A (GENETICS INSTITUTE INC (US); JACOBS K; MCCOY JM; KELLEHER K; CARLIN M) 27 February 1997 (1997-02-27) ---	
A	TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 30 July 1993 (1993-07-30), pages 600-603, XP000673204 abstract ---	
A	YOKOYAMA-KOBAYASHI M. ET AL.: "A signal sequence detection system using secreted protease activity as an indicator" GENE, vol. 163, 1995, pages 193-196, XP002053953 abstract ---	
A	HEIJNE VON G.: "A new method for predicting signal sequence cleavage sites" NUCLEIC ACIDS RESEARCH, vol. 14, no. 11, 1986, pages 4683-4690, XP002053954 cited in the application abstract ---	

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INTERNATIONAL SEARCH REPORT

International Application No

B 98/02122

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	LOCKHART D.J. ET AL.: "Expression monitoring by hybridization to high-density oligonucleotide arrays" BIO/TECHNOLOGY, no. 14, 14 December 1996 (1996-12-14), pages 1675-1680, XP002074420 abstract -----	18

INTERNATIONAL SEARCH REPORT

International application No.

PCT/IB 98/02122

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See additional sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Invention 1, Claims 1-20 partially.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/IB 98/02122

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Invention 1: Claims 1-20, all partially.

Nucleic acid comprising the sequence as in Seq.ID:40, complementary sequence or fragments, host cell containing said nucleic acid. Polypeptide as in Seq.ID:141, encoded by said polynucleotide, or fragments, method of making said polypeptide. Antibody specifically binding to said polypeptide.

2. Claims: Inventions 2-233: Claims 1-20, all partially, as far as applicable.

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:41-140, 242-377, and corresponding polypeptides, where invention 2 is limited to Seq.ID:41 and 142, invention 3 is limited to Seq.ID:42 and 143,, invention 8 is limited to Seq.ID:47 and 148, invention 9 is limited to Seq.ID:48,49,110,149,150 and 211, invention 10 is limited to Seq.ID:50 and 151,, invention 32 is limited to Seq.ID:72 and 173, invention 33 is limited to Seq.ID:73,74,131,174,175 and 232, invention 34 is limited to Seq.ID:75 and 176,, invention 233 is limited to Seq.ID:377 and 513.

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

/IB 98/02122

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
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